_		
化化氯化铵 医克朗氏试验检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检检	(TM)	化多多多多多多多多多多多多多多多多多多 医多多多 医多多多 医多多多 医多多多
* * * * *	, 	****
* * * *		****
**		****
k k k k	 	****
k k k k		****
k k k		****
k k k	.	****
k k k		****
k k k	'	****
k k		***
K K K		****

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu May 20 09:26:24 1999; MasPar time 3339.47 Seconds -------1284:906 Million cell-updates/sec Run on:

Tabular output not generated.

>US-09-099-053-1 (1-1548) from US09099053.seq 1548 Description: Perfect Score: N.A. Sequence: Comp: Title:

1 GCTCGCGGGCTCCCATGGCC.......CCAACGCTCTGGGCTCCAGC 1548 CGAGCGCCCGAGGTACCGG......GGTTGCGAACCCGAGGTCG

Scoring table:

TABLE default Gap 6

646147 seqs, 1385953633 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Minimum Match 0% Listing first 45 summaries Post-processing:

emb158 Database:

Database:

Statistics:

Mean 11.063; Variance 5.685; scale 1.946

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11.2 9312 37 RERSV6 Rous sarcoma virus, co 5.25e-108 17.3 11.2 9392 37 ALRCG 17.3 11.2 5922 4 RECSRC Gallus gallus gene c-s 3.26e-107 17.1 1.5 25.2 4 RECSRC Gallus garcoma virus, (pr 5.25e-108 17.2 11.1 1759 24 RECSRC Gallus garcoma virus (pr 5.25e-108 17.3 11.0 518 37 RSVPRSRC Rous Sarcoma virus (pr 3.26e-107 RSVSRC Rous Sarcoma virus (pr 2.03e-106 10.9 3125 37 RECSRC Rous Sarcoma virus (pr 2.03e-106 10.9 3255 37 RECSRC Rous Sarcoma virus (pr 2.03e-106 ROUS SARCOMA virus (pr 2.03e-106 ROUS SARCOMA virus (pr 2.03e-106 10.9 3255 37 RALRDAD ROUS SARCOMA virus (pr 2.03e-106 10.1 10.3 RSVSRC ROUS SARCOMA virus (pr 2.03e-106 10.2 10.3 RSVSRC ROUS SARCOMA virus (pr 2.03e-101 10.4 1578 37 RSVSRC ROUS SARCOMA virus pho 3.00e-103 10.4 1578 37 RSVSRCHM ROUS SARCOMA virus pho 3.00e-103 10.4 1578 37 RSVSRCHM ROUS SARCOMA virus pho 3.00e-103 10.4 1578 37 RSVSRCHM ROUS SARCOMA virus pho 3.00e-103 10.4 2293 37 REFESV ROUS SARCOMA virus pho 1.77e-97 10.4 2354 29 HUMFCR ROUS SARCOMA virus (pr 1.77e-87 11.0 2025 37 REFESV GARCHET SARCOMA virus (pr 1.77e-87 11.0 3.16 13 RESSRCA ROUS SARCOMA virus (pr 1.77e-87 11.0 3.16 13 RECSRCY GARCHET SARCOMA virus (pr 1.77e-87 11.0 4 2.259 37 REFESV GARCHET SARCOMA virus (pr 1.77e-87 11.0 4 2.259 37 REFESV GARCHET SARCOMA virus (pr 1.77e-87 11.0 5.2 1529 37 RESSRCA ROUS SARCOMA virus (pr 1.77e-87 11.0 5.2 1529 37 RESSRCA ROUS SARCOMA virus (pr 1.77e-87 11.0 5.2 1529 37 RESSRCA ROUS SARCOMA virus (pr 1.77e-87 11.0 5.2 1529 37 RESSRCA ROUS SARCOMA virus (pr 1.77e-87 11.0 6.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10	MUSSRM 2560 bp mRNA ROD 10-FEB-1999 MOUSE MRNA for srm (tyrosine kinase), complete cds. 1049471 D49477 D494
489799999999999999999999999999999999999	RESULT 1 LOCUS DEFINITION ACCESSION NID NID NEB CORRES SOURCE AUTHORS TITLE JOURNAL FEFERENCE AUTHORS TITLE JOURNAL FEATURES COS COS
<u> </u>	

```
Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                              1051 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                 1111
                                                                                                                                                                                                                                                                             1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                              1821
 991
                        1461
                                                                           1521
                                                                                                                          1581
                                                                                                                                                                                                                            1701
                                                                                                                                                                                                                                                                                                     1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
 à
                    g
                                             δ
                                                                      g
                                                                                                 δ
                                                                                                                       ద
                                                                                                                                                 ò
                                                                                                                                                                          g
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                        à
                                ANVEDCSEPAPRARLERALYDETARCABELSVSRGDRIYALKEGGDY ITAGASTERS
TGLVPVTYLARATPEPPSDQPWYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGY
TGLVPVTYLARATPEPPSDQPWYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGY
SLSVRAQARVCHIRLORPSGSLYLQGEQQLFPSDALLAYKTRWKLIQNPLLQDCIP
QIPLVQDEWERPRESEVLRKIGEGFFGEVWEGLMLGSIPVAKVIKADDLTK
ENEALKSLRHERLIRLHAICSLGEPVYIYTELMGKGNLOVYLGSSEGRALSLPHLGF
PVKWTAPEAMYRVFRDLAARNVLVGDDLTCKVADFGLARLLKDDVYSPSSGSKI
PVKWTAPEAANYRVFSQKSDVWSFGILLYEVFTYGQCPYEGMTWHETLQQISRGYRLP
2560
         /db_xref="GI:684972" --
/translation="MEPFLRKRLTFLSFFWDKIWPADESEEDIPRIGGHDDNPVPEGA
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        981 CCCAGTGGCAGCCTCTATCTGCAGGAGGCCCAACTCTTCCCCCAGCCTGGATGCACTGCTG 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1400
                                                                                                                                                                                                                                                      330
                                                                                                                                                                                                                                                                                                                                          800
                                                                                                                                                                                                                                                                                                                                                                                                                                            920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571 GCTGATGGCAGCCTCTACCTGCAGAAGGGACGCTCTTTCCCGGCCTGGAGGAGCTGCTC 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810
                                                                                                                                                                                                                                       621 CTCTTCCGCGCGCTCTACGACTTCACTGCTCGATGTGCAGAGGAACTGAGCGTCAGCCGT 680
                                                                                                                                                                                                                                                                                        681 GGGGACAGACTCTACGCCCTCAAGGAGGGGGGACTACATCTTTGCCCAAAGGCTCTCT 740
                                                                                                                                                                                                                                                                                                                                                                  390
                                                                                                                                                                                                                                                                                                                                                                                           860
                                                                                                                                                                                                                                                                                                                                                                                                                  450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          921 GGCTATICICIATCAGGCCCAGGCCAAAGICTGCCACTACCGCAICTGCAIGGCA 980
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                     391 CTCTCAGACCCTGGTACTTTAGCGGGTCAGTCGGACCCAGGCACAGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCACCCAGCACCGGACTAGTTCCTGTCACCTAGCCTTGCCAAGGCTACCCCGGAGCCG
                                                                                                                                                                                                                                                                                                                                                       861 ITGICICCTGCCAATGCACCAGGGCCTTCCTCATCCGCCCAGCGAAAGCAGCATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 CTCTCCCCACCCAACGAACCAGGGGCCTTCCTCATCCGGCCCAGCGAGCAGCAGCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101 CAGATACCCTTGGTTCAGGACGAGTGGGAACGACCACGTTCAGAATTTGTCCTTCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1161 AAGCTGGGTGAAGGTTTCTTCGGGGAGGTGTGGGAAGGCCTGTGGCGTGGGCTCTATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1221 GTGGCAGTGAAGGTTATCAAATCAGCTGACATGAAGCTGGCAGACCTCACCAAGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTCAGACCAACCTTGGTACTTCAGTGGGATCAGCAGGGCTCAGGCCCAGCAGTTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .041 GCTTACTACAAGACCAACTGGAAGCTGATCCAGAACCCTCTGCTGCAGCCCTGCATACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1341 GGTGAACCTGTGTACATCGTTACTGAACTCATGGGCAAGGGCAACTTGCAAGTCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1281 GAGGCACTGAAGAGCTTGAGGCATGAGGGCTGATCCGGCTGCACGCTATATGTTCCCTC
                                                                                                                                                                                                              ö
                                                                                                                                                                                     Length 2560;
                                                                                                                                                                                    Score 827; DB 32; Length 25
Pred. No. 0.00e+00;
0; Mismatches 246; Indels
                                                                                                                                                  550 t
/db_xref-"PID:g684972"
                                                                                                                                                    Б
                                                                                                                                                  669
                                                                                                                                                                                    Query Match
Best Local Similarity 81.3%;
Matches 1073; Conservative
                                                                                                                                                742 c
                                                                                                                                                  ಹ
                                                                                                                                     polyA_site
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                       741
                                                                                                                                                                                                                                                                                                                                                                                          801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

```
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases 1 to 2393)

1 (Chases 1 to 2393)

Direct Submission

Submitted (24-DEC-1993) to the DDBJ/EMBL/GenBank databases. Naohiro Kohmura, National Institute for Physiological Sciences, Lab.

Neurobiology & Behavioral Genetics; 38 Nishigonaka, Myodaiji, Okazaki, Aichi 444, Japan (Tel:0564-55-7744, Fax:0564-55-7741)
                                                                                                                                                                                                                                                                                                                                              1700
                                                                                                                                                                                                                                                                                                                                                                                                                                             1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1880
1881 ATACTGAGGGAGAAGCTGAATGCCATAAACAGACGCCTCCATCTGGGGCCTCACGTGACC 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1999 complete cds
                                                                                                                                                                                                                                                                                                                                         Department of Neurobiology and Behavioral Genetics National
                                               GCTGAGGGCATGAGCTACCTGGAGGAGGGGCGTGTCGTCCACCGGGACTTGGCTGCCAGG
                                                                             AACGTGCTGGTGGGTGATGACCTCACCTGCAAGGTAGCTGATTTTGGCCTGGCCAGACTG
                                                                                                                                                                                                                                                                     1171 CTCAAGGACGACATCTACTCCCCGAGCAGCACCTCCAAGATCCCGGTCAAGTGGACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1291 CTGCTGCACGAGGTTTTCACCTATGGCCAGTGTCCCTATGAAGGGATGACCAACAACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine-specific protein kinase.
Mus musculus adult lung cDNA to mRNA, clone_lib:5' stretch.
                                                                                                                                                                                              AACGTGCTCGTGGACGGCCTGGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCTACAGCAGATTAGTCGTGGATACCGGCTGCCACGCCCAGCTGTCTGCCCAGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTATGTGCTCATGGTAGAGTGCTGGAAGGGCAGCCCTGAGGAGCGTCCCACCTTTGCC
                                                                                                                                                                                                                                            CTCAAGGATGATGTCTACTCCCCAAGCAGTGGCTCCAAGATCCCTGTCAAGTGGACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2393)
Kohmura, N., Yagi, T., Tomooka, Y., Oyanagi, M., Kominami, R., Takeda, N., Chiba, J., Ikawa, Y. and Aizawa, S.
A novel nonreceptor tyrosine kinase, Srm: cloning and tar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSTSPK 2393 bp mRNA ROD
Mouse mRNA for tyrosine-specific protein kinase,
D26186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute for Physiological Sciences
Myodaiji, Okazaki 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 14 (10), 6915-6925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="5' stretch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-Dec-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9529072
D26186.1 GI:529072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phone: 0564-55-7741
Fax: 0564-55-7744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nachiro Kohmura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disruption
```

 \sim

•

```
Location/Qualifiers
1. .2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ო
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
                        1113
                                                                 1173
                                                                                                           1233
                                                                                                                                166
                                                                                                                                                     1293
                                                                                                                                                                        1051
                                                                                                                                                                                              1353
                                                                                                                                                                                                                  1111
                                                                                                                                                                                                                                       1413
                                                                                                                                                                                                                                                                                1473
                                                                                                                                                                                                                                                                                                     1231
                                                                                                                                                                                                                                                                                                                          1533
                                                                                                                                                                                                                                                                                                                                               1291
                                                                                                                                                                                                                                                                                                                                                                    1593
                                                                                                                                                                                                                                                                                                                                                                                                             1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
    811
                                                                                                                                                                                                                                                                                                                                                                                          1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                            g
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                               .
B
                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                    g
                                            ö
                                                              ద
                                                                                     ò
                                                                                                          В
                                                                                                                                à
                                                                                                                                                유
                                                                                                                                                                       δ
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                       /product="tyrosine-specific protein kinase"
/product="tyrosine-specific protein kinase"
/protein_id="BAA05331.1"
/db_xxef="pic_id1005873"
/db_xxef="pic_id1005873"
/db_xxef="pic_id105873"
/db_xxef="ci:529073"
/translation="MePFLRKLTFLSFFWDKIWPADESEEDIPRIQGHDDNEVPEQA
AAVEPGSFPARALERALFARALERALFARALERALSOFFARALERESISGESIGGY
SLSVRAQAKVCHYRICMAPSGSLYLQEGQLEPSLDALLAYYKTNWKLIGNPLLQPES
TGLVPYTYLAKATPEPPSDQWYFSG1SRQAQQQLLLSPANAPGAFLIRPSESSIGGY
SLSVRAQAKVCHYRICMAPSGSLYLQEGQLEPSLDALLAYYKTNWKLIGNPLLQPET
OIPLVODEWBRPRSEEVFGRKLGEGFFEWWEGLWLGSIPVAKVKIKADDATK
EIEALKSLRHERLIRLHAIGSLGEPVITYTELMGKGNLQVYLGSSEGRALSLPHLGF
ACOVARGMSTLEERRRVHADLAARNULYGDDLTCKVADFGLARLLKDDVTSPSSGSKI
PVKWTAPEAANYRVFSOKSDVWSFGILLYEVFTYGQCPYEGWTWHETLCOISRGYRLP
RPAVCPAEVYLMVECWKGSPEERPFFALLREKLNAINRRLHLGIT"
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTGGGTGAAGGTTTCTTCGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCTATCCCT 1052
                                                                                                                                                                                                                                                                                                                                                                               572
                                                                                                                                                                                                                                                                                                                                                                                                                       632
                                                                                                                                                                                                                                                                                                                                                                                                                                            390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CICTICCGCGCGCTCTACGACTTCACTGCATGTGCAGGAACTGAGCGCTCAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGCAGTGAAGGTTATCAAATCAGCTGACATGAAGCTGGCAGACCTCACCAAGGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTCAGACCAACCCTGGTACTTTAGCGGGGTCAGTCGGACCCAGGCACAGCAGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGATACCCTTGGTTCAGGACGAGTGGGAACGACCACGTTCAGAATTTGTCTTCGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCAGCCCAGCGCCCGGGCTCGTGCCCATCACCCACGTGGCCAAGGCTTCTCCTGAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTCAGACCAACCTTGGTACTTCAGTGGGATCAGCAGGGCTCAGGCCCAGCAGTTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTATTCTCTATCAGTCAGGGCCCCAGGCCAAAGTCTGCCACTACCGCATCTGCATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCAGTGGCAGCCTCTATCTGCAGGAGGGCCAACTCTTCCCCAGGCTTGGATGCACTGGTG
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                          Length 2393;
                                                                                                                                                                                                                                                                                         Score 825; DB 32; Length 23
Pred. No. 0.00e+00;
0; Mismatches 247; Indels
/dev_stage="adult"
/tissue_type="lung"
279. .1769
                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                             655
                                 /gene="srm"
279. .1769
/gene="srm"
/codon_start=1
                                                                                                                                                                                                                          1934. .2008
2369. .2374
2393
                                                                                                                                                                                                                                                                                          Query Match 53.3%;
Best Local Similarity 81.3%;
Matches 1072; Conservative
                                                                                                                                                                                                                                                            688 c
                                                                                                                                                                                                                           repeat_region
polyA_signal
polyA_site
: COUNT 525
                                                                                                                                                                                                                                                                                                                                     453
                                                                                                                                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631
                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                       573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053
                                                                                                                                                                                                                                                                                                                                                                              513
                                                                                                                                                                                                                                                                                                                                                                                                                                            331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751
                                            CDS
                                                                                                                                                                                                                                                            BASE CO
ORIGIN
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     硆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
non-receptor
                                                                                                                  1232
                                                                                                                                                                                                                                                                           1352
                                                                                                                                                                                                                                                                                                                                                                                                                                    1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICTATGTGCTCATGGTAGAGTGCTGGAAGGGCAGCCCTGAGGAGCGTCCCACCTTTGCC 1712
870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2507)

Mitchell, P.J., Barker, K.T., Martindale, J.E., Kamalati, T., Lowe, P.N., Page, M.J., Gusterson, B.A. and Crompton, M. R. Cloning and characterisation of cDNNs encoding a novel non-retyrosine kinase, brk, expressed in human breast tumours oncogene 9 (8), 2383-2390 (1994)

2 (Dases 1 to 2507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAR-1994) P.J. Mitchell, Institute of Cancer
Research, Haddon Labs, 15 Cotswold Road, Sutton, Surrey, SM2
UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGCTACAGCAGATTAGTCGTGGATACCGGCTGCCACGCCCAGCTGTCTGCCCAGCAGAG
  GTGGCGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGATC
                                                          GGTGAACCTGTGTACATCGTTACTGAACTCATGGGCAAGGGCAACTTGCAAGTCTACCTG
                                                                                                                                      GCTGAGGGCATGAGCTACCTGGAGGAGCGGCGTGTCGTCCACCGGGACTTGGCTGCCAGG
                                                                                                                                                                                                                                                                                               CTCAAGGATGATGTCTACTCCCCAAGCAGTGGCTCCAAGATCCCTGTCAAGTGGACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGAGGCTGCTAATTACCGTGTCTTTTCCCAAAAGTCAGATGTCTGGTCTTTGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGCACTGAAGAGCTTGAGGCATGAGAGGCTGATCCGGCTGCACGCTATATGTTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATACTGAGGGAGAAGCTGAATGCCATAAACAGACGCCTCCATCTGGGCCTCACGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSBRK 2507 bp mRNA FOR TYROSINE Kinase. V X78549 4515025 X78549.1 GI:515025 A78549.1 GI:515025 A78649.1 GI:515025 AF gene; Tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2507)
Mitchell, P.J.
Direct Submission
```

05-MAR-1997

PAT

Barker, K.T.,

4

```
/protein_id="CAA02687.1"
/db_xref="PID: e305207"
/db_xref="PID: e305207"
/db_xref="PID: e305207"
/db_xref="PID: e305207"
/db_xref="CI: 29297809"
/translation="MVSRDQAHIGPRYVGLWDFKSRTDEELSFRAGDVFHVARKEEQWWATLLDEAGGAVAQGYVPHNYIAERETVESEPWFFGCISKSBAVRRLQAEGNTGAF
LIRVSREVSADYVLSYRDYDAWRYKIWRKAGGRLHLNEAVSFLSLEELDELWNYHRAQSE
SHGLRLAAPCRKHEPEPLPHWDDWERPREEFTLCRKLGSGYFGEVFEGLWKDRVQVAI
RVJRRDMLHQQMLQSETQAMKKLRHKHILALYSAVSVGOPYYITTELMAKGSLLELL
RDSDEKYLPVGELLDTAWQVABGMCYLESQNYITHRDLAARNILLYGEWTLGYGOFGLAR
RLIKEDVYLSHDHNIPYKWTAPEALSRGHYSTKSDVWSFGILLHEWFSRGQVPFPGBGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHEAFLRVDAGY RMPCPLECPPSVHKLMLTCWCRDPEQRPCFKALRERLSSFTSY ENP
                         1168 GTTCAGCAGGGGTCAGGTGCCCTACCCAGGCATGTCCAACCATGAGGCCTTCCTGAGGGT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 GGATGACTGGGAGAGGCCGAGGGAGGAGTTCACGCTCTGCAGGAAGCTGGGGGTCCGGCTA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        691 TTCTCGAGACAACCTCCTGCACCAGCAGATGCTGCAGTCGGAGATCCAGGCCATGAAGAA 750
                                                                                                      1365 CATGCGAGGGTACCGGCTGCCGGCCGGCTGCCTGCCGGCGGAGGTCTACGTGCTCTA
                                                                                                                                                                 1288 GCTGACATGCTGGTGCAGGGACCCCGAGCAGAGACCCTGCTTCAAGGCCCTGCGGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  828 CAAGTCAGCCAACATGAAGCTC-A-CTGACCTCGCCAA-GGAGATCCAGACACTGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         631 CTTTGGGGAGGTCTTCGAGGGGCTCTGGAAAGACCGGGTCCAGGTGGCCATTAAGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768 CTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCCCGTGGCGATCAAGGTCAT
                                                                                 1228 GGACGCCGGCTACCGCATGCCCTGCGCCTCTGGAGTGCCCGGCCCAGCGTGCACAAGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 191; DB 25; Length 25
Pred. No. 2.43e-122;
0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in unidentified
unclassified.

1 (bases 1 to 2507)
is Gusterson, B.A., Crompton, M.R., Mitchell, P.J., Bar Kamalati, T., Page, M.J. and Spence, P.
PROTEIN TYROSINE KINASE AND LIGANDS THEREOF PATENT: WO 9502057-A 1 19-JAN-1995;
CANCER RES INST (GB)
Other publication AU 7080994 950206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 t
                                                                                                                                                                                                                                                                                                                                    2507 bp DNA
NN Sequence 1 from Patent W09502057.
A42329
92297808
A42329.1 GI:22007007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 809 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.3%;
Best Local Similarity 64.1%;
Matches 502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 726 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458
                                                                                                                                                                                                                                                 1348 GCT 1350
                                                                                                                                                                                                                                                                                      GCT 1487
                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                        1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                               g
                                                                                                                                                             g
                                                                                                                                                                                                       à
                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                         δ
                                                                                                                         ò
                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                            SHGLRLAAPCRKHEPPEPLPHWDDWERPREEFTLCRKLGSGYFGEVFEGLWKDRVQVAI
KVISRDNLLHGQMLOSEIQAWKKLRHKHILALTAVNSVGDPYYITELMAKGSLLELL
RDSDEXVLPVSELLDIAWQAGGWCYLESQNYIHRDLAARNIIVGENTLCKVGDFGLA
RLIKEDYYLSHDHNPYKWTAPEALSRGHYSTKSDVWSFGILLHEMFSRGOVPYPGWS
NHEAFLRVDAGYRMPCPLECPPSVHKLMLTCWCRDPEQRPCKALRERLSSFTSYENP
                                                                                                                                                                                                                                                                                                                                               /translation="MYSRDQAHLGPRYVGLWDFKSRTDEELSFRAGDVFHVARKEEQW
WMATLLDEAGGAVAQGYVPHNYLAERETVESEPWFFGCISRSEAVRRLQAEGNATGAF
LIRVSEKPSADYVLSVRDTQAVRHYKIWRRAGGRLHLNEAVSFLSLPELVNYHRAQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1185 CTACTCCCCGAGCAGCACCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGGGGGCGAA 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  945 CATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCCCCGAGGG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1108 CCGAGGCCATTACTCCACCAAATCCGACGTCTGGTCCTTTGGGATTCTCCTGCATGAGAT 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1245 TTATCGIGICTTTCTCCCAGAAGICAGACGICTGGICCTICGGCGICCTGCTGCACGAGGI 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 GGATGACTGGGAGAGGCCGAGGGAGGAGTTCACGCTCTGCAGGAAGCTGGGGTCCGGCTA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICTCGAGACAACCTCCTGCACCAGCAGATGCTGCAGTCGGAGATCCAGGCCATGAAGAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708 GGACGTGTGGGAGCGGCCACACTCCGAATTCGCCCTTGGGAGGAAGCTGGGTGAAGGCTA 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGGGGAGGTCTTCGAGGGGCTCTGGAAAGACCGGGTCCAGGTGGCCATTAAGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828 CAAGTCAGCCAACATGAAGCTC-A-CTGACCTCGCCAA-GGAGATCCAGACACTGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCTCTCC -- CATGACCAC - AATATCCCCTACAAGTGGACGGCCCCTGAAGCGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     768 CTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGCTCCCTGCCCGTGGCGATCAAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCGGCACAAACACATCCTGGCGCTGTACGCCGTGGTGTCCGTGGGGGACCCCGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCATCACGGAGCTCATGGCCAAGGGCAGCTGCTGGAGCTGCTCCGCGACTCTGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 GAAAGICCIGCCCGITICGGAGCIGCIGGACAICGCCIGGCAGGIGGCIGAGGGCAIGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         931 TTACCTGGAGTCGCAGAATTACATCCACCGGGACCTGGCCGCCAGGAACATCCTCGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAAACACCCTCTGCAAAGTTGGGGACTTCGGGTTAGCCAGGCTTATCAAGGAGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 191; DB 29; L
Pred. No. 2.43e-122;
0; Mismatches 275;
                                       /tissue_type="breast carcinoma"
/cell_type="epithelial like"
/cell_line="T-47D"
                                                                                                                                                                                                                          /codon_start=1
/product="tyrosine kinase"
/protein_id="CA455295.1"
/db_xref="PID:9515026"
/db_xref="GI:515026"
/db_xref="GI:515026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 t
/organism="Homo sapiens"/db_xref="taxon:9606" .
                                                                                        /clone_lib="lambda Zap"
/clone="lambda T2"
29. .1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809
                                                                                                                                                               /gene="brk"
29. .1384
                                                                                                                                                                                                       /gene="brk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 12.3%;
Local Similarity 64.1%;
nes 502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1051 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            811
                                                                                                                                              gene
                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

ς. ..

Gaps

9

Length 2507;

S

```
Similarity
                                                                                                                                                                                                                      855
                                                                                                                                                                                                                                                                                                                493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 1322
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                      COUNT
                                                                                                                                                                                                                                                                                                                                                  546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1322
                                                                                                                                                                                                                                                                                                                                                                                                                          909
                                                                                                                                                                                                                                                                                                                                                                                                                                                              747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203
                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
Q
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703579.1 GI:212712
703579.1 GI:212712
703579.1 GI:212712
703579.1 GI:212712
703579.1 GI:212712
705579.1 GI:212712
705579.1 GI:212712
705579.1 GI:212712
705579.1 GI:212712
70579.1 GI:212712
705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA VRT 29-JUL-1992 protooncogene (c-tkl) mRNA, complete cds
                                                                                                                                                                                                                                                                                             1050
                                                                                                                                                                                                                                                                                                                                                                                                                                           1167
                                                                                                                                                                                1064
                                                                                                                                                                                                                                                        1124
                                                                                                                                                                                                                                                                                                                                 1184
                                                                                                                                                                                                                                                                                                                                                                   1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1424
                                                                                                          1004
                                                                                                                                                                                                                                                                                                                                                                                      990
                                                                                                                                                                                                                                         CATCATCACGGAGCTCATGGCCAAGGGCAGCCTGCTGGAGCTGCTCCGCGACTCTGATGA
                                                                                                                                                                         GGAAAACACCCTCTGCAAAGTTGGGGACTTCGGGTTAGCCAGGCTTATCAAGGAGGACGT
                                                                                                                                                                                                                                                                                                                                                                 CTACCTCTCC -- CATGACCAC-AATATCCCCTACAAGTGGACGGCCCCTGAAGCGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCGAGGGTACCGGCTGCCGCGGCTGCCCGGCGGAGGTCTACGTGCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGACATGCTGGTGCAGGGACCCCGAGCAGACCCTGCTTCAAGGCCCTGCGGGAGAG
GCTGCGGCACAACACATCCTGGCGCTGTACGCCGTGGTGTCCGTGGGGGACCCCGTGTA
                                                                                                                                              GAAAGTCCTGCCCGTTTCGGAGCTGCTCGACATCGCCTGGCAGGTGGCTGAGGGCATGTG
                                                                                                                                                                                                                    TTACCTGGAGTCGCAGAATTACATCCACCGGGACCTGGCCGCCAGGAACATCCTCGTCGG
                                                                                                                                                                                                                                                                                                                               CGACGGCCTGGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGGCTGCTCAAGGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGAGGCCATTACTCCACCAAATCCGACGTCTGGTCCTTTGGGATTCTCCTGCATGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCAGCAGGGGTCAGGTGCCCTACCCAGGCATGTCCAACCATGAGGCCTTCCTGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="c-tkl tyrosine kinase (EC 2.7.1.112)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 84, 8778-8782 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/db_xref="taxon:9031"
<1. .3701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="c-tk1 mRNA"
22. .1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHKTCKL 3701 bp
Chicken tyrosine kinase
J03579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .3701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Nat
88097370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCT 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                      811
                                                                                                                                                                                1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
751
                                                                                                                                            871
                                                                                                                                                                                                                    931
                                                                                                                                                                                                                                                                                                                             13.25
                                                                                                                                                                                                                                                                                                                                                                 1051
                                                                                                                                                                                                                                                                                                                                                                                                     1185
                                                                                                                                                                                                                                                                                                                                                                                                                                         1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                             991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                    셤
                                                                                                                                      g
                                  ò
                                                                                                                                                                                                                  g
                                                                                                        ò
                                                                                                                                                                                ò
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                   පි
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

```
/db_xref="G1:2121313"
/translation="MSPPCSPLQDKLVVALYDYEPTHDGDLGLKQGEKLRVLEESGEWWRAGSLTTGGGEGLIPHNEYAMVNSLEBEPWFFKNLSKRNAREARLLASGRYTHGSFLIRE
SETSKGSYSLSYRDFDGNGGETYRKIRNINDNGGYISPRVFFSSLHELVEYYSSS
DGLCTRLGKPCRTQKPQKPWWQDEWVPRESLKLVEKLGAGGFGEVWMGFYNGHTKVA
IKNLKGGSMSPGAFLAEANLMKNLQHPRLVELYSKTSTYTTEYMREKGSLVDFLK
TSEGIKLSINKLLDMAAQIAEGMAFISERNYIHRDLRANVTKEPIYITTEYMRKGSLVDFLK
TSEGIKLSINKLLDMAAQIAEGMAFISERNYIHRDLRANNILVSFALCCKIADFGLAR
ILEDNEYTAREGARFPIKWTAPEAINYGTFTIKSDWWGFGILLTEIVYTVGRIPYPGMT
NPEVIQNLERGYRMPQPDNCPQELYELMMQCWKEQPEERPTFEYMKSVLEDFFTATEG
                                                                                                                                                                                                                                                                                                                                                                                                                                    ις.
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGCAGAAGCCGTGGTGGCAGGACGAGTGGGAGGTGCCCACGAGAGTCGCTGAAGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGAAGCTGGGAGCCGGCCAGTTTGGAGAAGTCTGGATGGGCTTCTACAACGGCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGGAAGGCCTGTGGCTGGGGCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGGTAGCCATCAAGAACCTGAAGCAGGGCAGTATGTCCCCCCAGCGCCTTCCTGGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCAAGACCTCAGAGGCATCAAGCTCAGCATCAACAAACTTCTGGACATGGCCGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1047 GGTGGCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCAACATCCTCGTGTCGGAGGCCCTGTGCTGCAAAATCGCTGACTTCGGGCTGGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107 CCGGAACGTGCTCGTGGACGACGCCTGCCAAGGTGGCTGACTTCGGCCTGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1167 GCTGCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGGTCTACGTGCTCATGCTGGAGTGCTGGA-GGAGCAGCCCCGAGGAACGGCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCAACCTGATGAAGAACCTGCAGCACCCACGGCTGGTGCGGCTCTACGCTGTG-G-T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCAAGGAGCCCATCTACATCATCACAGAGTACATGGAGAAGGGCAGCCTGGTGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCATCGAGGACAACGAATACACAGGACACGAGAAGGGGGCTAAATTCCCCCATCAAGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCACCGGAGGCTATCAATTACGCCACGTTCACCATCAAGTCTGACGTCTGGTCTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCCTGCTCACTGAGATTGTTACCTACGGCCGGATCCCGTATCCAGGGATGACCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGTGATCCAGAACCTGGAGCGCGGGCTACCGCATGCCGCAGCCCGACAACTGCCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCTGTACGAACTGATGATGCAGTGCTGGAAGGAGCAGCCT-GAGGAGCGGCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTGCTGAAGGCATGGCCTTCATCGAAGCCAAGAACTACATCCACCGTGACCTGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                       ς.
Έ
                                                                                                                                                                                                                                                                                                                                                                                  Length 3701;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                                                  Score 180; DB 24; I Pred. No. 1.43e-113;
                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                                                                                                                                                                         703
/protein_id="AAA49081.1"
/db_xref="PID:9212713"
                                                                                                                                                                                                                                                                                                         1089 g
                                                                                                                                                                                                                                                                                                                                                                                11.6%;
llarity 63.1%;
Conservative
                                                                                                                                                                                                                                                                                 QYQQQP"
1054 c
```

Length 1759

9

RESULT

ó

```
ďq
ch 11.4%;
1 Similarity 63.3%;
455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGYRKA 1982 by
G.gallus yrk mRNA.
X67786 X68973
g63895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X67786.1 GI:63895
yrk gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                   066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
NID
                             Matches
                                                                                                                                                                                                                                1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                        g
                                                                                    Ω
                                                                                                               셤
                                                                                                                                             δ
                                                                                                                                                                      g
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                        Hanafusa, H.

Unpublished (1983)
2 (bases 1 to 1759; 1 to 1759)
2 (bases 1 to 1759; 1 to 1759)
3 Liverand Hanafusa, H.

Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus (211 32 (3), 881-890 (1983)
8315564
[2] reports the sequence of c-src without its introns and includes the following table of the predicted splicing junctions based upon the structural similarity between c-src and v-src.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLNPENPRGTFLVRESETTKGAYCLGYSDFDNAKGLNVKHYKITKLDSGGFYTTSRT
QFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWETPRESLRLEVKLGQG
CFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAVVSEEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMÄAQÍASGMAYVERMNYVHRDLRAANI
LVGENLVCKVADFGLARLIEDNEYTARQGAKEPIKWTAPEAALYGRFTIKSDVWSFGI
LLTELTTKGRVPYPGMVNREVLDQVERGYRMPČPPECPESLHDLMCQCWRRDPEERPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGSSKSKPKDPSQRRRSLEPPDSTHHGGFPASQTPNKTAAPDTH
RTPSRSFGTVATEPKLFGGFNTSDTVTSPQRAGALAGGVTTFVALYDYESRTETDLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
                                                                                                                                                                                                                                                                                                                                                                                    The revision in [1] was a private communication via C. Van Beveren. 19-MAY-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (61bp) cgcccacag/aftgcatccg
(118bp) cccgccag/yfgccaagtt
(79bp) cttccacag/ygatggtcaa
to GenBank features:
                                                      19-JUL-1995
                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
                                                                  Chicken c-src gene, complete cds (introns deleted). J00844
                                                                                                                               src oncodene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             messenger RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              description
                                                                                                                           c-myc proto-oncogene; proto-oncogene; Gallus gallus DNA.
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEYLQAFLEDYFTSTEPQYQPGENL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1759
/organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/protein_id="AAA70194.1"
/db_xref="PID:9901820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            acgacaaaag/gtgatccctg
tactactcca/gtgtgtatgg
gtctggatgg/gtaaggacag
atgagcaagg/gtgaggcacg
ggctgctcag/gtggttcct
) gcacggcaag/gtgagagcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL features not translated
                                                                                                                                                                                                                                                                                                                                                                                                     ggacgtgcag/gtaaggcatg
gcactggctg/gtcagtgtgg
tcaacaacac/gtgagtgtcc
aggctgaaga/gtaattgcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:901820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 >1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="src"
/citation=[2]
a 554 c 5
                                                     1759 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /qene="src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="src"
                                                                                                            J00844.1 GI:212700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                  (bases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                  370
                                                                                               g212700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      old_sequence
1466 T 1466
                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                  DEFINITION
                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                            JOURNAL
                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                               NID
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                     TITLE
```

```
μ'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is expressed at elevated levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1109
                                                                                                                                                                                                                                                                                                                       1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCGAGGCAGCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT 1460
                                                                                                                                                                                                                                         1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1161 GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGAT 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1221 TGCATCCGGCATGGCCTATGTGGAGGATGAACTACGTGCACCGAGACCTGCGGGGGG 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1230 GCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGT 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGCTGACTGACCTGACCACCAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 GAAGCTGGGGCAGGGCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1581 GCTGCATGACCTCATGTGCCAGTGCTGGCGGAGGGACCCTGAGGAGCGGCCCACTTTTG 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1993
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sudol, M., Greulich, H., Newman, L., Sarkar, A., Sukegawa, J. and
Yamamoto, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 1982)
                                                                                                    984 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTGCAGGAAGC
                                                                                                                                                                                                                                       1044 CCAAGTGATGAAGAAGCTCCGGCATGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1341 CATCGAGGACAACGAGTACACAGCACGGCAAGGTGCCAAGTTCCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                AG---AGCCCATCTACATCGTCACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                            1281 CAACATCCTGGTGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
Έ
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRT
Score 176; DB 24; L
Pred. No. 2.17e-110;
0; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel Yes-related kinase, Yrk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural and hematopoietic tissues
Oncogene 8 (4), 823-831 (1993)
93205395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1982)
Sudol,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
```

.

```
Genetics,
                                       1230 GCCTGAGGCGCCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCTTCGGCGT 1289
                                                                                                                       1623 GGTGCTGGAGCAGGTGGAGGGGGGTACCGCATGCAGTGCCGGGCGGCGGCTGCCCCCATC 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bodor, J.
Direct Submission
Submitted (25-MAY-1990) Bodor J., Institute of Molecular Geneti
Czechoslovak, Academy of Sciences, Flemingovo 2, 166 37 Prague.
Czechoslovakia
                                                                                                                                                                                                                      1410 GGTCTACGTGCTCATGCTGGAGGAGCAGCCCCCGAGGAACGCCCCTCCTTG 1468
                                                                                                                                                                                                   1683 CCTGCACGATGTGATGGTGCAGTGCTGGAAGCGGGAGCCGGAGGAGCGTCCAACCTTTG 1741
                                                                                                                                                                                                                                                                                                                         14-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3775)
Bodor,J., Rozkot,F. and Svoboda,J.
Sequence organization of the adjacent chromosomal flanks the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Euther
Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
1 (bases 1 to 3775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10036"
/haplotype="21-21 hypodiploid"
/dev_stage="sarcoma cell from renal metastas1s"
/tissue_type="mesenchymal"
                                                                                                                                                                                                                                                                                                    MAVSCR 3775 bp RNA ROD ...
M.auratus H-19 proviral sequence (LTR,v-3scrl,LTR).
X52822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /proviral
/db_xss7
522..537
/note="direct repeat of integration"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mesocricetus auratus"
/db_xref="taxon:10036"
1. 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mesocricetus auratus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392. 401
/note="Spl binding site"
531...3509
/organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 3775
/organism="Rous sarcoma virus"
/db_xref="taxon:11886"
148. 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148. .161
/note="minicircle gap site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="polymorphic"
/cell_line="H-19"
/clone_lib="71,lNM1149"
/clone="71,lH19c1C2.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207. .214 /note="MSV enhancer" 392. .401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .3775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740. .746
763. .768
1242. .2822
/gene"v-3src-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1242. .2822
/gene="v-3src-1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          provirus; src oncogene golden hamster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                   949656
X52822.1 GI:49656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA_signal
polyA_signal
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhancer
                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                     NID
                                         g
                                                                                                                       a
                                                                                                                                                                                                 셤
                                                                                ò
                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDFNNFHAAAYSPPVPFSGPGFYPCNTLQAHSSITGGGYTLFIALYDYBARTEDDLSF
QKGEKFHIINNTEGDWWEARSLSSGATGYIPSNYVAPVDSIQAEEWYFGKIGRKDAER
OLLCHGNCRGTFLIRESETTKGAYSLSIRDWDEAKGDHVKHYKIRKLDSGGYIITTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFDTIQQLVQHYIERAAGLCCRLAVPCPKGTPKLADLSVKTKDVWEIPRESLQLLQKL
GROGFGEVWARGTWRYAKTLKPGTWAPREALEBAQIMARLHBHDKAYVSE
EPIYIVTERNSQGSLLDFLKDGDGRYLKLPQLVDWAAQIAAGRAYIERNNYIHBDLRA
ANILVGDNLVCKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALFGKFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMQCPGGCPPSLHDVMVQCWKREPEE
RPTFEYLQSFLEDYFTATEPQYQPGDNQ"
621 c 655 g 318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGCVHCKEKISGKGQGGSGTGTPAHPPSQYDPDPTQLSGAFTHI
                      Rockefeller University, 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026 GAAGTIGGCCAACGGCCAGTICGGGGAAGTGTGGGATGGGGACGTGGAACGGCACCACCAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1086 GGTGGCAGTGAAGACGCTGAAGCCGGGCACCATGTCCCCCGAGGCCTTCCTGGAGGAGGCC 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1146 TCAGATCATGAAGCGGCTGCGGCACGACAAGCTGGTGCAGCTCTACGCCGTGGTGTCGGA 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1263 AAAGGACGGGATGGCCGCTACCTGAAGCTGCCCCAGCTGGTGGACATGGCTGCGCAGAT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCCAAGATCCCGGTCAAGTGGACAGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1323 CGCCGCGGGCATGGCTTACATTGAGCGGATGAACTACATCCACCGGGACCTGCGTGCTGC 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1443 CATCGAGGACAACGAGTACACGGCGCGCCCAGGGTGCCAAATTCCCCATTAAGTGGACAGC 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGGAGGCAGCCCTGTTTGGGAAGTTCACCATCAAGTCAGACGTGTGGTCCTTCGGCAT 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 CGTGGCGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGAT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 CGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GGAACCCATCTACATCGTCACCGAGTTCATGAGCCAAGGCAGCTTGCTGGACTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1383 CAACATCCTGGTGGGTGACCTGGTGTGCAAGATCGCCGACTTTGGGCTCGCCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1982;
Direct Submission
Submitted (22-0CT-1992) M. Sudol; The Rockefe
York Ave. New York NY 10021, M. Box 288, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 176; DB 24; L
Pred. No. 2.17e-110;
0; Mismatches 261;
                                                                                                                                                                               /tissue_type="brain"
/clone_lib="cDNA lambda gt10"
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="G1:63896" - ...../db_xref="SWISS-PROT:Q02977"
                                                                                            /organism="Gallus gallus"
/strain="white leghorn"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                         /product="p60yrk"
/protein_id="CAA47996.1"
/db_xref="PID:g63896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 g
                                                                                                                                                              /dev_stage="adult'
                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                    /clone="pY20"
205. .1815
                                                                                                                                                                                                                                      205. .1815
/gene="yrk"
205. .1815
/gene="yrk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.4%;
Best Local Similarity 63.3%;
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
_
_
_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388
  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1503
                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                CDS
                                                           FEATURES
```

В ò 엄 ò g ò g ò g ò g ò g ò g õ

```
mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                2591
                                                                               1290
                                                                                                                2651
                                                                                                                                              1350
                                                                                                                                                                              2711
                                                                                                                                                                                                           1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                          RESULT
                                              g
                                                                                                             g
                                                                                                                                                                            g
                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                          οχ
                                                                                                                                            ò
                                                                                                                                                                                                           ò
                                                                               ò
                                                                                                                          QFGSLQQLVAYYSKHADGLCHRLTNVCPTSKPOTOGLAKDAWEIPRESLELEAKLGGG
CFGEVWMGTWGTTRVALKTLKPGTMSPEAFLOEAQVMKKLHHEKLVQLYAVVSEEPI
YIVIEYMSKGSLLDFLKGEMGKYLLPQLVDMAAQIASGMAYVERMIYVHRDLRANI
LVGENLVCKVADFGLARLIEDMEYTARQGAKPPIKWTAPEAALYGRRTIKSDVWSFGI
LLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKDPEERPT
FKLQAQALLPRAVLEVAE"
3375. 3381
3503. 3508
                                            /db_xref="SPTREMBL:060367"
/translation="MGSSKSKPKDPSQRRRSLEPPDSTHHGGFPASQTPDETAAPDAH
RNPSRSFGTVATEPKLFWGFNTSDTVTSPQRAGALAGGVTTFVALYDYESWTETDLSF
                                                                                              KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
LLLNPENPRGTFLVRKSETAKGAYCLSVSDFDNAKGPNVKHYKICKLYSGGFYITSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2054 GAAGCTGGGGCAGGGCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2114 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTACAGGAAGC 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1050 GGCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCG 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2291 GAAGGGAGAGAGGCCAAGTACCTGCGGCTGCGACACCGTCGATATGGCTGCTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2234 AG---AGCCCATCTACATCGTCATTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 CGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2411 CAACATCCTGGTGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTCGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2471 CATCGAGGACAACGAGTACACAGCACGCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                      /organism="Mesocricetus auratus"
/db_xref="taxon:10036"
/haplotype="21-22 hypodiploid"
/dev_stage="sarcoma cell from renal metastasis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 177; DB 32; L
Pred. No. 3.49e-111;
0; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="mesenchymal"
/cell_type="polymorphic"
/cell_line="H-19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA37004.1"
/db_xref="PID:949657"
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="71,1NM1149"
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="71,1H19c1C2.1"
3608
                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="enhancer core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3640. .3651
/note="enhancer core"
                             /db_xref="GI:49657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.4%;
Best Local Similarity 63.0%;
Matches 466; Conservative
                                                                                                                                                                                                                                                                          3509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     878
                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                          TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                      enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhancer
                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
```

CCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT 2590

```
HIDDYCSDEVOLWGPTARIFASILAPGVAAAQALKEIERLACWSVKQANLTTSLLGDL
LDDVTSIRHAVLQNRAAIDFLLLAHGHGCEDVAGMCCFNLSDHSESIQKKFQLMKEHV
NKIGVDSDPIGSWLRGLFGGIGEWAVHLLKGLLLGLVVILLLVVVCLPCLLQIVCGNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGSSKSKPKDPSQRRCSLEPPDSTHHGGFPASQTPNKTAAPDTH
RTPSRSFGTVATEPKLFGGFNTSDTVTSPQRAGALAGGVTTFVALYDYESRTETDLSF
KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="IPSRPVGGPCYLGKLTMLAPNHTDILKILANSSRTGIRRKRSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rous sarcoma virus (recovered td mutant 1441) env-src-3'LTR region. K00928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses. 1 (bases 1 to 3110)
2 (bases 1 to 3110)
2 (bases 1 to 3110)
3 (bases 1 to 3110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transforming ability (presumably by picking up the cellular src gene from the host) after having lost transforming ability by deletion of the src gene. This particular recovered ASV is known to be derived from a transformation defective deletion mutant of Rous sarcoma virus Schmidt-Ruppin strain, subgroup A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c-myc proto-oncogene; env protein; src oncogene.
RASV1441 (recovered avian sarcoma virus 1441; derived from td
mutant of Rous sarcoma virus Schmidt-Ruppin strain, subgroup A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A recovered avian sarcoma virus is a virus which has regained
GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGGCCCACCTTTAA
                                                                                                                                                                       CCTGCTGACTGACCTGACCACCAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA
                                                                                                                                                                                                                                                                          742
/note="env-Pr95 polyprotein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rous sarcoma virus"
/db_xref="taxon:11886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="src-p60 phosphoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMINNSISYHTEYKKLQKAYGQPESRIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAA42564.1"
/db_xref="PID:9210188"
/db_xref="GI:210188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA42565.1"
/db_xref="PID:9210189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125. .739
/note="glycoprotein-37"
1121. .2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="glycoprotein-85'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:210189'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2771 GTACCTGCAGGCCCAGCTGC 2790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1470 CACGCTGCGGAGAGCTGC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA to genomic RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g210187
K00928.1 GI:210187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rous sarcoma virus
```

LIR

셤

g

ò

q

ò

g

ò

a

ò

Q

ò

셤

ò

g

ô

QQ

ò

g

ò

g

ò

ద

g

ö

```
QFGSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEIPRESLRLEAKLGGG
CFGEVWMGYTRYALTKYLKPGTWSPEAFLQBAQVMKKLRHEKLVQLXAVVSEEP1
YLIEYWRSKGSLLDFLKGEWGKYLRLPQLVDWAAQIASGMAYVERMNYVHRDLRAANI
LVGENLVCKYADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGI
LLTELLTKGRVPYPGMVNREVLDQVERAYRMDCPPECPESLHDLMCQCWRKDPEERPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MGSSKSKPKDPSQRRRSLEPPDSTHHGGFPASQTPDETAAPDAH
WRPSRSFGYTYATEPKLEWGRYNTSDYVTSPQRAAGGYTFYALYDYESWTETDL.ST
KKGRRLQIVNNTEGDWWLABLITTGOTGYIBSNYAPSDSIQAEBWYEGKITRRESEP
LLLNPENPRGTFLYRKSETAAKGAYCLSVSDFDNAKGPNVKHYKICKLYSGGFYITSRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="sarcoma cells induced by XC rescued PR-RSV-C"
/cell_line="H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                   hamster genome by src
                                                                                                                                                                                                                                                  Bodor J., Institute of Molecular Genet
Sciences, Flemingovo 2, 166 37 Prague,
                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
1 (bases 1 to 3123)
                                                long terminal repeat; oncogene; provirus; src oncogene; src
                                                                                                                                                                                                                                                                                                                                                                  provirus
                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3123)
Bodor, J., Poliak, E., Pichrtova, J., Geryk, J.
Complete nucleotide sequence of LTR, v-src,
Nucleic Acids Res. 17 (21), 8869 (1989)
90067864
                                                                                                                                                                                                                                                                                                                                                                                                                              The H-19 proviral seq was generated in the mRNA reverse transcription and integration. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mesocricetus auratus"
/db_xref="taxon:10036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hamster DNA"
/organism="Mesocricetus auratus'
/db_xref="taxon:10036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rous sarcoma virus"
/db_xref="taxon:11886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /haplotype="21-22 hypodiploid"
/tissue_type="mesenchymal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121. .3097
/organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    831. .2411
/note="pp60v-src (AA 1-526)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="G1:61707"
/db_xref="SWISS-PROT:P25020'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121...126

/note="direct repeat 1"

/note="sis LTR"

329..335

/note="put. TATA-box"

352..357

/note="pot. polyA signal"

359..357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="direct repeat 2 (R) 756. 2992 /note="exon (v-src)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="lambda NM1149"
/clone="H19c1C2.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'protein_id-"CAA33404.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:11886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="PID:961707"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKYLQAQLLPACVLEVAE"
2760. 3091
/note="3' LTR"
                                                                                                                                                                                                   Bodor,J.
Direct Submission
Submitted (26-MAY-1989) |
Czechoslovak Academy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                               Mesocricetus auratus
                       GI:61706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /proviral
                                                                   oncogene viral.
                                                                                        qolden hamster
                                                                                                                                                                                                                                                                                            Czechoslovakia
g61706
X15345.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                               ORGANISM
                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                        SOURCE
                QFSSLQQLVAYYSKHADGLCHRUTNVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQG
CFGEVWMGTWGTTRYALKFGTMGFBAFLCEAQYMKKLHEKLVQLXAVYSEBPI
YIVTEYMSKGSLLDFLKGEMGKYLRHPQLVDMAAQIASGMAYVERMNYVHRDLRAANI
LVGENLVCKVADFGLARLIEDMEYTARQGAKFPIKWTAFBAALYGFRFTIKSDYWSFGI
LLTELTTKGRYPYPGMGNGEVLDRVERGYRMPCPPECPESLHDLMCQCWRRDPEERPT
FELLQADLLPACVLEVAE"

2926. .3110
/note="3" LIR"
LLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKİRKLDSGGFYITSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349
                                                                                                                                                                                                                                                                                                                                                             1933 GAAGCTGGGGCAGGGCTGCTTTGGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2170 GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACACCTCGATATGGCTGCTGCTGAA 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1110 GAACGTGCTCGTGGACGACGCCTGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGCT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1230 GCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCTTCGGCGT 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1993 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCGGAGGCCTTCCTGGAGGAAGC 2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2590 GCTGCATGACCTTATGTGCCAGTGCTGGCGGAGGGACCCTGAGGAGCGGCCCACTTTTGA 2649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                         750 GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2053 CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTACAGCTGTACGCAGTGGTGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2410 CCCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2470 CCTGCTGACTGAGCTGACCACCAAGGGCCGGGTGCCATACCCAGGGATGGGCAACGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2113 AG----AGCCCAICTACATCGTCACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2290 CAACATCCTGGTGGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2350 CATCGAGGACAACGAGTACACAGGACGCAAGGTGCCAAGTTCCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                                   э,
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3110;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RERSVH19 3123 bp RNA ROD Hamster H-19 proviral DNA (LTR- v-src -LTR). X15345
                                                                                                                                                                                                                                                                  Score 175; DB 37; I
Pred. No. 1.35e-109;
0; Mismatches 272;
                                                                                                                                                                                                   655 t
                                                                                                                                                                                                 912 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1470 CACGCTGCGGAGAAGCTGC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2650 GTACCTGCAGGCCCAGCTGC 2669
                                                                                                                                                                                                                                                                  Query Match 11.3%;
Best Local Similarity 62.8%;
Matches 465; Conservative
                                                                                                                                                                                                   812 c
                                                                                                                                                                                                                        EcoRI site.
                                                                                                                                                                                                 731 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
                                                                                                                                                                                                 BASE COUNT
ORIGIN
```

RESULT

```
/organism="Moscoricetus auratus"
/db_xref="taxon:10036"
/haplotype="21-22 hypodiploid"
/tissue_type="mesenchymal"
/cell_type="sarcoma cells induced by XC rescued PR-RSV-C"
/cell_type="lambda NM1149"
/clone="H19c1c2.1"
a 843 c 936 g 628 t
                                                                                                                                                                                                                                                                                                                                                   Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACACACTCGTCGATATGGCTGCTCAGAT 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1643 GAAGCTGGGGCAGGGCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                          1703 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTACAGGAAGC 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTCGGA 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1823 AG---AGCCCATCTACATCGTCATTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1940 TGCATCCGGCATGGCCTATGTGGAGAGAATGAACTACGTGCACCGAGACCTGCGGGGGGG 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2120 CCCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2180 CCTGCTGACTGACCTGACCACCAAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2300 GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGCCCCCCTTTAA 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 CGTGGCGATCAAGGTCATCAAGTCAACCATGAAGCTCACTGACCTCGCCAAGGAGAT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 CGGGGGAGCCTGTGTAACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT 989
                                                                                                                                                                                                                                                                                                                                                                                                             GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGGCTGGGCTCCCTGCC 809
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2060 CATCGAGGACAACGAGTACACAGCACGGCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000 CAACATCCTGGTGGGGGAGAACCTGGTGCAAGGTGGCTGACTTCGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                      Length 3123;
                                                                                                                                                                                                                                                                                                                   Score 175; DB 32; Length 312
Pred. No. 1.35e-109;
0; Mismatches 272; Indels
2964. .2970
/note="put. TATA-box" ..
2986. .2991
/note="pot. polyA signal"
2993. .3013
                                                                       /note="direct repeat 2 (R)
                                                                                        3092. .3097
/note="direct repeat 1"
                                                                                                                        3098. .>3123
/note="hamster DNA"
                                                                                                                                                                                                                                                                                                                    Query Match 11.3%;
Best Local Similarity 62.8%;
Matches 465; Conservative
                                                                                                                       3098.
                                                              repeat_region
                                                                                           repeat_region
                               misc_feature
   promoter
                                                                                                                        source
                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                           750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
St
                                                                                                                                            Rous sarcoma virus.
Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
1 (bases 1 to 1653)
                                                                                                                                                                                                                          Submitted (14-MAR-1989) Hackett P.B., University of Minnesota, Department of Genetics and Cell Biology, 250 Biosciences Centre, Paul MN 55108-1095, U S A. (bases I to 1653)
Liu, Z.J. and Hackett.P.B.
Sequence variation of the Rous sarcoma virus PrA src gene
Nucleic Acids Res. 17 (10), 3986 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 CGTGGCGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            948 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTGCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTCTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1068 AG---AGCCCATCTACATCGTCATTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1185 TGCATCCGGCATGGCCTATGTGGAGAGAATGAACTACGTGCACCGAGACCTGCGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1245 CAACATCCTGGTGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTCGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1305 CATCGAGGACAACGAGTACACAGCACGCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳
:
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                          VRL
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 173; DB 37; L. Pred. No. 5.25e-108; 0; Mismatches 273;
                                                      Rous sarcome virus Pra src gene (pp60). X14718
                                                                                                                                                                                                                                                                                                                                                   1. 1653 /
/organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                          283 t
                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:11886"
516 c 500 g
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
2360 GTACCTGCAGGCCCAGCTGC 2379
                        1470 CACGCTGCGGGAGAAGCTGC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.2%;
1 Similarity 62.7%;
464; Conservative
                                                                                                                         X14718.1 GI:61714
src gene.
                                                                                                                                                                                                  Hackett, P.B.
Direct Submission
                                                                                                                                                                                                                                                                                                                             *map: 7054-8706
                                                                                                                                                                                                                                                                                                                                                                                           ๙
                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 8
                                                             Ξ
                                                                                                                                       KEYWORDS
SOURCE
ORGANISM
                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990
                                                                                                  ACCESSION
                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                              COMMENT
 원
                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

Gaps

1755

1815

1875

1935

1995 1229 2055

ò

ò

ò

ò

```
Submitted (08-MAR-1990) Zubak S., Institute Mol. Biol. & Genet., Academy of Science Ukr SSr, 252627 Kiev, Str Zabolotnogo 150, U S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 4503)
Yatsula, B.A., Geryk, J., Svoboda, J., Rynditch, A.V., Calothy, G. and
                                                                                                                                                                                                                                                                                                                                                                  2056 CCTGCTGACTGACCTGACCACCAAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCTGGGGCAGGCCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 1578
                                                                                                                1579 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCGGAGGCCTTCCTGCAGGAAGC 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2116 GGTGCTGGACCAGGTGGAGGGGCTACCGCATGCCCTGCCCGCCGAGTGCCCCGAGTC 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2176 GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGGCCCCACTTTTG 2234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996 CCCCGAGGCAGCCCTCTATGCCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT
                                                                                                                                   870 ccagacacreaagegecrecegecaceagegercarecegerecacecagerereges
                                                                                                                                                                                                                                                                                       930 CGGGGGGCCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                            1756 GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGATATGGCTGCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             PR2257, a recent c-src transducing
                                                                          750 GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCC
                                                                                                                                                                                                                                                                   1699 AG---AGCCCATCTACATCGTCACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                         1816 TGCATCCGGCATGGCCTATGTGGAGAGGATGAACTACGTGCACCGAGACCTGCGGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1936 CATCGAGGACAACGAGTACACAGCACGCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1170 GCTCAAGGACGACATCTACTCCCGGAGCAGCACCTCCAAGATCCCGGTCAAGTGGACAGC
                                                                                                                                                                                         1639 CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1876 CAACATCCTGGTGGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷,
Mismatches 262; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     src protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian sarcoma virus
Viruses; Retroid viruses;
 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evolution and origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c-src gene; env gene;
Avian sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 4503)
Zubak, S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X51863.1 GI:394712
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           revised by [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dezelee, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9394712
 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                     1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                       g
                                                                                                                g
                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                   ŏ
                                                                                                                                                                                       셤
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVGENLVCKVADFGLARLIEDNEYTARÖGAKFPIKWTAPEAALYGRFTIKSDVWSFGI
LTELTTKRSVPYPGMVNRSVLDQVERGYRMPCPPECPESLHDLMCQCMRKDPEERPT
FEYLQAFLEDY FTSTEPPVPAWREPIGLELLLAPEASLWGTGAWLRAEGPRFGEQPQS
RMWHGEVSGAPSLIKTVLGHP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MGSSKSKPKDPSQRRRSLEPPDSTHHGGFPASQTPNKTAAPDTH
RTPSRSFGTVATEPKLFGGFNTSDTVTSPQRAGALAGGVTTFVALYDYESRTETDLSF
KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LILNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRT
OSSLQQLVAYYSKHADGLCHRLINVCPFSKPQTGLAKDAWEIPRESLALEVKGOG
CFGEVWMGTNNGTTFX IKTIKPGTMSPEAFLOEAQVNKKLHHRKLYQLYAVSEEPI
YIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASCMAYVERNIY VHRDLRANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      įυ
                                                                                                                                                                                                                                                                                                                                                                                                                                     9210264
M21526.1 GI:210264
Iong terminal repeat (LTR); p66-src protein; src oncogene.
Rous sarcoma virus (strain PR-C, replication-defective mutant PR2257) RNA, passed in quail embryo fibroblast cell line C7.
Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 4413)
Gerk, J., Dezelee, P., Barnier, J.-V V., Svoboda, J., Nehyba, J.,
Karakoz, I., Synditch, A.V., Yatsula, B.A. and Calothy, G.
Transduction of the cellular src gene and 3' adjacent sequences
avian sarcoma virus PR2257
                                                                                                                                                                   GGTGCTGGACCAGGTGGAGAGGGGCTACCGCATGCCCTGCCCGGCCCGAGTGCCCCGAGTC 1544
                                                                                                                               Draft entry and computer-readable sequence for [1] submitted P.Dezelee 30-NOV-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                ALRSRCAC 4413 bp ss-RNA VRL 28-JUL-1995,
Rous sarcoma virus defective mutant-PR2257 src.geng encoding
P66-src protein, complete cds.
                 CCTGCTGACTGACCTGACCACCAAGGGCCGGGTGCCATACACAGGGATGGTCAACAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 174; DB 37; Length 4413; Pred. No. 8.43e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rous sarcoma virus"
/db_xref="taxon:11886"
1. 335
/note="5, long terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4079. .4413
/note="3'_long terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235. .255
/note="5' LTR R-region"
/707. .2470
/note="p66 src protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA42583.1"
/db_xref="PID:9210265"
/db_xref="GI:210265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4313. .4333 /
/note="3' LTR R-region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 bp upstream of EcoRI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 63, 481-492 (1988)
89094972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1269 g
                                                                                                                                                                                                                                                                                   1470 CACGCTGCGGGAGAGCTGC 1489
                                                                                                                                                                                                                                                GTACCTGCAGGCCCAGCTGC 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1226 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .4413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                   1425
                                                                                          1485
                                                                                                                              1350
                                                                                                                                                                       1545
                                                                                                                                                                                                                                              1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                            1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                          엄
                                                                                                                                                                 a
                                                                                                                                                                                                                                              g
```

S

```
mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SnRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
FEATURES
                                                                                                                                                                                                      2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                 g
                                                                                                    ö
                                                                                                                                 g
                                                                                                                                                                  δý
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                 /product="src protein"
/protein_id="CA36156.1"
/protein_id="CA36156.1"
/db_xxref="g1:34713"
/db_xxref="g1:34713"
/db_xxref="SWISS-PROT:P15054"
/translation="MOSSESERENDEORRESLEPPDSTHHGGFPASOTPNKTAAPDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFSSLOOLVAYYSKHADGLCHRLTNYCPTSKPOTOGLAKDAMEIPRESLRLEVKLGOG
CEREVWARTHWOTTRVALKTRIKREDANEDEADGAOVAKKHENKLVOLYAVVSEBPI
YVTBEYMSKGSLLEFKGEMORYTRLPODAAQIASKMAYVERMNYVHRDLRAANI
LVGENLVCKVADDFGLARLIEDNEYTAROGAKFPIKWTARFAAALKGRFTIKSDVWSFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTPSRSFGTVATEPKLFGGFNTSDTVTSPQRAGALAGGVTTFVALYDYESRTETDLSF
KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
LLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKDPEERPT
FEYLQAFLEDYFTSTEPPVPAWREPIGLELLLAPEASLWGTGAWLRAEGPRFGEQPQS
                                Direct Submission
Submitted (16-JUL-1993) Dezelee P., URA 1443 CNRS, Institut
Curie-Biologie Bat. 110, Centre Universitaire Orsay 91405, France
On Sep 3, 1993 this sequence version replaced gi:61895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1519 GAAGCTGGGGCAGGGCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAG 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTGCAGGAAGC 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1639 CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGA 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1699 AG --- AGCCCATCTACATCGTCACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGAT 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 CGTGGCGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 CGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 262; Indels
                                                                                                                                                                                   <1. .>4503
/note="Avian Leukemia Virus leader mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .>4503
/function="gp37 env gene (partial)"
                                                                                                                                                                                                                                                                                  707. 2470
/standard_name="p66src"
/function="protein tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 174; DB 37; 1
Pred. No. 8.43e-109;
                                                                                                                                   /organism="Avian sarcoma virus"
                                                                                                                                               /note="Quail sarcoma DNA" /db_xref="taxon:11876"
                                                                                                                                                                                                                                                                                                                                                       /evidence=experimental
                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1295 g
                                                                                                                                                                                                                                                                    'note="5' LTR"
                                                                                                                                                                                                                                                                                                                                      /codon_start=1
3 (bases 1 to 4503)
Dezelee, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.2%;
1 Similarity 63.1%;
454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1249 c
                                                                                                                 1. .4503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ๙
                                                                                                                                                                                                                     misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                     source
                                                                                                                                                                                     5'UTR
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  066
                                                   JOURNAL
                                                                                                                                                                                                                                                     LIR
                                                                                                     FEATURES
                                    TITLE
                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
IGCNCATASAPPPPYVGSGLYPSLAGVGGQGGGDTPPGAEQSRAEPGHAGQAPGPA
TUDMARVREBLASTGPPVVAMPVVITRGPAMPTDERKLITALLADDTYRKGLRSBITM
AEVBALMSSPLLPHDYTNLARPITGPAPYALWMDAWGVQLQTVIAATRDPRIBANG
GRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLAEPAGPW
ADINGSPESESYDFANRLIKAYEGSDLPSARARDYIIOFGRKSQPDLOQLIRTABST
LITPGELIKYVLDRGYTAPLITGOAAMSSAIQPLIMAVVNRERGGTGSGGRARGL
CYTGGSPGHYQAQCPKKRKSGNSRERCQLCNOMGHNAKOCRRNGNOGORPGKGLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"SWISS-PROT:P03322"
/translation-"MENVIKVISSACKTYCGKTSPSKKEIGAMLSLLOKEGLLMSPSD
/translation-"MENVIKVISSACKTYCGKTYGALKAREEGVTSEGAKFWIGLGG
GRVSPGSWDPTTAALSORAMILGKGEEKTWGLVLGALKAAREEGVTSEGAKFWIGLGG
GRVSPPGFBCLIEKABATERRIINKGEEVGETTVQRDAKMAPEETATPKTVGTSCYHCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWPGPEPPAVSLAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISE
EDWPTDWPVMEAANPQIHGIGGGIPWRKSRDMIELGVINRDGSLERPLLLFPAVAMVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses
1876 CAACAICCIGGIGGGGAGAACCIGGIGIGCAAGGIGGCIGACITIGGGCIGGCACGCCI 1935
                                                                                                                                                                                                                                                    2176 GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGGCCCACTTTTG 2234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coat protein; endonuclease; oncogene; reverse transcriptase.
Rous sarcoma virus.
                                                                                                                                                                 1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGC
                                                  1110 GAACGIGCICGIGGACGACGACGCCIGCAGGIGGCIGACTICGGCCIGGCCCGGCI
                                                                                                            1936 CATCGAGGACAACGAGTACACGACGCCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                         CCCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT
                                                                                                                                                                                                                                                                                                                                         CCTGCTGACTGACCTGACCACCAAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RERSV6 9312 bp DNA VRL
Rous sarcoma virus genome, strain Prague C (Pr-C).
V01197
V01197 I GI:61695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 9312)
Schwartz,D.E., Tizard,R. and Gilbert,W.
Uncleotide sequence of Rous sarcoma virus
Call 32 (3), 853-869 (1983)
83155662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .9312
/organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="reading frame p27"
1844. .2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reading frame p10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="polyprotein gag"
/protein_id="CAA24512.1"
/db_xref="PID:g61696"
/db_xref="G1:61696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:11886"
22. .101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSILGRDCLQGLGLRLTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22. .101
/note="U5 RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="p19"
380. .2485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
```

```
mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'UTR
                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                              ACCESSION
                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8237
                                                                                                                                                                                                                                                                                                                          7941 GAAGCIGGGCAGGGCIGCTITGGAGAGGICIGGAIGGGGACCIGGAACGACACCACCAG 8000
                                                                                                                                                                                                                                                                                                                                                                                           8001 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTGCAGGAAGC 8060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1050 GGCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCCG 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCTCCCAAGATCCCGGTCAAGTGGACAGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 CGTGGCGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCCAAGGAGAT 869
                                                                                                                                                                                                                                                                                                                                                           750 GAAGCIGGGIGAAGGCIACTITGGGGAGGIGIGGGAAGGCCCIGIGGCIGGGCICCCIGCC 809
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           870 ccagacacidaagggccigcggcacgacggciccarccggcigcacgcaggggggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8121 AG----AGCCCATCTACATCGTCATTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8238 IGCAICCGGCAIGGCCIAIGIGGAGAGAAIGAACIACGIGCACCGAGACCIGCGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1110 GAACGTGCTCGTGGACGACGGCCTGGCAGGTGGCTGACTTCGGCCTGGCCCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8418 CCCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8598 GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGGCCCACCTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 GGGGGGGCCTGTGTACTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACATCCTGGTGGGGGAGAACCTGGTGTGCCAAGGTGGCTGACTTCGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8358 CATCGAGGACAACGAGTACACGACGCCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8478 CCTGCTGACTGACCTGACCACCAGGGCCGGTGCCATACCCAGGGATGGTCAACAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8538 GGTGCTGGACCAGGTGGAGAGGGGCTACCGCATGCCCTGCCCGCCGGAGTGCCCGAGTC
                                                                                                                                                                                                                                                                                             э;
                                                                                                      5054. 6865

/note="reading frame env (envelope protein)"

7129. 8709

/note="transforming gene src"

/note="U3 RNA"

1 2359 c 2681 g 2060 t
                                                                                                                                                                                                                                                             Length 9312;
                                                                                                                                                                                                                                                                                            Indels
                                                                                          (reverse transcriptase)"
                                                                                                                                                                                                                                                         Score 173; DB 37; L/Pred. No. 5.25e-108; 0; Mismatches 273;
reading frame pl2"
/product-"reading frame pl5"
2503 .5187
/note="pol (rever-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8658 GTACCIGCAGGCCCAGCIGC 8677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1470 CACGCTGCGGGAGAAGCTGC 1489
                                                                                                                                                                                                                                                         Query Match 11.2%;
Best Local Similarity 62.7%;
Matches 464; Conservative
                                                                                                                                                                                                             ๙
                                                                                                                                                                                                           2212
                                          mat_peptide
                                                                           mat_peptide
                                                                                                          mat_peptide
                                                                                                                                            mat_peptide
                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                           SURNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

03-DEC-1998

VRL

RNA

9392 bp

AF033808

```
/db_xxef="G1:2801462"
/db_xxef="G1:2801462"
/translation="WEAVIRAFLICYPGKTSKKDSKERPLATSKKDPEKTPLLPTRVN
/translation="WEAVIRAFLICYPGKTSKKDSKERPLATSKKDPEKTPLLPTRVN
ILIIGOLVLCEVTGVRADVHLLEOPGNLWITWANRTGGTDFCLSTGSATSPFCLT
GIPSPESBGDPFKGYYSDTNCSTYGTDRLVLSASITIGGPDNSTTLTYRKVSCLLLKLNU
SMWDBPPELQLLGSQSLPNVTNITQVSGVAGGCVYFAPRATGLFLGWSKQGLSRFLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSTOGSFTKPKALPPAIFLICCDRAWGIPSRPVGGPCYLGKUTMLAPNHTDIIKLIA
NSSRTGIRRKRSVSHLDDTCSDEVQLWGPTARIFASILAPGVAAAQALREIERLACWS
NKQANUTTSLLGDLLDDYTSRRHAVLQNRAALDFLLAHGHGCEDVAGMCCFNISDHS
ESIQKKFQLMKKHVNKIGYDSPDFIGSWLRGIFGGIGEWAVHLLKGLLGLVVILLLLV
CLPCLLQFVSSSIRKHNSSRNYTEFRKWQGGAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGCNCATASAPPPPYVGSGLYPSLAGVGEQQGGGDTPPGAEGSRAEPGHAGQAPGPA
LTDWARVREELASTGPPVVAMPVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSFITM
AEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQLQTVIAAATRDPRHPANGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPFTSTSNSTEPFTVVTADRHNLFMGSEYCGAYGYRFWELYNCSGTRNTYRCGDVGGT
GLPETWCRGKGGIWVNQSKEINETEPPSFTANCTGSNLGNVSGCCGEPITILPLGAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLLMSPSJ
LYSPGSWDPITAALSQRAMILGKSGELKTWGLVLGALKAAREEQVTSEQAKFWLGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGERTULNRLKGLADGMVGNPQGQAALLRPGELVAITÄSÄLQAFREVARLAEPAGPW
ADINGOPESESPUDFANRLIKAYBGSDALPSARRAVIIOCREVOKGQPDIOQLIKTÄRST
LITPGELIKYVLDRGKTAPLTDGGIAAAMSALQPLIMAVVNRERDGOTGSGGRARGI
CYTCGSPGHYQAQCPKKRRSGNSRERCQLCNGMGHNAKOCRKRDGNOGORPGKGLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRVSPPGPECIEKPATERRIDKGEEVGETTVQRDAKMAPEETATPKTVGTSCYHCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWPGPEPPAVSLAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISE
                                                                                                                                                                                                                                                                                                        Appendix 2: Retroviral taxonomy, protein structure, sequences, and
                                                                                                                                                                                                                                                                                                                                                                                                                  Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, NY, USA (1997)
2 (bases 1 to 9392)
Chappey, C.
Direct Submission
Submitted (12-NOV-1997) NIH, NLM, Rockville Pike, Bethesda, MD 20894, USA
                                                                                                                                                                                    Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="gPr95 polyprotein precursor"
22. .102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="gpr95 polyprotein precursor"
/protein_id="AAC82562.1"
/db_xref="PID:92801462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Pr180 polyprotein precursor'
/protein_id="AAC82561.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /exception="ribosomal slippage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .9392
/organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(380. 397,5078. 6865)
/gene="env"
Rous sarcoma virus, complete genome.
AF033808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gag-pol"
join(1. .397,5078. .9392)
/gene="env"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="PID:92801461"
/db_xref="G1:2801461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:11886"
1. .9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "p19"
                                                                                                                                                                                                                                                                                                                                           genetic maps
(in) Coffin, J.M. (Ed.);
RETROVIRUSES: 757;
                                                      92801459
AF033808.1 GI:2801459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="gag-po]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380. .844
/gene="gag"
/product="pl9
380. .2485
/gene="gag"
                                                                                                                                                                                                                                           1 (bases 1 to 9392)
Petropoulos, C.J.
                                                                                                                                                       Rous sarcoma virus.
Rous sarcoma virus
```

```
RAGFTISPDKVQREPGVQYLGYKLGSTYVAPVGLVAEPRIATLMDVQKLVGSLQMLRP
ALGIPPRLMGPFYEQLRGSDPNEAREWNLDMKMAWREIVRLSTTAALERWDPALPLEG
AVARCEQGAIGVLGQGLSTHPRPCLMLFSTQPTKAFTAMLEVLTLLITKLRASAVRTF
                                                                                                                                                                                                                                   GKEVDIÍLLPACFREDLPLPEGILLALKGFÄGKIRSSDTPSIFDIARPLHVSLKVRYT
DHPVPGPTVFTDASSSTHKGVVVWREGPRWEIKEIADLGASVQQLEARAVAMALLLWP
TTPTNVYTDSAFVAKMLLKMGQEGVPSTAAAFILEDALSQRSAMAAVLHVRSHSEVPG
                                                                                                                                                                                                                                                                                                                        FFTEGNDVADSQATFQAYPLREAKDLHTALHIGPRALSKACNISMQQAREVVQTCPHC
NSAPALEAGVNPRGLGPLQIMQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTS
VAVQHHWATAIAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMV
                                                                                                                                                                                                                                                                                                                                                                                                             ERANRLLKDRIRVLAEGDGFMKRIPTSKOGELLAKAMYALNHFERGENTKTPIOKHWR
PTVLFBGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDITOK
DEVTKKDEASPLFAGISDWIPWEDEQEGLOGETASNKOERPGEDTLAANES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLLMSPSD
LYSPGSWDPTTAALSQRAMLGKSGBEKTWGVIAGALKAREREQYTSQAKFWLGLGG
GRYSPPEDED IEKPYTERRIDKGEBYGETTYQRDAKMAPEETATPKTYGTSCYHCGTA
IGCNCATASAPPPYVGSGLYPSLAGYGEQOGGGDTPPGAEQSRAEPGHAGQAPGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTTPGEIIKYVLDRQKTAPLTDQGIAAAMSSAIQPLIMAVVNRERDGQTGSGGRARGL
CYTCGSPGHYQAQCPKKRKSGNSRERCQLCNGMGHNAKQCRKRDGNQGQRPGKGLSSG
PWPGPEPPAVSLAMTMEHKDRPLVRYILTNTGSHPVKQRSVYITALLDSGADITIISE
                                                         ALTQLVEKELQLGHIEPSLSCWNTPVFVIRKASGSYRLLHDLRAVNAKLVPFGAVQG
APVLSALPRGWPLMVLDLKDCFFSIPLAEQDREAFAFTLPSVNNQAPARRFQWKVLPQ
                                                                                                                   GMTCSPTICQLVVGQVLEPLRLKHPSLCMLHYMDDLLLAASSHDGLEAAGEEVISTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIDWARVREELASIGPPVVAMPVVIKIEGPAWIPLEPKLIIRLADIVRIKGLRSPIIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQLQTVIAAATRDPRHPANGQ
GRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLAEPAGPW
EDWPTDWPVMEAANPQIHGIGGGIPMRKSRDMIELGVINRDGSLERPLLLFPAVAMVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adimogpsesfydfanrlikavegsdlppsarapyiidcfroksopdioolirtapst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDWPTDWPVMEAANPQIHGIGGGIPMRKSRDMIELGVINRDGSLERPLLLFPAVAMVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Pr76 polyprotein precursor"
/protein_id="AAC82560.1"
/db_xref="IDI92801460"
/db_xref="GI:2801460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="pl2 NC"
join(2102. 2482, 2482. 2502)
/product="pl5 PR"
2482. 5190
/gene="pol"
2503. 4218
/gene="pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7129. .8709
/gene="src"
/note="p60'SRC phosphoprotein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC82563.1"
/db_xref="PID:92801463"
/db_xref="G1:2801463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSILGRDCLQGLGLRLTNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="p60 src"
7129. .8709
/gene="src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="p60 src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="p27 CA"
1844. .2110
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="gp37 TM"
7129. .8709
/gene="src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="p68a RT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="gp85 SU"
6269. .6862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="p32 IN"
249. .6268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="pp10"
1097. 1816
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /qene="qaq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4219. .5187/gene="pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
```

CDS

gene

gene

CDS

mRNA

```
QFGSLQQLVAYYSKHADGLCHRLANVCPTSROTOGLAMAINTAINLIAGSTILTSK

QFGSLQQLVAYYSKHADGLCHRLANVCPTSROTOGLAMAINTAINLIAGSTILTSK

CGEGVAMGTWNDTTRVAIKTLKRGTMSPEAFLQEAOVMKKLRHEKLVOLYAVVSEEPI

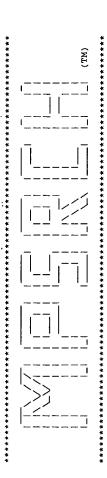
XIVIEYMSKGSLLDFLKGEMGKYLRLPQLVDWAAQIASGMAYVERMNYVHRDLRAANI

LLYEBLTKCKVADFGLARLIEDNEYTARQGAKRPIKWTAPEAALYGRFTIKSDVWSFGI

EKYLQAQLLPACVLEVAE"

7132. 8706
                                KKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
LLLNPENPRGTFLVRKSETAKGAYCLSVSDFDNAKGPNVKHYKIYKLYSGGFYITSRT
/translation="MGSSKSKPKDPSQRRHSLEPPDSTHHGGFPASQTPDETAAPDAH
                  RNPSRSFGTVATEPKLFWGFNTSDTVTSPQRAGALAGGVTTFVALYDYESWTETDLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8597
                                                                                                                                                                                                                                                                                                                                         GAAGCTGGGGCAGGGCTGCTTTGGAGAGGTCTGGATGGGGACCTGGAACGACACCACAG 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCTACGTGCTCATGCTGGAGTGCTGGAGGAGCAGCCCCGAGGAACGGCCCTCCTTTGC 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCATGACCTCATGTGCCAGTGCTGGCGGAAGGACCCTGAGGAGCGGCCCACCTTTAA
                                                                                                                                                                                                                                                                                                                                                                        750 GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                         8001 AGTGGCCATAAAGACTCTGAAGCCCGGCACCATGTCCCCGGAGGCCTTCCTGCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTGGCGATCAAGGTCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAGTGATGAAGAAGCTCCGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccagacacreaagggccrecegecacgagggccrcarcegecrecacgcaggrererege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCGAGGCAGCCCTCTATGGCCGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGCTGACTGACCTGACCACCAAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8121 AG----AGCCCATCTACATCGTCATTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 CGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGGAGAGATGGGCAAGTACCTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACATCCTGGTGGGGGAGAQCTGGTGTGCAAGGTGGCTGACTTCGGGCTGGCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCGAGGACAACGAGTACACAGCACGCCAAGGTGCCAAGTTCCCCATCAAGTGGACAGC
                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                            Length 9392;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                         Score 173; DB 37; L. Pred. No. 5.25e-108; 0; Mismatches 273;
                                                                                                                                                                                           /product="pp60 SRC"
9058. .9292
2378 c 2704 g
                                                                                                                                                                                                                                                                          11.2%;
ilarity 62.7%;
Conservative
                                                                                                                                                                             /gene="src'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCTGCAGGCCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1470 CACGCTGCGGGAGAGCTGC
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                              Ø
                                                                                                                                                                                                                                                                              Query ...
Best Local Similar
                                                                                                                                                               mat_peptide
                                                                                                                                                                                                            3'UTR
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                         7941
                                                                                                                                                                                                                                                                                                                                                                                                                                       810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990
                                                                                                                                                                                                                                                                                                                                         .
QD
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

US-09-099-053-1.rge



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. database search, using Smith-Waterman algorithm п. В. MPsrch_nn

Thu May 20 14:58:36 1999; MasPar time 400.17 Seconds828:882-Million-cell-updates/sec Run on:

Tabular output not generated

>US-09-099-053-1 (1-1548) from US09099053.seq 1548 Description: Perfect Score: N.A. Sequence: Comp:

1 GCTCGCGGGCTCCCATGCC.......CCAACGCTCTGGGCTCCAGC 1548 CGAGCGCCCGAGGGTACCGG.......GGTTGCGAACCCGAGGTCG

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

271905 segs, 107135622 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq35 Database:

1:part 2.part 3.part 4.part 4.part 5.part 5.part 7.part 7.part 8.part 8.part 9.part 9.par

Mean 9.225; Variance 5.916; scale 1.559 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Pred. No.	.0.00e+00	1.95e-101	4.84e-93	5.48e-77	2.36e-62	2.17e-37	3.65e-36	6.68e-32	1.08e-30
			Description	Human SAD encoding cD	Breast tumour kinase,	Chicken pp60 c-src ge	Human pp60 c-src gene	Lck gene fused with p	gD.trkA fusion useful	Human c-trk oncogene.	c-abl gene.	Human c-abl oncogene.
SUMMARIES			Ц	V81743	081189	046687	046688	Q13983.	T51456	V20445	T61865	V20457
			re Match Length DB I	1548 59								
	æ	Query	Match	100.0	12.3	11.5	o.	8.4	5.8	5.7	5.2	5.1
			Score	1548	191	178	153	130	90	88	81	79
		Result	NO.	-	7	٣	4	S	ø	7	80	6

886-223 86-223 86-223	18e-2 70e-2 02e-1 02e-1	2386-1-1-2386-1-1-2386-1-1-2386-1-1-1-2386-1-1-1-2386-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	23.6	2000 0000
c-abl gene. Potential tyrosine ki Rat orphan tyrosine k Human receptor tyrosi DNA encoding cytoplsm Human matK CDNA.	karyocyte sine Kinas related PT related PT	PH-Jike receptor prouse fik-2 cDNA. urine fik-2 cDNA. Ik2 receptor protei urine fik-2 cDNA.	ine fik-2 recent foctal live fix-3 recent live 2/fit3 tyrosin related PTK crelated PTK C-2/neu oncogen receptor kina	Rat neu promoter. elk CDNA. Sequence encoding a c Human HER2 gene. Her-2/neu (ERBB2/c-er gD.trkB fusion useful Human trkB receptor D Murine flk-2 cDNA seg Embryonic stem cell k Human neurotrophic fa Human embryonal kinas
186 072 022 023 488 488	061 753 066 065	20064 20064 2001 2001	2111 873 065 065 073 073	T01590 053471 046083 T71253 T01585 T51457 T00689 T72320 099277 062461
2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	15 15 15	13	30 23 115 7 7	17 9 17 17 20 20 11 11 11
877000	000000000000000000000000000000000000000	0044444	444000777	3955 4281 4289 4530 3060 3194 3453 3453 3707
N44444				a
				0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
110 111 114 114	16 118 119	22222222222222222222222222222222222222	333311008875 333311008875	8 8 8 8 9 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

```
10-MAR'1999 (first entry)

Human SAD encoding cDNA.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

type I receptor serimo-/threonine kinase; cancer; leukaemia; lymphoma;
neurodegenerative disease; neuronal survival; Alzheimer's disease;
Parkinson's disease; Huntington's disease; ss.
                                                           Location/Qualifiers
49..1515
/*tag= a
      BP.
     V81743 standard; cDNA; 1548
V81743;
                                                                             WO9849317-A2
RESULT
```

~

```
present sequence encodes human SAD. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 840
                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                       9
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                   ctcaggaggcggctggccttccttcttctgggacaagatctggccggcggcggc
                                                                                                                                                                                                                                                                        gagooggaccatggcaccccggggtccctggaccccaacactgacccagtgcccacgctc
                                                                                                                                                                                                                                                                                                                   gtcagtcggacccaggcacagcagctgctctctcccaacgaaccaggggccttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCTCTTTCCCGGCCTGGAGGAGCTGCTCACCTACTACAAGGCCAACTGGAAGCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 tgggaaggcctgtgggctccctgcccgtggcgatcaaggtcatcaagtcagccaac
                                                                                                                                                                                                                                                                                                                                                 cccgccgagccttgcagccccttccctcagctcttccttgcgctctatgacttcacggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggctctttcccggcctggaggagctgctcacctacaaggccaactggaagctgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagaaccccctgctgcagccctgcatgccccagaaggccccgaggcaggacgtgtgggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cggccacactccgaattcgcccttgggaggaagctgggtgaaggctactttggggaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCACACTCCGAATTCGCCCTTGGGAGGAGGCTGGGTGAAGGCTACTTTGGGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                         59; Length 1548;
                                                                                                                                                     263 T;
                                                                                                                                                                                             0; Indels
                                                                                                                                                     494 G;
                                                                                                                                                                        8; DB 59;
0.00e+00;
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                         Score 1548;
Pred. No. 0.
                                                                                                                                                     533 C;
                                                                                                                                                     258 A;
                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 1548; Conservative
                                                                                                                                                     BP;
                                                                                                                                                    1548
                                                                                                                                                      Seguence
                                                                                                                                           proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                         н
                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721
   셤
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                               òγ
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
1140
                                                                                                                                                                                                                   1200
                                                                                                                                                                                                                                    1200
                                                                                                                                                                                                                                                       1260
                                                                                                                                                                                                                                                                                                                                                                      1440
                                                                                                                                                                                                                                                                                                                                                                                        1440
                                                                                                     1020
                                                                                                                      1020
                                                                                                                                         1080
                                                                                                                                                           1080
                                                                                                                                                                                                                                                                         1260
                                                                                                                                                                                                                                                                                            1320
                                                                                                                                                                                                                                                                                                              1320
                                                                                                                                                                                                                                                                                                                                 1380
                                                                                                                                                                                                                                                                                                                                                   1380
                                                                                                                                                                                                                                                                                                                                                                                                                     960
        840
                                                                                  960
                                                                                                                                                                                                                                                                                            agcagccccgaggaacggccctcctttgccacgctgcggggagaagctgcacgccatccac
atgaagctcactgacctcgccaaggagatccagacactgaagggcctgcggcacgagggg
                                     ctcatccggctgcacgcagtgtgctcggggggggggggctgtgtacatagtcacggaactc
                                                                                                     atgegeaaggggaacctgcaggccttcctgggcacccccgaggcccgggccctgcgtctg
                                                                                                                                          ccgccactcctgggctttgcctgccaggtggctgagggcatgagctacctggaggagcag
                                                                                                                                                 aaggtggctgacttcggcctggcccggctcaaggacatctactccccgagcagc
                                                                                                                                                                                                                                     AAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTCAAGGACGACATCTACTCCCCGAGCAGC
                                                                                                                                                                                                                                                        agctccaagatcccggtcaagtggacagcgcctgaggcggccaattatcgtgtcttctcc
                                                                                                                                                                                                                                                                          AGCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                      ctgccgcgcccggctgcctgcccggcggaggtctacgtgctcatgctggagtgctggagg
                                                                                                                                                                                                                                                                                                                                                                               CTCATCCGGCTGCACGCAGTGTGTCTCGGCGGGGAGCCTGTGTACATAGTCACGGAACTC
                                                                                                                      ATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCCCGAGGGCCGGGCCCTGCGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                                                                                                                                                                                                                               agatgccaccctgagtcctcacgtgacccaacgctctgggctccagc 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           081189;
12-AUG-1995 (first entry)
Breast tumour kinase, brk.
Breast tumor kinase; brk; protein-tyrosine-kinase; PTK;
Breast tumor metastasis; prognosis; diagnosis; T-47D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamalati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gusterson |
ence P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
29..1384
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barker KT, Crompton MR, Gust
Mitchell PJ, Page MJ, Spence
WPI; 95-066901/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1993; GB-014233.
11-MAR-1994; GB-004817.
(CANC-) CANCER RES INST
(WELL ) WELLCOME FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JAN-1995.
08-JUL-1994; G01479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9502057-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  081189 s
081189;
                                             841
                                                                                                                      961
                                                                                                                                                                                                                                    1141
                                                                                                                                                                                                                                                                         1201
                                                                                                                                                                                                                                                                                                                                                                                       1381
                                                                                                                                                                              1081
                                                                                                                                                                                                1081
                                                                                                                                                                                                                  1141
                                                                                                                                                                                                                                                                                                                                                  1321
                                                                                                                                                                                                                                                                                                                                                                     1381
                                                                                                                                                                                                                                                                                                                                                                                                          1441
                                                                                                     961
                                                                                                                                         1021
                                                                                                                                                                                                                                                       1201
                                                                                                                                                                                                                                                                                            1261
                                                                                                                                                                                                                                                                                                              1261
                                                                                                                                                                                                                                                                                                                                 1321
                                                                                                                                                                                                                                                                                                                                                                                                                            1441
                                                                                                                                                                                                                                                                                                                                                                                                                                              1501
                           841
                                                                 901
                                                                                  901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
        ò
                         g
                                             δ
                                                               g
                                                                                  δ
                                                                                                   g
                                                                                                                      δ
                                                                                                                                         임
                                                                                                                                                           ò
                                                                                                                                                                            а
                                                                                                                                                                                               δ
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

m

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              움
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                             ů,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870
                                                                                                                                                                                                                                                                                                                                                              810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990
                                                                                                                                                                                                        ggatgactgggagagaggccgagggaggagttcacgctctgcaggaagctggggtccggcta 630
                                                                                                                                                                                                                                767
                                                                                                                                                                                                                                                         690
                                                                                                                                                                                                                                                                                  827
                                                                                                                                                                                                                                                                                                           750
                                                                                                                                                                                                                                                                                                                                     884
                                                                                                                                                                                                                                                                                                                                                                                       944
                                              Disclosure; Page 29-31; 52pp; English.

A brk (breast tumor kinase) CDNA fragment was used to screen a CDNA increase tumor cell line T-47D.

CDNA library propared from human breast tumor cell line T-47D.

CDNAs were isolated. The slightly longer clone lambda-t2 (Q81189) encoded brk, which was identified as a novel putative non-receptor kinase of use as a prognostic/diagnostic of breast tumour metastasis, Sequence 2507 BP; 48 R, 726 C; 809 G; 514 T;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                GGACGTGTGGGAGCGGCCACACTCCGAATTCGCCCTTGGGAGGAAGCTGGGTGAAGGCTA
                                                                                                                                                                                                                                                          ctttgggggaggtcttcgaggggctctggaaagaccgggtccaggtggccattaaggtgat
                                                                                                                                                                                                                                                                         ttctcgagacaacctcctgcaccagcagatgctgcagtcggagatccaggccatgaagaa
                                                                                                                                                                                                                                                                                                                                                                                      ccreceecaceaececrecareceecrecaeceaecrecaececeeceeceeceaecrerera
                                                                                                                                                                                                                                                                                                                                                                                                                catcatcacggagctcatggccaagggcagcctgctggagctgctgcgcgactctgatga
                                                                                                                                                                                                                                                                                                                                                                                                                                        CATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCCCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaaagtcctgcccgtttcggaagctgctggacatcgcctggcaggtggctgagggcatgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttacctggagtcgcagaattacatccaccgggacctggccgccaggaacatcctcgtcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACGGCCTGGCCTGCAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTCAAGGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccgaggccattactccaccaaatccgacgtctggtcctttgggattctcctgcatgagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1245 TTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTGGCGCGCCTCTGCTGCAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaacgccggctaccgcatgccctcgcagagtgcccgcccagcgtgcacaagctgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGCGAGGGTACCGGCTGCCGCGCCCGGCTGCCTGCCCGGCGGAGGTCTACGTGCTCAT
                                                                                                                                                                                                                                                                                                                                   CAAGTCAGCCAACATGAAGCTC-A-CTGACCTCGCCAA-GGAGATCCAGACACTGAAGGG
                                                                                                                                                                                                                                                                                                                                                              gctgcggcacaaacacatcctggcgctgtacgccgtggtgtccgtgggggaccccgtgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggaaaacaccctctgcaaagttggggacttcggggttagccaggcttatcaaggaggacgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctacctctcc--catgaccac-aatatcccctacaagtggacggcccctgaagcgctctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gttcagcaggggtcaggtgccctacccaggcatgtccaaccatgaggccttcctgagggt
          Novel protein tyrosine kinase and its DNA - isolated from human breast tumour, useful for diagnosis and prognosis of cancerous
                                                                                                                                                                               9
                                                                                                                                                    Length 2507;
                                                                                                                                                 Score 191; DB 13; Length 25
Pred. No. 1.95e-101;
0; Mismatches 275; Indels
                                                                                                                                                   Query Match
12.3%;
Best Local Similarity 64.1%;
Matches 502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gct 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCT 1487
                                       tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1485
                                                                                                                                                                                                        571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1348
                                                                                                                                                                                                                                708
                                                                                                                                                                                                                                                         631
                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                           691
                                                                                                                                                                                                                                                                                                                                     828
                                                                                                                                                                                                                                                                                                                                                              751
                                                                                                                                                                                                                                                                                                                                                                                       885
                                                                                                                                                                                                                                                                                                                                                                                                                811
                                                                                                                                                                                                                                                                                                                                                                                                                                        945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
셤
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                οŽ
                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                   δ
```

```
1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cctgctgactgaccaccaaccaagggccgggtgccatacccagggatggtcaacaggga 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1170 GCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               870 CCAGACACTGAAGGGCCTGCGGCACGAGCGGCTCCATCCGGCTGCACGCAGTGTGCTCGGG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagetgggggcagggctgctttggagggtctggatggggacctggaacggcaccag 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 GAAGCTGGGTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCC 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        They can also
                                                                                                                                                                                                                                                                                                                                                                                                 cell migration, urokinase-type plasminogen activator activity, and reduced monourclear cell adhesion and fibronectin prodn The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have be used to improve the success of surgical procedures such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   873 agtggccataaagactctgaagcccggcaacatgtccccggaggccttcctgcaggaagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1050 GCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       993 ag---agcccatctacatcgtcactgagtacatgagcaaggggagcctcctggatttcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1050 gaagggagagatgggcaagtacctgcggctgccacagctcgtcgatatggctgctcagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1170 caacatcctggtggggggagaacctggtgtgcaaggtggctgactttgggctggcacgcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1110 GAACGIGCICGIGGACGACGGCCIGGCAGCIGGCIGACIICGGCCIGGCCCGGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catcgaggacaacgagtacacagcacggcaaggtgccaagttccccatcaagtggacagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1290 ccccgaggcagccctctatggccggttcaccatcaagtcggatgtctggtcttcggcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1230 GCCTGAGGCGCCCAATTATCGTGTTTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     810 CGTGGCGATCAAGGTCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 CGGGGAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                Genetically engineered endothelial cells – which exhibit enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coronary angioplasty, heart bypass surgery, vessel graft and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 1602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260; Indels
                                                                                                              ຮູ
                                                                                                              c-src;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.84e-93;
0; Mismatches 260
                                                                                                                                                                                                                                                                                                SL;
                                                                             Chicken pp60 c-src gene.
Endothelial; tyrosine kinase protein; pp60
                                                                                                                                                                                                                                                                                                Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 178;
                                                                                                                                                                                                                                                                                                   Madri JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
larity 63.4%;
Conservative
                                                       (first entry)
  standard; cDNA to
                                                                                                                                                                                                                                                                                                Luthringer DJ,
                                                                                                                                                                                       22-JUL-1993.
05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA.) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1602 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 456; Conser
                                                                                                                                                                                                                                                                                             Bell L, Luthringe
WPI; 93-243209/30.
P-PSDB; R39705.
                                                                                                                                     Gallus gallus.
WO9314193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implantation
                                                    23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
046687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οŻ
```

```
J03201994-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nisc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                1300
                                                                                                                                                        1231
                                                                                                                                                                                                   1360
                                                                                                                                                                                                                                                                                         1420
                                                                                                                                                                                                                                                                                                                                                                            1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938
                                                                                                         g
                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                        δλ
                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetically engineered endothelial cells - which exhibit enhanced T cell migration, urokinase type plasminogen activator activity, and reduced monouclear cell adhesion and fibronectin prodn and reduced monouclear cell adhesion and fibronectin prodn conscioure; Page 69-72; 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60 construction or produce increased amounts of pp60 constructions are dotterably to pp60 constructions of the constructions. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced monouclear cell adhesion. They can also coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
1060 aagggggagacaggcaagtacctgcggctgcctcagctggtggacatggctgctcagatc 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1110
                                                                                                                             943 caggicaigaagaagcigaggcaigagaagciggigcagitgiatgcigtggiltcaga- 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --ggagcccatttacatcgtcacggagtacatgagcaaggggagtttgctggactttctc 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1111 AACGIGCICGIGGACGACGGCCIGCCIGCAAGGIGGCIGACTICGGCCIGGCCCGGCIG 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         823 aagctgggccagggctgctttggcgaggtgtggatggggacctggaacggtaccaccagg 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 AAGCTGGGTGAAGGCTACTITGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTCCCTGCCC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931 GGGGAGCCTGTGTACATACTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 giggccatcaaaacccigaagcciggcacgaigtciccagaggcciiccigcaggaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1051 GCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.7%; Pred. No. 5.48e-77; es 442; Conservative 0: Mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 T;
                                                                                                                                                                                                                                                                                                                                                        SS
                                                                                                                                                                                                                                                                                                                                                        c-src;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warren SL;
                                                                                                                                                                                                                                                                                                                          Human pp60 c-src gene.
Endothelial; tyrosine kinase protein; pp60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 C;
                                                                                                                                                                                                                                         r 4
Q46688 standard; cDNA to mRNA; 1611 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
Bell L, Luthringer DJ, Madri JA,
WPI; 93-243209/30.
P-PSDB; R39705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 A;
                                                                                                                                                                                                                                                                                                      23-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1611 BP;
                                                                                                                                                                                                                                                                                                                                                                       Homo sapien.
W09314193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                046688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1002
                                                                                                                                                                                                                                       RESULT

23 A LO

24 A LO

25 A LO

26 A LO

27 A LO

28 A LO

28 A LO

29 A LO

20 A
                                        Dp
                                                                                   δý
                                                                                                                           g
                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
3
1240 attgaagacaatgagtacacggcgcggcaaggtgccaaattccccatcaagtggacggct 1299
                                                     1171 CTCAAGGACGACATCTACTCCCGGAGCAGCACCTCCAAGATCCCGGTCAAGTGGACAGCG 1230
                                                                                                                                                                                                                                                 1419
                                                                                                                                                                                                                                                                                                          gtgctggaccaggtggagcggggctaccggatgccctgcccggagtgtcccgagtcc 1479
                                                                                                                                                                                                                                                                                                                                                                                                                               tgaagcagctgcaaccagcggctggttcggctctacgctgtg-g-tcacccagg-agc 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 ccatctacatcactgaatacatggagaatgggagtctagtggattttctcaagaccc 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttcaggcatcaagttgaccatcaacaaactcctggacatggcagcccaaattgcagaag 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multi-cloning site.

Disclosure: Fig 4.2: 15pp; Japanese.

The sequence consists of the first 78 bp encoding the N-terminal amino acids of the beta galactosidase gene fused with the lck gene. It is prepd. by a claimed process in which a DNA contg. the lck gene is inserted into an E.Coll expression vector. The vector has DNA contg. part or all of the beta-galactosidase gene at the appropriate site of the multi-cloning site. It is useful for producing an antibody specifically immunoreactive with only a lck gene-derived polypeptide in T cells. The antibody may recognise lck gene-derived polypeptides in human cells.

Sequence 1254 BP; 291 A; 361 C; 365 G; 237 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcgcccacctt 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1411 GTCTACGTGCTCATGCTGCAGGAGGAGCAGCCCCGAGGAACGGCCCTCCTT 1466
                                                                                                                           ccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatc
                                                                                                                                                                                    CCTGAGGCGCCCAATTATCGTGTGTTTCTCCCAGAAGTCAGACGTCTGGGTCCTTCGGCGTC
                                                                                                                                                                                                                                             ctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "beta-galactosidase gene fragment"
/>po.1254 /
/*tag= b
/note= "lck gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1991 (first entry)
Lck gene fused with part of beta-galactosidase gene.
Multi-cloning site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 130; DB 2;
Pred. No. 2.36e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 5
Q13983 standard; DNA; 1254
Q13983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %.4%;
Local Similarity 62.1%;
hes 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TOKU ) TOKUYAMA SODA KK.
WPI; 91-300980/41.
P-PSDB; R14201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1991.
28-DEC-1989; 338268.
28-DEC-1989; JP-338268.
```

tyrosine kinase receptor

588 T;

836 G;

867 C;

ហ

ò

ò

g

ò

g

ò

g

ö

유

ö

셤

ò

ò

```
characterise potential (ant)agonists of rPTKs, study ligand receptor interactions, measure phosphatase activity and identify rPTK ligands
                  identify and characterise potential faut) agonists of TRR
Example 3; Fig12a-9; 148pp; English.

DNA constructs (T51456-58) respectively code for gD.trkA (W11940),

DNA constructs (T51456-58) respectively code for gD.trkA (W11940),

DL.KB (W11941) and gD.trkC (W11942), comprising fusions between
herpes simplex virus glycoprotein D filag polypeptide and human
receptor protein tyrosine kinases (FTKs) trkA, B and C, which are
involved in the interaction between neurotrophins and their target
cells. The gD.trk constructs can be expressed e.g. in dp12.CHO
host cells and used in kinase receptor activation, enzyme-linked
immunosorbent assays (KIRA BLISA) to measure autophosphorylation of
FPTK kinase domains. These assays are used to identify and
   Measuring auto-phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                          529 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 5.8%;
Local Similarity 61.6%;
nes 278; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T
V20445 standard; DNA; 2301
V20445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human c-trk oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                              clinical samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT

1D V2

AC V2

DT 17

DE HU

KW CA

CA

CA

PP 15

g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1076 agaacctggagcgaggctaccgcatggtgcgccctgacaactgtccagaggagctgtacc 1135
                                                                                                                                                                      1016 cggaaattgtcacccacggccgcatcccttacccagggatgaccaacccggaggtgattc 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1136 aactcatgaggctgtgctggaaggagcgcccagaggaccggcccacctttgactacctgc 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1418 TGCTCATGCTGGAGTGCTGGAGGAGCAGCCCCGGAGGAACGGCCCTCCTTTGCCACGCTGC 1477
                                                                              1058 GCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGGGAACGTGC 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9D.trkA fusion useful in kinase receptor activation assay.
Kinase receptor activation; KIRA; receptor protein tyrosine kinase;
rPTK; signal transduction; autophosphorylation; gD.trkA;
enzyme-linked immunosorbent assay; ELISA; ds.
                                                                                                                                                                                                                                                                                                                                                                       956 ccattaactacgggacattcaccatcaagtcagatgtgtggtcttttgggatcctgctga
                        gcatggcattcattgaagagcggaattatattcatcgtgaccttcgggctgccaacattc
                                                                                                                                                                                                                                                          896 acaacgagtacacagccagggagggggccaagtttcccattaagtggacagcgccagaag
                                                                                                                                       tggtgtctgacaccctgagctgcaagattgcagactttggcctagcacgcctcattgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/product= gD.trkA fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "begin gD from pchadIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong WLT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/note= "trkA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             early polyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "sp6 RNA start"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "mature trkA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sadick MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric herpes simplex virus; Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= f
/note= "SV40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .T 6
T51456 standard; DNA; 2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293..2740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461..2737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995.

18-NOV-1994; U13329.

23-NOV-1994; US-157563.

20-DEC-1993; US-170558.

05-AUG-1994; US-286305.

GETH) GENENTECH INC.

GGGOWSKI PJ, MARK MR, 6

WPI: 95-207042/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380..460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9514930-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1196 g 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1478 G 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_rna
                                                                                                                                       836
                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cds
```

```
present invention.
                                                                                                    ccctgggtctggggcagctggcggtggctagccaggtcgctgcgggggatggtacc 2267
                                                                                                                                   31-MAR-1998.
15-SEP-1994; 306691.
15-SEP-1994; US-306691.
15-SEP-1994; US-306691.
Calabretta B, Skorski T;
WPI; 98-229882/20.
Anticancer composition comprising two anti-sense oligo:nucleotide(s)
- targetting cytoplasmic and nuclear oncogene(s)
claim 1; Column 99-102; 32pp; English.
The present sequence represents an oncogene from the present inventi
                                                                                                                                                                                                                               tggcgggtctgcattttgtgcaccgggacctggccacacgcaactgtctagtggggccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCCCCGAGCAGCACCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgcagggacgtgagttggagcggccacgtgcctgcccaccagaggtctacgccatcatgc
                                                                                                                                                                                                                                                                                                                                                                                                              accgigigaggccgcaccatgctgccattcgctggatgccgcccgagagcatcctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accgtaagttcaccaccgagagcgacgtgtggagcttcggcgtggtgctctgggagatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcacctacggcaagcagccctggtaccagctctccaacaggaggcaatcgactgcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; c-trk; ds.
                                                      'n
Score 90; DB 28; Length 2820;
Pred. No. 2.17e-37;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggggctgctggcagcgggagccccagcaacg 2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1427 TGGAGTGCTGGAGGAGCAGCCCCGAGGAACG 1457
```

US-09-099-053-1.rng

```
The present invention describes a composition which comprises two antisense oligonuclectides. The first oligonuclectide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonuclectide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fgs, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha , AMLL/MTGB, E2A/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells, 403 T; 568 C; 785 G; 403 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccctggggtctggggcagctggcggtggctagccaggtcgctgcgggggatggtgtacc 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1803 accgtaagttcaccaccgagagcgacgtgtggagcttcggcgtggtgctctgggagatct 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense RNA molecule that inhibits expression of c-Abl gene product - useful in killing malignant cells in cancer, optionally in combination with DNA damaging agent the Example 9; Page 76-83; Il4pp; English.

The c-abl gene (161864 and 161865) encodes a non-receptor tyrosine kinase that is activated DNA damaging agents. Antisense constructs kinase that c-abl gene can be used to selectively inhibit the expression c-Abl following exposure of cells to a DNA damaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gactggtggtcaagattggtgattttggcatgagcagggatatctacaggcaccgactatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgcagggacgtgagttggagcggccacgtgcctgcccaccagaggtctacgccatcatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTGGCCTGCAAGGTGGCTGACTTCGGCCTG-GCCGGCTG-CTCAAGGAC-GACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accgtgtgggaggccgcatgctgcccattcgctggatgccgccgagagcatcctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1863 tcacctacggcaagcagccctggtaccagctctccaacagggaggcaatcgactgcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1367 receasestaccescrecescescescescesses receases and receases and receases receases and receases receases and receases receases receases and receases recease receases receases receases receases receases receases receased receases receased receases receases receases receases receases receases recease receases recease receases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natch 5.7%; Score 88; DB 40; Length 2301;
Local Similarity 61.9%; Pred. No. 3.65e-36;
Les 267; Conservative 0; Mismatches 161; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c-Abl gene; antisense RNA; cancer; therapy; DNA damage; radiotherapy; mitomycin C; cytostatic; tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kufe DW, Weichselbaum RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00-MAR-1997, 013922.
30-AUG-1995; US-520923.
(ARCH-) ARCH DEV CORP.
(DAND) DANA FARBER CANCER INST INC.
Kharbanda S, Kufe DW, Weichselbaum I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 8
T61865 standard; DNA; 5520 T
T61865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggggctgctgg 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1427 TGGAGTGCTGG 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9708184-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c-abl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT TO THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                    88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
```

```
1413
                                                                                                                                                                                                                                                                                                                                                1071
                                                                                                                                                                                                                                                                                                                                                                                                              1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1431
                                                                                                                                                                                                                                                                                    ccgtgaagaccttgaaggagacaccatggaggtggaagagttcttgaaagaagctgcag 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcagccatggagtacctggagaagaagacttcatccacagagatcttgctgcccgaaac 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatgagctgctagagaaggactaccgcatggagcgcccagaaggctgcccagagaaggtc 1551
                                                                                                                                                                                                                                                                                                                 873
                                                                                                                                                                                                                                                                                                                                                                               933
                                                                                                                                                           892
                                                                                                                                                                                       698 cccccaggcaggacgrgrggaggcgccacacrccgaarrcgcccrrgggaggaagcrgg 757
agent such as ionising radiation or mitomycin C. When used in combination with DNA damaging agents, the antisense RNA provides a synergistic cell killing effect useful for killing malignant cells
                                                                                                                                                          833 cccccaactacgacaagtgggagatggaacgcacggacatcaccatgaagcacaagctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tatgaactcatgcgagcatgttggcagtggaatccctctgaccggccctcctttgc 1607
                                                                                                                                                                                                                                                                                                                                                1013 tca-tgaaagagatcaaacaccctaacctggtgcagctccttggggtctgcacccgggag
                                                                                                                                                                                                                                                                                                                                                                                                              cccccgttctatatcatcactgagttcatgacctacgggaactcctggactacctgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcgggggccagtacgggggaggtgtacgagggggtgtggaagaaatacagcctgacggtgg
                                                                                                                                                                                                                                         CGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGA-GATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           934 GAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gagtgcaaccggcaggaggtgaacgccgtggtgctgctgtacatggccactcagatctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accecedadeseces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1054 GAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acaggggacacctacacagcccatgctggagccaagttccccatcaaatggactgcaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctttgggaaattgctacctatggcatgtccccttacccgggaattgacctgtcccaggtg
                                                                                                                                                                                                                                                                                                                                                                               gagagcctggcctacaacaagttctccatcaagtccgacgtctgggcatttggagtattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; c-abl; ds.
                                                               Ë
                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 330; Indels
                                                                                              Length
                                                               1593 G;
                                                                                            Score 81; DB 29; Pred. No. 6.68e-32;
                                                               1671 C;
                                                               1193 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
ID V20457 standard; DNA; 3623 BF
AC V20457;
DT 17-JUN-1998 (first entry)
DE Human c-abl oncogene.
DE Human; oncogene; proto-oncoge
KW cancer; antisense oligonuclec
OS Homo sapiens.
PN US5734039-A.
PD 31-MAR-1998.
                                                                                            / Match 5.2%;
Local Similarity 56.8%;
                                                                                                                           441; Conservative
                                                in cancer treatment
                                                            5520 BP;
                                                                  Seguence
                                                                                            Query Match
                                                                                                                             Matches
                                                                                                                                                                                                                        893
                                                                                                                                                                                                                                                                                                                                                                                                              1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1432
                                                                                                                                                                                                                                                                                    953
                                                                                                                                                                                                                                                                                                                 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1312
                                                                                                                                                                                                                                                     758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1372
 888888
                                                                                                                                                          g
                                                                                                                                                                                       δ
                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                 ÓΣ
                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
Homo sapiens.
WO9708184-A1.
                                                                                                                                                                                                                     T61864;
06-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                           NAME OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                Tricancer composition comprising two anti-sense oligo:nucleotide(s)

- targetting cytoplasmic and nuclear oncogene(s)

- targetting cytoplasmic and nuclear oncogene(s)

- targetting cytoplasmic and nuclear oncogene from the present invention.

The present sequence represents an oncogene from the present invention.

The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-fms, c-ros, c-kit, c-spi, cytoplasmic oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cytoplasmic oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cytoplasmic selected from is used for treating cancer. The composition is used for treating cancer. The composition of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1252 tgcctggtaggggagaaccacttggtgaaggtagctgattttggcctgagcaggttgatg 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatgagctgctagagaaggactaccgcatgaagcgcccagaaggctgcccagagaggtc 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcgggggccagtacggggaggtgtacgagggcgtgtggaagaaatacagcctgacggtgg 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              934 GAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGC 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccccaactacgacaagtgggagatggaacgcacggacatcaccatgaagcacaagctgg 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCGAGGCAGGACGTGTGGGAGCGCCACACTCCGAATTCGCCCTTGGGAGGAAGCTGG 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGAAGGCTACTTTGGGGAGGTGTGGGAAGGCCTGTGGCTGGGCT-C--CCTGCCCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cogtgaagaccttgaaggaggacaccatggaggtggaagagttcttgaaagaagctgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGATCAAGGTCATCAAGTCAGCCAACATGAAGCTCACTGACCTCGCCAAGGA-GATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tca-tgaaagagatcaaacaccctaacctagtgcagctccttgggggtctgcacccgggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcagccatggagtacctagagaagaaaacttcatccacagagatcttgctgccgaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCTCGTGGACGACGCCTGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1312 acaggggacacctacacagcccatgctggagccaagttccccatcaaatggactgcaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagagcctggcctacaaacaagttctccatcaagtccgacgtctggggcatttggagtattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072 cccccgttctatatcatcactgagttcatgacctacgggaacctcctgggactacctgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gagtgcaaccggcaggaggtgaacgccgtggtgctgctgctacatggccactcagatctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctttgggaaattgctacctatggcatgtccccttacccgggaattgaccgttcccaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score 79; DB 40; Length 362
red. No. 1.08e-30;
0; Mismatches 331; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79;
Pred. No.
15-SEP-1994; US-306691.
(UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%;
Best Local Similarity 56.7%;
Matches 440; Conservative
                                                                     Calabretta B, Skorski T;
WPI; 98-229882/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953
```

QQ

ò

g

엄 ò 유 ò g ά g

ò

g

ò

QQ

ö g ò

ö

g

요

ò

οy

g

```
1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccccqttctatatcatcatcaggttcatgacctacgggaacctcctggactacctgagg 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1050 cccccaactacgacaagtgggagatggaacgcacggacatcaccatgaagcacaagctgg 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcggggccagtacgggggaggtgtacgagggcgtgtggaagaaatacagcctgacggtgg 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acaggggacacctacacagcccatgctggagccaagttccccatcaaatggactgcaccc 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marbanda S, Kufe DW, Weichselbaum RR:
MPI; 97-179167/16.
Antisense RNA molecule that inhibits expression of c-Abl gene
product - useful in Killing malignant cells in cancer, optionally in
Example 9; Page 70-75; 114pp; English.

Example 9; Page 70-75; 114pp; English.

The c-abl gene (F61864 and T61865) encodes a non-receptor tyrosine
Kinase that is activated DNA damaging agents. Antisense constructs
Ainase that is activated by admaging agents. Antisense constructs
Adirected to the c-abl gene can be used to selectively inhibit the
expression c-Abl following exposure of cells to a DNA damaging
agent such as ionising radiation or mitomytch C. When used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
combination with DNA damaging agents, the antisense RNA provides a synergistic cell killing effect useful for killing malignant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccgtgaagaccttgaaggacaccatggaggtggaagagttcttgaaagaagctgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gagtgcaaccggcaggaggtgaacgccgtggtgctgtacatggccactcagatctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1114 GIGCICGIGGACGACGGCCTGGCTGCAAGGIGGCTGACTICGGCCTGGCCCGGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   698 CCCCGAGGCAGGACGTGGGGAGCGGCCACACTCCGAATTCGCCCTTGGGAGGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tca-tgaaagagatcaaacacctaacctagtgcagctccttggggtctgcaccggggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcagccatggagtacctagagaagaagaaattcatccacagagatcttgctgcccgaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1054 GAGGCCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCCCGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgcctggtagggggaaccacttggtgaaggtagctgattttggcctgagcaggttgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         934 GAGCCTGTGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ι,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 5.1%; Score 79; DB 29; Length 3780; Local Similarity 56.7%; Pred. No. 1.08e-30; nes 440; Conservative 0; Mismatches 331; Indels
                                                                                                                                                                                                                                                                                                                           SS.
                                                                                                                                                                                                                                                                                             cancer; therapy; DNA damage; cytostatic; tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1166 G;
                                                                                                                                                                                                                                                                                                                                                                                 WOY, ver. 1997.

06-MAR-1997.

30-AUG-1995; US-520923.

A (ARCH-) ARCH DEV CORP.

A (DAND ) DANA FARBER CANCER INST INC.

"--handa S, Kufe DW, Weichselbaum RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1136 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 A;
                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                         c-abl gene.
c-Abl gene; antisense RNA;
radiotherapy; mitomycin C;
                                                                                                                                          r 10
r61864 standard; DNA; 3780
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3780 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1529
```

φ

```
448 cccgcctgggtgtatgccctcatgatcgagtgctgga 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                        328
                                                                                                                                  388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                               ID DATE OF THE PROPERTY OF T
                                                                            δ
                                                                                                                               g
                                                                                                                                                                                   ò
                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying agonists and antagonists, and new recombinant cells for identifying agonists and antagonists, and new recombinant cells and nucleic acid producing trkB, for diagnosis and treatment of neurological disease

Disclosure: Fig 15; 156pp; English.

The sequence is that of potential tyrosine kinase receptor fragment RR-3, isolated from cDNA from human neuroblastoma cell line SY9Y. It may be of use in the treatment of neurodegenerative disease/neurotrauma including motor neuron disorders such as amyotrophic lateral sclerosis, werding-Hoffman disease, chronic proximal spinal muscular atrophy and cuillain-Barre syndrome. It may also be of use in the treatment of neurological disorders associated with diabetes, Parkinson's disease, Alzheimer's disease and Huntington's chorea. See also Q30715-Q30728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>;</u>
                                                                                                                                                                                                                                                               1709 tatgagctgctagaaggaactaccgcatgaagcgcccagaaggctgcccagagaaggtc 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagategeggeggggatggagtacetatecageeaceaegtggtteacaaggaeetggee 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    1769 tatgaactcatgcgagcatgttggcagtggaatccctctgaccggccctcttgc 1824
1174 AAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCT
                                                                                                    1234 GAGGCGCCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGTCCTG
                                                                                                                                                        1649 ctttgggaaattgctacctatggcatgtccccttacccgggaattgaccgttcccaggtg
                                                                                                                                                                                                           148 accegeaatgtgetagtgtacgacaagetgaacgtgaagateteagaettgggeetette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgagaggtgtatgccgccgattactacaagctgctggggaactcgctgctgcctatccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1165 CGGCTGCTCAAGGACGACATCTACTCCCCGA-GCAGCAG--CTCCAAGATCCCGGTCAAG
                                              1589 gagageetggeetacaacaagttetecateaagteegaegtetggggeatttggagtattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1105 GCCCGGAACGTGCTCGTGGACGACGGCCTGGCCTGCAAGGTGGCTGACTTCGGCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggatggccccagaggccatcatgtacggcaagttctccatcgactcagacatctggtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1991; US-690199.
26-JUL-1991; US-736559.
(REGE-) REGENERON PHARM INC.
Addrich TH, Distephano P, Furth ME, Glass D, Masiakowski, Maison-Pierre PC. Squinto SP, Stitt T, Yancopoulos GD; WPI; 92-381778/46.
P-PSDB; R28605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 4.9%; Score 76; DB 5; Length 755; Local Similarity 61.5%; Pred. No. 6.98e-29; nes 244; Conservative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1993 (first entry)
Potential tyrosine kinase receptor fragment RTK-3.
Tyrosine kinase receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r 11
Q30725 standard; DNA; 755 BP.
Q30725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1992; U03376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09218149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                           1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESCIENCE OF THE SCIENCE OF THE SCIE
                                              g
                                                                                                                                                     g
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                    ò
                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1999 (first entry)
Rat orphan tyrosine kinase receptor RTK-3 encoding DNA.
Receptor tyrosine kinase, Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
neurotrophin activity; trKB; proto-oncogene; tyrosine kinase receptor;
binding protein; BDNF; NT-3; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example, Fig 15; 194pp; English.

The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins: Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat orphan tyrosine kinase receptor Rtk-3 from the present invention.

Sequence 755 BP; 147 A; 257 C; 217 G; 134 T;
                                                                                                                                                                             1342 AACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCGCCCGGGTGCCTGC 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1045 CAGGIGGCIGAGGGCAIGAGCIACCIGGAGGAGCAGCGCGIIGIGCACCGGGACIIGGCC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1165 CGGCTGCTCAAGGACGACATCTACTCCCCGA-GCAGCAG--CTCCAAGATCCCGGTCAAG 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1222 TGGACAGCGCCTGAGGCGCCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagatogoggogggatggagtacctatccagccaccacgtggttcacaaggacctggcc 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 acccgcaatgtgctagtgtacgacaagctgaacgtgaagatctcagacttgggcctcttc 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \ensuremath{\mathsf{DNA}} encoding receptor tyrosine kinase proteins - and corresponding proteins
                            1282 TICGGCGTCCTGCTGCACGAGGTTTTCACCTATGGCCAGTGTCCCTATGAAGGGATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgagaggtgtatgccgccgattactacaagctgctggggaactcgctgctgcctatccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaccaggatgtggagatgatccggaaccggcaggtgctgccttgccccgatgactgt
tacggtgtggtcctgtggggaggtcttcagctacggcctgcagccctactgcgggtattcc
                                                                                                                    aaccaggatgtggtggagatgatccggaaccggcaggtgctgccttgccccgatgactgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tggatggccccagaggccatcatgtacggcaagttctccatcgactcagacatctggtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tacggtgtggtggtgggaggtcttcagctacggcctgcagcctactgcgggtattcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; DB 54; Length 755; Pred. No. 6.98e-29; 0; Mismatches 150; Indels
                                                                                                                                                                                                                                      (REGE-) REGENERON PHARM INC.
Maisonpierre PC, Masiakowski P, Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                 JT 12
V70224 standard; DNA; 755 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 4.9%;
Local Similarity 61.5%;
les 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1993; US-144992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995; US-469537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 99-044584/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W83166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
US5843749-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1998
```

σ

ò

```
Breast; cancer; matk; CSK homologous kinase; CHK; detection; diagnosis; cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator; mitogenic signalling; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1106 tgtacattgtcatggagcacgtgagcaagggcaacctggtgaactttctgcggacccggg 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1226 tggagtacctggagagagcaagagcttgtgcaccgcgacctggccgccgcacatcttgg 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy
Claim 7; Page 49-50; Sapp; English.
This DNA encodes a cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation. It was isolated from the human UT-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are usful for screening agents for inhibiting or activating activity on the tyrosine kinase, for sequence 1942 BP; 85 A; 615 C; 651 G; 311 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       941 TGTACATAGTCACGGAACTCATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1166 gtcgagccctcgtgaacaccgctcagctcctgcagttttctctgcacgtggccgagggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1061 IGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGGAACGTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encodes N-terminally truncated form of the common (co. p71122)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 14; Length 1942;
Pred. No. 4.18e-24;
0; Mismatches 78; Indels (
                                                                                                                                                                                                                                                                                                                                            domain (see
DNA encoding cytoplsmic tyrosine kinase. cytoplasmic; tyrosine kinase; blood; cell differentiation; screening; anticancer agent; ds.
                                                                                                                                                                                                                                                                                 R71130)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic tyrosine kinase and antibody recognising it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1121 TGGACGACGGCCTGGCTGCAAGGTGGCTGACTTCGGCCTGGCC 1164
                                                                                                                                        /product= cytoplasmic_tyrosine_kinase
/note= "see R71133"
349..540
                                                                                                                                                                                                                                                                                                                    /*tag= d
/note= "encodes tyrosine kinase
                                                                                                                                                                                                                          (see
                                                                                                                                                                                                                                                                                   (see
                                                                                                                                                                                                 /*tag= b
/note= "encodes SH3 domain
                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                            of the enzyme (see R71132)
                                                                                                                                                                                                                                                               /*tag= c
/note= "encodes SH2
                                                                             Location/Qualiflers
208..1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1995.
25-AUG-1994; J01411.
25-AUG-1993; JP-210403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 15
V44497 standard; cDNA; 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.2%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V44497;
16-OCT-1998 (first entry)
Human matk cDNA.
                                                                                                                                                                                                                                                                                                                                                            R71131)"
331..1728
                                                                                                                                                                                                                                                                                                 ..1641
                                                                                                                                                                                                                                        571..795
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= e
                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-106842/14
P-PSDB; R71129-33
                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakano S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
ID V4
AC V4
DT 16
DE HU
KW Br
KW CY
        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 27; 194pp; English.

The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins: Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes human ROR-2. Sequence 4092 BP; 884 A; 1229 C; 1171 G; 808 T;
                                                                                                                  V70230;
11-FEB-1999 (first entry)
Human receptor tyrosine kinase ROR-2 encoding DNA.
Receptor tyrosine kinase; ROr-1; ROr-2; Ehk-1; Ehk-2; detection;
neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
binding protein; BDNF; NT-3; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2291 aaccaggatgtggtggagatgcggaaccggcaggtgctgcttgccccgatgactgt 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1991 cagatcgcggcggggatggagtacctatccagccaccactggttcacaaaggacctggcc 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2051 accogcaatgigctagigtacgacaagcigaacgigaagatcicagactigggccictic 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2111 cgagaggtgtatgccgccgattactacaagctgctggggaactcgctgctgcctatccgc 2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tacggtgtggtcctgtgggaggtcttcagctacggcctgcagccctactgcgggtactcc 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1282 TTCGGCGTCCTGCTGCAGGTTTTCACCTATGGCCAGTGTCCCTATGAAGGGATGACC 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1045 CAGGTGGCTGAGGGCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1165 CGGCTGCTCAAGGACGACATCTACTCCCCGA-GCAGCAG--CTCCAAGATCCCGGTCAAG 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 regacadedecregadecedecaarrarcerererereceagaagreagaceregere 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding receptor tyrosine kinase proteins - and corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1105 GCCCGGAACGTGCTCGTGGACGACGGCCTGCCAAGGTGGCTGACTTCGGCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggatggccccagaggccatcatgtacggcaagttctccatcgactcagacatctggtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76; DB 54; Length 409
Pred. No. 6.98e-29;
0; Mismatches 150; Indels
  1402 cceccesacercracercrarecresacresa 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masiakowski P, Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 14
084888 standard; cDNA to mRNA; 1942 BP.
084888;
26-OCT-1995 (first entry)
                                                                                                                                                                                                                                                        Location/Qualifiers 200..3031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.9%;
Best Local Similarity 61.5%;
Matches 244; Conservative
                                                                             т 13
V70230 standard; DNA; 4092
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                 /*tag= a
                                                                                                                                                                                                                                                                                                                                    01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-146952.
06-JUN-1995; US-469537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99-044584/04.
P-PSDB; W83168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonpierre PC,
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                      US5843749-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2171
                                                                                                                                                                                                                                                               Key
                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
```

셤

셤

ò

ò

8

ò

g

g

8

硆

ò

g

ò

ò

ö

Gaps

ö

```
FIT Key 263.1846

74197 Another CHK

WOOSB30704-A1.

WOOSB3070
```

```
Query Match

Query Match

Best Local Similarity 65.2%; Pred. No. 4.18e-24;

Matches 146; Conservative 0. Mismatches 78; Indels 0; Gaps 0;

Db 1161 tgtacattgtcatggagcaagggcaacctggtgaactttctggggacccggg 1220

Qy 941 TGTACATAGTCACGAACTCATGCCAAGGGGAACCTGCAGGCCTTCCTGGGGGACCCCCC 1000
```

g

1121 TGGACGACGCCTGCCTGCAAGGTGGCTGCATTCGGCCTGGCC 1164

Search completed: Thu May 20 15:22:29 1999 Job time : 1433 secs.

vz75d05.rl Soares mous stray9f04.rl Soares_NHHM Exf00140 Activated T-c yx73h12.rl Scares meta mn85b11.rl Stratagene qz48f07.xl NCI_CGAP_Ki A023R Heat. Britatagene Ex7180795 Jurkat T-cel zk26h10.rl Scares_preg my22f12.rl Scares_preg my22f12.rl Barstead mo ve29ff03.rl Knowles Sol ve2b12.rl Scares_mult zx56a12.rl Scares_mult zx56a12.rl Scares_feta Lib39618.sprime LD Dros vk45e12.rl Scares_mous mz5a06.rl Barstead mo o919a12.xl NCL_CGAP_Ki 97SN1787 Rice Immature Sc22G05 Porcine small syu05h03.rl Scares_tota zw90c01.rl Scares_tota qz17c04.xl NCL_CGAP_Cl yu85677.rl Scares_tota qz17c04.xl NCL_CGAP_Cl yu80507.rl Scares mous

ALLS9486

AA256288

N3236285

N3236285

AA098002

AA098002

AA098002

AA098002

AA098002

AA098002

AA098002

AA098002

AA09806

AA098002

 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00
 0.00

US-09-099-053-1.rst

		O (
	(ML)	υ
Release 3.1A John F. Col. Copyright (c) 1993-1998 Distribution rigi	3.1A John F. Collins, Biocomputing Research Unit. t (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	υ
MPsrch_nn n.a n.a.	database search, us	
Run on: Thu May 20 Tabular output not generated	7 20 13:27:11 1999; MasPar Line 2933.07 Seconds 1236.663 Million cell updates/sec ated.	U
Title: >US-09- Description: (1-1548 Perfect Score: 1548 N.A. Sequence: 1	>US-09-099-053-1 (1-1548) from US09099053.seq 1548 I GTCGCGGGCTCCCATGGC	υ
Scoring table: TABLE d Gap 6	default	
Nmatch STD : Dbase 0	0; Query 0	υ
Searched: 2883791	. segs, 1171580779 bases x 2	
Post-processing: Minimum Listing	Minimum Match 0% Listing first 45 summaries	
Database: embl-est58	bl-est58 1:em_est10_2:em_est11 3:em_est17 4:em_est18 5:em_est2	RES
Database: genbank 8:0b- 13:0b 17:9b 27:9b 25:9b	/:em_gss1 9:gb_est10 10:gb_est11 4 14:gb_est15 15:gb_est 8 18:gb_est19 19:gb_est 1 22:gb_est22 23:gb_est 5 26:gb_est26 27:gb_est 9 30:gb_est3 31:gb_est	DEF ACC NID VER KEY
34:9b 39:9b	35:gb_est8	0
Statistics: Mean 11.202;	202; Variance 2.630; scale 4.260	REF

1.11e-151 1.41e-151 1.02e-111 4.49e-110 6.77e-103 6.77e-103 6.77e-95 8.90e-94

vp06c03 r1 Scares mous vz45q04.r1 Scares 2NbM EST63065 Jurkat T-cell vs36h03.r1 Stratagene vq48h02.r1 Barstead bo EST177341 Jurkat T-cel z141g09.r1 Scares_preg 71B11 Human retina CDN mu04h04.r1 Scares con zt98e10.r1 Scares_test

AA763708 AA940351 AA354687 AA646158 AA646158 AA869202 AA306381 AA149096 AA149096 AA20981 AA420981

13 13 13 13 13 13 13 13 13

639 334 634 553 577 724 586

77.000000000

1122 1110 93 93 93 93 88 87 83

108433710

ě

Description

DB

Length

Score

Result No.

% Query Match

the number of results predicted by chance to have a than or equal to the score of the result being printed of by analysis of the total score distribution.

Pred. No. is the score greater th and is derived b SUMMARIES

Source

FEATURES

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 547) Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Marra,M., Hillier,L., Allen,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU HHMI Mouse EST Project
WashU HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1026 ACTCCTGGGCTTTGCCTGCCAGGTGGCTGAGGCCATGAGCTACCTGGAGGAGCAGCGCGT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1206 CAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAA 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1266 Greadacereregreerresegerecrecrecrecaceaegrinicaceraregeeagrere 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AGAATTTCCCATTAAGTGGACAGCACCAGAAGCCATTAACTATGGGACCTTCACCATCAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 ACTITIGGACAIGGCAGCCCAGAIIGCAGAGGGCAIGGCGIICCAICGAAGAACAGAAITA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 CATCCATCGGGACCTGCGCGCCGCCAACATCCTGGTGTCTGACACGCTGAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1086 TGTGCACCGGGGACTTGGCCGCGGGAACGTGCTCGTGGACGACGCTGGCCTGCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 TGCAGACTTTGGCCTGGCGCGCCTCATTGAGGACAATGAGTACACGGCCCGGGAAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1146 GGCTGACTTCGGCCTGGCCCGGCTGCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 GTCAGACGTGTGGTCCTTCGGGATCTTGCTTACAGAGATCGTCACCCACGGTCGAATCCC
                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2287662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.41e-131;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.1%; Score 110; DB 21; Best Local Similarity 62.1%; Pred. No. 1.41e-131; Matches 282; Conservative 0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 483.
Location/Qualifiers
1. .547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1329462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="4 weeks"
/lab_host="DH10B"
155 c 143 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 g
        Mus musculus
                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:689006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                      REFERENCE
                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                   I 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pryray vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatina
                                                                                                                                                                                                                 /strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA940351 547 bp mRNA EST 01-MAY-1998 vz45904.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1329462 5' similar to gb:M12056 Mouse rearranged lck gene encoding lymphocyte-specific protein (MOUSE);, mRNA sequence.
AA940351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1198 AGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGGCCAATTATCGTGTTTT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1018 CTGCCGCCACTCCTGGGCTTTGCCTGCCAGGTGGCTGAGGCCATGAGCTACCTGGAGGAG 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1078 CAGCGCGTTGTGCACCGGGACTTGGCCGCGGGAACGTGGTGGACGACGACGGCCTGGCC 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1138 recaasgreecreacricescerescecescrecreaassacareracreecesase 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1258 TCCCAGAAGTCAGACGTCTGGTCCTTCGGCGTCCTGCTGCTGCAGGGTTTTCACCTATGGC 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1318 CAGTGTCCCTATGAAGGGATGACCAACCACGAGACGTGCAGCAGAGATCATGCGAGGGTAC 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1378 CGGCTGCCGGCCCGGCTGCCTGCCCGGCGAGGTCTACGTGCTCATGCTGGAGTGCTGG 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 GAAGGAGCCAAGTTCCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGTTCCTTC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 ACCATCAAGTCAGATGTCTGGTCCTTTGGTATCCTGCTGATGGAAATTGTCACCTATGGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 CGGATCCCTTACCCAGGTATGTCAAACCCAGAGGTGATTCGGGCACTAGAGCATGGGTAC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 CIGCCAAAACICATIGACTICICAGCCCAGAICTCAGAAGGCAIG-GCTICATIGAGCAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AGGAACTACATCCACCGAGACCTGAGGGCTGCCAACATCTTAGTCTCTGCATCACTGGTG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 CGTATGCCTCGACCAGATAACTGTCCAGAAGAGCTCTACAATATCATGATCCGCTGCTGG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 TGTAAGATTGCTGACTTTGGACTGGCACGAATCATCGAGGACAATGAGTACACAGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1067812"
/clone_lib="Soares mouse mammary gland NbMMG"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 122; DB 18; Length 639
Pred. No..1.11e-151;
0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 474. Location/Qualifiers ...
                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 AAGAACCGCCCCGAGGAACGGCCCACCTTTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA940351.1 GI:3099895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93099895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289;
```

Query Match

Matches

δ g Qγ g δ g ò g ò qq δy g οχ g

BASE COUNT ORIGIN

ö

ö

1145

1205

224

~

RESULT

LOCUS

ACCESSION

KEYWORDS SOURCE

VERSION

Length 336;

```
Query Match 6.3%;
Best Local Similarity 65.7%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA646158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                            а
                                                                                                                                          ô
                                                                                                                                                                                     유
                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J.D., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fitchman, J.L., Geoghagen, N.S.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Fenzie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y. F., Wing, J., Li, H., Meissner, P.S., Olsen, H.,

Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699055
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                 /organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                         1326 CTATGAAGGGATGACCAAACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCC 1385
345 TTACCCAGGAATGACCAACCCTGAAGTCATTCAGAACCTGGAGAGAGGCTACCGCATGGT 404
                                                                                                                                                                                                                                                                                                                           AA354687 336 bp mRNA EST 21-APR-1997
EST63065 Jurkat T-cells V Homo sapiens cDNA 5' end similar to
                                                                                         GAGACCTGACAACTGTCCGGAAGAGCTGTACCACCTCATGATGCTGTGCTGGAAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Apr 14, 1993 this sequence version replaced gi:785388 Other_ESTs: THC170446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="ATCC (inhost):155014"
/db_xref="taxon:9606"
/map="2; 13412"
/clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
a 95 c 93 g 65 t
                                                                                                                                                                                                              1446 CCCCGAGGAACGCCCTCTTTGCCACGCTGCGG 1479
                                                                                                                                                                                 465 CCCAGAGGACCGGCCCACGTTTGACTACCTTCGG 498
                                                                                                                                                                                                                                                                                                                                                                      tyrosine kinase lck, mRNA sequence.
AA354687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     g2007078
AA354687.1 GI:2007078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                       405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                              g
                                                                                                                                                                                                                               ò
                                           ò
                                                                                    g
                                                                                                                                     ö
```

```
/organism="Mus musculus"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
Corst; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 634)
Mariar, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vs36h03.rl Stratagene mouse Tcell 937311 Mus musculus CDNA Clone IMAGE:1140341 5' similar to gb:X13529 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (HUMAN); gb:X03533 Mouse mRNA for tyrosine protein kinase p56-tck (MOUSE);, mRNA sequence. AA646158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:621613
                                                                                                                                                                                                                                                                                1261 CAGAAGTCAGACGTCTGGGCGTCCTGCTGCAGGTTTTCACCTATGGCCAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1141 AAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTCAAGGACGACATCTACTCCCCGAGCAGC 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                         61 GGGCCCAAGTTTCCCATTAAGTGGACAGCGCCAGAAGCCATTAACTACGGGACATTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                 121 ATCAAGTCAGATGTGTGTGTTTTTGGGATCCTGCTGACGGAAATTTTCACCCACGGCCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ATGGTGCGCCCTGACAACTGTCCAGAGGAGCTGTACCAACTCATTGAGGCTGTGCTGGAA 300
                                                                                                    1 AAGATTGCAGACTTTGGCCTAGCACGCCTCATTGAGGACAACGAGTACACAGCCAGGGAG 60
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AICCCTTACCCAGGGAIGACCAACCCGGAGGIGATICAGAACCTGGAGCGAGGCTACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 12, 1996 this sequence version replaced g1:1407219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; cont
                                       ï
                                0; Mismatches 112; Indels
Pred. No. 1.02e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28ml3 revl ET from Amersham High quality sequence stop: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1440 GAGCACCCGAGGAACGCCCTCTTTG 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R. The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GGAGCGCCCAGAGGACCGGCCCACCTTTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92572587
AA646158.1 GI:2572587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   634 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996
```

셤

ò

ద

δ g δŽ g

g

Q

. Q

ò

g

ò

 \dot{Q}

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                              ä
3′ ~3′ adaptor sequence: 5′ CTCGAGTTTTTTTTTTTTTTTT 3′"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                              1104 CGCCCGGAACGTGCTCGTGGACGACGCCTGCCAGGTGCTGGACTTCGGCCTGGC 1163
                                                                                                                                                                                                                                                                                                                                                       1164 CCGGCTGCTCAAGGACGACGACTTTACTCC-CCGAGCAGCAGCTCCAAGATCCCGGTCAAGT 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1283 resecercerserseassatrreacerarsseassatreacerarsasses 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303
                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                    GCGCCTCATTGAGGACAATGAGTACACGGCCCGGGAGGGGCCACAATTTCCCATT-AAGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 CGGAAGAGCTGTACCACCTCATGATGCTGTGGAAGGAGCGCCCAGAGGACCGGCCCA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA869202 553 bp mRNA EST 16-MAR-1998 vq48h02.rl Barstead bowel MPLRB9 Mus musculus cDNA clone IMAGE:1097523 5'.similar_to_gb:M64608 Mouse lyn protein mRNA.complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                GGACAGCACCAGAAGCCATTAACTATGGGACCTTCACCATCAAGTCAGACGTGTGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TCGGGATCTTGCTTACAGAGATTGTCACCCACGGTCGAATCCCTTACCCAGGAATGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ACCCTGAAGTCATTCAGAACCTGGAGAGGCTACCGCATGGTGAGACCTGACAACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gi:2282426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                              5;
                                                                                                                                                                           Length 634;
                                                 Tcell 937311"
                                                                                                                                                                                                              Indels
                                                                                                         resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Jan 19, 1998 this sequence version replaced
                                                                                                                                                                         Score 97; DB 16; Le
Pred. No. 4.49e-110;
0; Mismatches 133;
                             /clone="IMAGE:1140341"
/clone_lib="Stratagene mouse Tc
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA869202.1 GI:2964647
                                                                                                                                                                         6.3%;
llarity 64.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1463 CCTTTGCCACGCTGCGG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 CGTTTGACTACCTTCGG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                            Local Similarity
les 242; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                        150
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                വ
                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

```
ö
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:603755
Seg primer: -20ml3 rev2 ET from Amersham
High quality sequence stop: 505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGACATCTACTCCCCGAGCAGCAGCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-1997
end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGTCCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TGAAGACCTTGCAACATGACAAGCTAGTGCGGCTGTACGCTGTGGTCACCAAGGAGGAGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   878 TGAAGGGCCTGCGGCACGAGCGGCTCATCCGGCTGCACGCAGTGTGCTCGGGCCGGGGAGC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 CCATCTACATCACCGAGTTCATGGCTAAGGGTAGTTTGCTGGATTTCCTCAAGAGTG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTGGACGACGCCTGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AIGAAGGIGGCAAGGIGCIGCIGCCCAAGCICATIGACITCICGGCCCAGAITGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATGGCGTACATCGAGCGGAAGAACTACATCCACCGTGATCTGCGAGCTGCTAACGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1058 GCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGGAACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTCTCTGAGTCACTCATGTGCAAGATTGCAGACTTTGGCCTCGCGAGAGTCATCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCATCAACTICGGCTGCTICACTATCAAATCTGACGTGTGGTCCTTCGGAATTCTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAACGAGTACACAGCAAGGGAAGGTGCGAAGTTCCCTATCAAGTGGACAGCTCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA306381 577 bp mRNA EST
EST177341 Jurkat T-cells VI Homo sapiens cDNA 5'
similar to tyrosine kinase lck, mRNA sequence.
AA306381
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1097523"
/clone_lib="Barstead bowel MPLRB9"
/fissue_type="bowel"
/dev_stage="8 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 93; DB 20; L
Pred. No. 1.58e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAGATTGTCACCTATGGGAAGGATCCCTA 546
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĀA306381.1 GI:1958708
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 6.0%;
L Similarity 60.3%;
272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q1958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local
```

S

```
1118 TCGTGGACGACGGCCTGGCCTGCAAGGTGGCTGACTTCGGCCTGGCCCGGCTGCTCAAGG 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA149096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                  1238
                                                                                                                                                                                                                                                                                                                                                                                               1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                               원
                                                                                                  οy
                                                                                                                                               9
                                                                                                                                                                                                                                               DD.
                                                                                                                                                                                                                                                                                                  Óγ
                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                  δy
                                   Eucharyota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eucharyota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fitne, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Kalley, J.M., Kalley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.Tar:Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGGGCCGGCCCTGCGTCTGCCGCCACTTTGCCTGCCAGGTGAGG 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 GCATGAGCTACCTGGAGGAGCAGCGCGTTGTGCACCGGGACTTGGCCGCCGGGAACGTGC 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIGIGIACAIAGICACGGAACICAIGCGCAAGGGGAACCIGCAGGCCTICCIGGGCACC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCTACATCATCATCATGAATACATGGAGAATGGGAGTCTAGTGGATTTTCTCAAGACCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TGAAGCAGCTGCAACACCCAGCGGCTGGTTCGGCTCTACGCTGTG-G-TCACCCAGG-AGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCAGGCATCAAGTTGACCATCAACAAACTCCTGGACATGGCAGCCCAAATTGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGGCATTCATTGAAGAGCGGAATTATATTCATCGTGACCTTCGGGCTGCCAACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 IGGIGICTGACACCCIGAGCIGCAAGAITGCAGACTITGGCCTAGCACGCCTCATIGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 21, 1992 this sequence version replaced gi:276421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 11; Length 577;
Pred. No. 6.77e-102;
0; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
The Institute for Genomic Research
The Modical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="ATCC (inhost):160506"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
163 c 149 g 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .577
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.7%;
Matches 328; Conservative
                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                  REFERENCE
                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
/organism="Homo sapiens"
/note="Organ: uterus; Vector: pT713-Pac; Site_1: Not I:
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                      Z141909.T1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:504544 5' similar to gb:M16591 TYROSINE-PROTEIN KINASE HCK (HUMAN), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 748 Std Error: 0.00
Seq primer: -28M13 rev2 from Anersham
High quality sequence stop: 381.
Location/Qualifiers
                                                                                                                                                1297
                                                                                                                                                                                                                                                                                                                                          CAGCAGATCATGCGAGGGTACCGGCTGCCCGGCTGCTGCCGGGGGAGGTCTAC 1416
                                                                                                                                                                                                                                                                                                   571
                                                                                                                                                                                                 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 467)

Hiller, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Materston, R., Milliamson, A., Wohldmann, F., Trevaskis, E., Wash Wackeston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                            453 CGGAAATTGTCACCCACGGCCGCATCCCTTACCCCAGGGATNACCAACCCGGAGGTGATT
                                                                                                                                                                                                                                1298 ACGAGGTTTTCACCTATGGCCAGTGTCCCTATGA-AGGGATGACCAACCACGAGGACGCTG
                                                                                                                                                                                                                                                                                                   513 CAGAACCTGGAGCGAGGCTACCGCATGGTGGGCCTGACAAC-TGTCCAGAGGAGCTGTAC
333 ACAACGAGTACACAGCCAGGGGGGCCCAAGTTTCCCATTAAGTGGACAGCGCCAGAAG
                                                                                                 On Sep 12, 1996 this sequence version replaced gi:1407090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="limAGE:504544"
/soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
140 c 133 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA149096.1 GI:1719549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
```

ø

δ

δy g Qγ g δ g

```
Q
 142
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                    g
                                                                                                                                                                         ö
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: eye, Vector: lambda gt10; Site_1: ECORI;
Site_2: ECORI; The library used for sequencing was a
sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated,
cleaved with Tsp5091, size selected, and cloned into lamda
gt10. Individual plaques were arrayed and used as
templates for ECR amplification and these PCR products
were used for sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Human retina cDNA Tsp509I-cleaved sublibrary" /sex="mixed (males and females)"
                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W22649 724 bp mRNA EST 06-MAY-1996
71B11 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens
cDNA not directional, mRNA sequence.
W22649
                                                                                                                                                                                                                                                                                                                                                 1265 AGTCAGACGTCTGGTCCTTCGGCGTCCTGCTGCACGAGGTTTTCACCTATGGCCAGTGTC 1324
                                                                                                                                  1205 CCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGA 1264
                                                                                                                                                                                                                                                                                     1325 CCTATGAAGGGATGACCAACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGC 1384
                                                                                                                                                                       AGTCAGACGTCTGGTCCTTTGGTATCCTGCTGAGAGATCGTCACCGCCGGATCC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homos sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 724)
Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1995)
On Oct 18, 1995 this sequence version replaced gi:1023853.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics
                                                                                              CCAAGITCCCCATCAAGIGGACAGCICCTGAAGCCATCAACTITGGCTCCTTCACCATCA
                                                                                                                                                                                                                                                CITACCCAGGGATGTCAAACCCTGAAGTGATCCGAGCTCTGGAGCGTGGATACCGGATGC
                                                                                                                                                                                                                                                                                                                           212 CTCGCCCAGAGAACTGCCCAGAGGAGCTCTACAACATGATGATGCGCTGCTGGAAAAACC
                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Johns Hopkins School of Medicine
725 North Wolf Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
                                                       0; Mismatches 83; Indels
                   Length 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: CITITGAGCAAGITCAGCCTGGTTAAGI
BACKWARD: GAGGTGGCTATGAGTAITTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAAIT.
Location/Qualifiers
               DB 9; L
5.12e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli strain K802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                 Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="retina"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%;
larity 67.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    272 GICCGGAG-AGCGGCCGACCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W22649.1 GI:1299482
       Query Match
Best Local Similarity
Matches 178; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91299482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                152
                                                                                                                                                                                                                                                                                                                                                                                                                                         1445
                                                                                              32
                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

```
SINCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA216991 586 bp mRNA EST 17-FEB-1997 mu04h04.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:638455 5' similar to gb:J03023 Murine macrophage gene, encoding bmk AA216991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 580
Marra_M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:390447
                                                                                                                                                                                                            1351 ACGUTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCGCCGGCTGCCCGGCGGGG 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                                                                                                                                                                 87 ATAGAAGACAATGAGTACACAGCAAGACAAGGTGCAAAGTTCCCCATCAAGTGGACGGCC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 TTACTCACAGAGCTGGTCACCAAAGGAAGAGTGCCATACCCAGGCATGAACAACCGGGAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 GTGCTGGAGCAGGTGGAGCGAGGCTACAGGATGCCCTGNCCGCAGGACTGCCCCATCTCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 CTGCATGAGCTCATGATCCACTGCTGGAAAAAGGACCCTGAAGAACGCCCCACTTTTG 384
                                                                                                                                                                                                                                                                                                                                                                                      147 CCCGAGGCAGCCCTGTACGGGAGGTTCACAATCAAGTCTGACGTGTGGTCTTTNGGAATC
                                                                                                                                                                               27 AACATTCTAGTGGGGAATGGACTCATATGCAAGATTGCTGACTTCGGATTGGCCCGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1397932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                            .;
0
                                                                       Length 724
145 others
                                                                                                                               0; Mismatches 136; Indels
                                                                       Score 88; DB 33;
Pred. No. 2.14e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amersham
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28ml3 rev2 ET from High quality sequence stop: 403. Location/Qualifiers
р
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g1826018
AA216991.1 GI:1826018
                                                                          5.7%;
  O
                                                                                                                          222; Conservative
168
                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
```

~

٠. <u>٠</u>

```
/organism="Homo sapiens"
//note="Wector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1159486 566 bp mRNA EST 02-OCT-1998 v275405.II Scares mouse mammary gland NbMMG Mus musculus cDNA clone ILMAGE:1332297 5' similat to 9b:M19722 PROTO-ONCOGRNE TYROSINE-PROTEIN KINASE FGR (HUMAN); 9b:X52191 Murine c-fgr mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1219 AAGTGGACAGCGCCTGAGGGGCGCCAATTATCGTGTCTTCTCCCAGAAGTCAGAGTCTGG 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1279 TCCTTCGGCGTCCTGCTGCACGAGGTTTTCACCTATGGCCAGTGTCCCTATGAAGGGATG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 TCTTTTGGGATCCTGCTGACGGAAATTGTCACCCACGGCCGCATCCCTTACCCAGGGATG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1339 ACCAACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCGCCCGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ACCAACCCGGAGT-GATTCAGAACCTGGAGGCGAGGCTACCGCATGGTGCGCCCTGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 TGTCCAGAGGAGCTGTACCAACTCATGAGGCTGTGCTGGAAGGAGCGCCCAGAGGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AAGIGGACAGCCCAGAAGCCATIAACTACGGGACATICACCAICAAGTCAGAIGIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB 13; Le
Pred. No. 2.50e-87;
0; Mismatches 85;
               Insert Length: 834 Std Error: 0.00
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         u
                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                     Location/Qualifiers
1. .519
                                                                                                                                                                                                                                                                                                                                                                                                                                                               b
                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
/lab_host="DH10B"
a 151 c 139 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOUSE);, mRNA sequence. A1159486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1459 CCCTCCTTTGCCACGCTGCG 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 CCCACCTTTGACTACCTGCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI159486.1 GI:3692668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%;
Best Local Similarity 66.9%;
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
AA420981 519 bp mRNA EST 09-NOV-1997 2t98e10,rl Scares_testis_NHT Homo sapiens cDNA clone IMAGE:730410 5' similar to gb:X13529 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK AM420981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCCTGCTGATGGAAATTGTCACCTATGGCCGGATCCCTTACCCAGGTATGTCAAACCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGTGATTCGGGCACTAGAGCATGGGTACCGTATGCCTCGACCAGATAACTGTCCAGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GAGCICTACAATATCAIGATCCGCTGCTGGAAGAACCGCCCCGAGGAACGGCCCACCTTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTCCTGAAGCCATCAACTTTGGTTCCTTCACCATCAAGTCAGATGTCTGGTCCTTTGGT 60
                                                                                                                                                                                                                                                                                                                                                         Score 87; DB 9; Length 586;
Pred. No. 8.90e-94;
0; Mismatches...77; Indels ---0; m-Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:430452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO
741: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                       Length 586;
                                                                                                                                                                                                                                                                                                   144 t
                                                                                                                                                                                                                                          /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                 132 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA420981.1 GI:2099922
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.0%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92099922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 G 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ò

ò

g ò ద ò g ò

```
(HUMAN);, mRNA sequence.
                                                   GI:1891797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.2%;
Best Local Similarity 61.2%;
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                   AA256258.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                 TITLE
JOURNAL
                  ACCESSION
                                                                                                                                                            REFERENCE
                                                                                                                                                                             AUTHORS
                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                     VERSION
                                                                                                                                                                                                                                                                                     COMMENT
                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA256258 574 bp mRNA EST 06-AUG-1997 zr79f04.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:681919 similar to gb:MI4676 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090 CACCGGGACTTGGCCGCCCGGAACGTGCTCGTGGACGGCCTGGCCTGCAAGGTGGCT 1149
                             Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is avallable royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150 GACTTCGGCCTGGCCCGGCTGCTCAAGGACGACATCTACTCCCCGAGCAGCAGCTCCAAG 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1210 ATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCA 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1270 GACGICIGGICCTICGGCGICCTGCTGCAGGITTTCACCTATGGCCAGTGTCCCTAT 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1330 GAAGGGATGACCAACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCGC 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCGAGACTTGAGGGCAGCCAACATCCTGGTGGGGGAATACCTAATATGCAAGATCGCT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTICGGGCTGGCACGCCTCCTAAGTGACAATGAGTATAACCCCCCACAAGGAACCAAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGTGTGGTCTTTGGGATTCTGCTCACTGAACTGATCACCAAGGGCAGAGTTCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 TTCCCCATCAAGTGGACAGCCCCCAGAGGCCGCCTCTTTGGCAGATTCACTGTCAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 CCAGGTATGAACAACCGGGAAGTGTTGGAACAGGTGGAGCATGGCTACCACATGCCGTGC
On Jan 19, 1998 this sequence version replaced gi:2152293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares mouse mammary gland NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB 23; Length 566
Pred. No. 6.16e-89;
0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 CCTCCAGGATGCCCTGCATCCTTGTATGAGGTCATGGAGCAGGCCTGG 425
                                                                                                                                                                                                           Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 t
                                                                                                                                                                                                                                                                Location/Qualifiers
1. .566
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:1332297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
153 c 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 5.4%;
Local Similarity 62.1%;
les 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonaldo."
                                                                                                                                                                                              MGI:691841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1390
                                                                                                                                                                                                                                                                    FEATURES
 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
// Order="Organization" and Saptems / Orde="Organization" and Saptems / Orde="Organization" or organization with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHDU, and fetal heart NbHH19W) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-348479. and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl, gov) for further information.
Insert Length: 1118 54d Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stp: 446.
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhin; Hominidae; Homo.

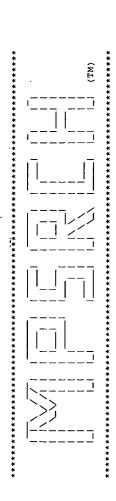
1 (bases 1 to 574)
Hiller, L., Aller, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Wahle, T., Wallen, T., Waterston, R. and Wilson, R.
Wash Wash T. Merce EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 AACGTGCTCGTGGACGACGCCTGCCTGCAGGTGGCTGACTTCGGCCTGGCCCGGCTG 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1231 CCTGAGGCGCCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGTC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 TTACTCACAGAGCTGGTCACCAAAGGAAGAGTGCCATACCCAGGCATGAACAACCGGGAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AACATTCTAGTGGGGAATGGACTCATATGCAAGATTGCTGACTTCGGATTGGCCGGATTG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 ATAGAAGACAATGAGTACACGGAAGAGGTGCAAAGTTCCCCATCAAGTGGACGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 CCCGAGGCAGCCCTGTACGGGAGGTTCACATTCAAGTCTGACGTGTGGTCTTTTGGAATC
                                                                                                                                                                                                                                                                                                                                            On Sep 12, 1996 this sequence version replaced gi:1290492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 4.02e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:681919"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
137 c 156 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pregnant uterus
```

```
g1152795
N32396.1
                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                RESULT
                        ò
                                               엄
                                                                         ò
                                                                                                                         à
                                                                                                                                                  음
                                                                                                                                                                                                                                 The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 11: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org Email: arkerlav@tigr.org information related to this EST, please check the TIGR Human Gene Information Information related to this EST, please check the TIGR Human Gene Seq primer: M13 Reverse.
                                                                                                                                      ç
          1351 ACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCCGCCGCCGGCGGAG 1410
                                                                                                                       AA352185 334 bp mRNA EST 21-APR-1997
ESTGO140 Activated T-cells XX Homo sapiens cDNA 5' end similar tyrosine kinase lck, mRNA sequence.
AA352185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
392 GTGCTGGAGCAGGTGGAGCGAGGCTACAGGATGCCCTGCCCGCAGGACTGCCCCATCTCT 451
                                                            452 CIGCAIGAGCICAIGATCCACIGCIGGAAAAAGGACCCIGGAAGNCGCCCCACIIITG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 12; Length 334;
Pred. No. 2.46e-79;
0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult" 69 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="ATCC (inhost):152375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
Bioinformatics
                                                                                                                                                                         92004505
AA352185.1 GI:2004505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%;
ilarity 67.4%;
Conservative
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 151; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                              RESULT 13
                                                                                                                                    DEFINITION
                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                              SOURCE
                       ö
                                              g
                                                                        ò
```

```
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Exx: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 257
Source: IMAGE Consortium, LLNL
This clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1009 Std Error: 0.00
Seq primer: T7
                                                                                                                           1375 TACCGGCTGCCGCCCCGCCTGCCTGCCGGCGGAGGTCTACGTGCTGATGCTGGAGTGC 1434
                        1255 TICTCCCAGAAGICAGACGICTGGTCCTTCGGCGTCCTGCTGCACGAGGTTTTCACCTAT 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N32396 401 bp mRNA 2NDHM HOMO SAPIENS CDNA CLONE SYNTAILS. IS SOARES MELANOSYLE SUBHM HOMO SAPIENS CDNA CLONE IMAGES:267431 5' Similar to gb.M14676 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 401)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
18 ITCACCATCAAGTCAGATGTGTGTGTCTTTTGGGATCCTGCTGACGGAAATTGTCACCCAC
                                                                                                   78 GCCGCGTTCCCTTACCCAGGGATGACCAACCCGGAGGTGATTCAGAACCTGGAGCGAGGC
                                                                                                                                                                                                      138 TACCGCATGCTGCGCCCTGACAACTGTCCAGAGGAGCTGTACCAACTCATGAGGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785619.
                                                                                                                                                                                                                                                                                                                                      198 TGGAAGGAGCCCCAGAGGACCGGCCCACCTTTGACTACCTGCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="melanocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 257.
Location/Qualifiers
1. 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:267431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:1152795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
```

```
Search completed: Thu May 20 14:58:13 1999 Job time : 5462 secs.
                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 11 to 56)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA098002 562 bp mRNA EST 15-FEB-1997 mRNA m85bll.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:550845 5' similar to 9b:M12056 Mouse rearranged lck gene encoding lymphocyte specific protein (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:331637
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 333.
Location/Qualifiers
1. :562
/organism="Mus musculus"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                      1111 AACGIGCICGIGGACGACGCCIGCCIGCAGGIGCTGACTICGGCCIGGCCGGCTG 1170
                                                                                                                                                                                                                                                                      1231 CCTGAGGCGGCCAATTATCGTGTCTTCTCCCAGAAGTCAGACGTCTGGTCCTTCGGCGTC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                            128 CCCGAGGCAGCCCTGTACGGGAGGTTCACAATCAAGTCTGACGTGTGGTCTTTTGGAATC 187
                                                                                                                                                                                                                                                                                                                                                                                                            188 TTACTCACAGAGCTGGTCACCAAAGGAAGAGTGCCATACCCAGGCATGAACAACCGGGAG 247
                                                                                                                                                                                                                                             68 AIAGAAGACAATGAGTACACAGCAAGACAAGGTGCAAAGTTCCCCATCAAGTGGACGGCC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 TGCCTGGAGCAGGTGGAGCGAGGCTACAGGATGCCCTGCCCG-CAGACTGCCCCATCTCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                               8 AACATICIAGIGGGAAIGGACICAIAIGCAAGAIIGCIGACIICGGAIIGGCCCGAIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 CIGCATGAGCTCATGATCCACTGCTGGAAAAAGGNCCCTGGAAGAACGCCCCCACTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63108
                                                                                                                         2;
                                                                               DB 32; Length 401;
/lab_host="DH10B (ampicillin resistant)" 99 c 109 g '83 t 4 others
                                                                             Score 78; DB 32; Length 401
Pred. No. 2.46e-79;
0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA098002.1 GI:1643555
                                                                             ch 5.0%;
1 Similarity 62.1%;
223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
                       ๙
                                                                                 Query Match
                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                     ORIGIN
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
1219 AAGIGGACAGCGCCIGAGGGGGCCAAITAICGIGICITCICCCAGAAGICAGACGICIGG 1278
                                                                                                                                                                                                                                                                                                                                       1338 GACCAACCACGAGACGCTGCAGCAGATCATGCGAGGGTACCGGCTGCCGCGCCCGCGCTGC 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 TCCTTCGGGATCTTGCTTATCAGAGATTGTCACCCACGGTCGAATCCCTTACCCAGGAAT 150
                                                                                                                                                                                                                                                        31 AAGTGGACAGCACCAGAAGCCATTAACTATGGGACCTTCACCATCAAGTCAGACGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                  GACCAACCCTGAAGTCATTCAGAACCTGGAGAGAGGCTACCGCATGGTGAGACCTGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲;
                                                                                                                                                                                              Length 562
                                                                                                                                                                                                                         0; Mismatches 90; Indels
                                                                                                                                                                                           Score 75; DB 36; Dred. No. 1.40e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCTCCTTTGCCACGCTGCGG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCACGITIGACIACCITCGG 292
                                                                                                                                                                                           / Match
Local Similarity 65.3%;
les 171; Conservative
```



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:13:59 1999; MasPar time 28.99 Seconds 357.975 Million cell-updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2

(1-488) from USO9099053.pep (1 of 6) 3671 1 MEPFLRRRLAFLSFFWDKIW......ERPSFATLREKLHAIHRCHP 488 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part11 12:part12 13:part13 14:part14 25:part25 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part25 26:part26 25:part28 29:part29 30:part30 31:part31 32:part32 33:part33 33:part33 33:part36 37:part37 38:part38

Mean 36.486; Variance 158.060; scale 0.231 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		đ			SUMMAKIES		
Result No.	Score	Query Match	Length DB	DB	ΠD	Description	Pred. No.
-				1			
-	3671	100.0	488	39	W89248	Human SAD.	0.00e+00
2	1355	36.9	451	12	R63088	Breast tumor kinase,	.7.03e-117
m	1332	36.3	505	ω	R41941	pTK gene LpTK-2 prod.	1.25e-114
4	1332	36.3	505	14	R85929	Protein tyrosine-kina	1.25e-114
വ	1326	36.1	533	œ	R39705	Chicken pp60 c-src pr	4.84e-114
Q	1315	35.8	536	∞	R39706	Human pp60 c-src prot	5.77e-113
7	1189	32.4	417	ო	R14201	(Beta-galactosidase N	1.17e-100
ω	1114	30.3	1146	m	R15156	Abelson Related Gene,	2.39e-93
σ	1072	29.5	1182	m	R15157	Abelson Related Gene,	2.92e-89
10	962	26.2	259	9	R32299	Sequence of pp60(c-sr	1.40e-78
11	926	25.2	620	17	R94535	ITK tyrosine kinase.	4.29e-75
12	904	24.6	629	17	R94534	BTK tyrosine kinase:	5.76e-73
13	006	24.5	441	17	R94538	Drosophila Src28C tyr	1.40e-72
14	894	24.4	466	13	R71132	N-terminal truncated	5.34e-72
15	894	24.4	507	13	R71133	Cytoplsmic tyrosine k	5.34e-72
16	893	24.3	629	20	W06708	Mouse haematopoietic-	6.67e-72

	2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2
karyocyte kinase tyrosine kinase karyocyte kinase krase na matk protein. Sine kinase dom matk protein. Sine kinase dom sex to protein to sex t	ph.related PTK Cek5 ph.related PTK Cek5 ph.related PTK Cek8 PH-like receptor pr rotein tyrosine-kin PH-like receptor pr
R844584 R8445381 R844533 R844533 R711831 R711831 R871628 R83147 R83147 R85102 R81466 R81466 R81466 R814513 R81466 R814513 R8147 R8166 R816	20000000000000000000000000000000000000
507 15 6430 17 6675 15 6675 15 8528 34 8928 19 991 15 998 1 998 1	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
22222222222222222222222222222222222222	
08888888888888888888888888888888888888	00000
11112222222222222222222222222222222222	

ALIGNMENTS

E Human SAD.

E Human Sapiens.

E Huntington's disease.

E Hunti pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the Ą. T W89248 standard; Protein; 488 10-MAR-1999 (first entry) Human SAD W89248; RESULT

 α

```
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dftarcggelsvrrgdrlcaleegggyifarrlsggpsaglvpithvakaspetlsdgpw 120
                                                                                                                                                                                                    9
                                                                                                                                    Gaps
                                                                                                                                                                   mepflrrrlaflsffwdkiwpaggepdhgtpgsldpntdpvptlpaepcspfpglflaly
                                                                                                                                                                                    fgevweglwlgslpvaikviksanmkltdlakeiqtlkglrherlirlhavcsggepvyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAVCSGGEPVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential regulatory tyrosine equivalent to Tyr-527 of c-src"
                                                                                                                                    ö
                                                                                                   488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strong indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "putative autophosphorylation site"
                                                                                                                                    Indels
                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; T-47D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "putative ATP binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1995 (first entry)
Breast tumor kinase, brk.
Breast tumor kinase; brk; protein-tyrosine-kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "similar to PTK SH2 domain"
                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "similar to PTK SN3 domain'
                                                                                                Score 3671; DB 39;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esponds to the stro
PTK specificity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312..317 /
/note= "corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; metastasis; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 2
R63088 standard; Protein; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subdomain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of
                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                  488; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78..169
/note= "s
198..203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15..68
                                                                   488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haihrchp 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9502057-A.
19-JAN-1995.
                                                                    Sequence
                                                 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                    Matches
                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULA

AC R6

AC R6

AC R6

AC R6

BE BE BE

COS BE

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쉱
 22222
                                                                                                                                                                                                    à
                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ά
                                                                                                                                                                                                                                                                                                                                                                                          Ω
```

```
vesepwffgcisrseavrrlqaegnatgaflirvsekpsadyvlsvrdtqavrhykiwrr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVP-ITHVAKASPET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggrlhlneavsflslpelvnyhrag-slshglrlaapcrkhepeplphwddwerpreef 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c-kit; megakaryocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 yvglwdfksrtdeelsfragdvfhvarkeeqwwwatlldeaggavaggyvphnylaeret 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                            Disclosure; Page 29-31; S2pp; English.

A brk (breast tumor kinase) cDNA fragment was used to screen a 20MA library prepared from human breast tumor cell line T-47D. 2 CDNAs were isolated. The slightly longer clone lambda-t2 (Q81189) encoded brk (R63088), which was identified as a novel putative non-receptor kinase of use as a prognostic/diagnostic of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTD-LAKEIQTLKGLRHERLIRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pTK gene LpTK-2 prod.
pTK; protein tyrosine kinase; catalytic domain; c-kit; megakaryoc;
lymphocyte; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | : | : | | | | | | | ADGSLYLQRGR-P-RQ-DVWERPHSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tlcrklgsgyfgevfeglwkdrvqvaikvisrdnllhqqmlqseiqamkklrhkhilaly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||:|| : |||:|||||||:||:|| DLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dlaarnilvgentlckvgdfglarlikedvy-lshdhnipykwtapealsrghystksdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wsfgillhemfsrgqvpypgmsnheaflrvdagyrmpcplecppsvhklmltcwcrdpeg
                                                                                                                                                                                       from human
cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1355; DB 12; Length 4
Pred. No. 7.03e-117;
73; Mismatches 151; Indels
                                                                                                                                                                                   Novel protein tyrosine kinase and its DNA - isolated breast tumour, useful for diagnosis and prognosis of
                                                                                                        Kamalati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avraham H, Cowley S, Groopman J, Scadden WPI; 93-320330/40.
                                                                                                      BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05.AUG-1993.
22.JAN-1993, UO0586.
22.JAN-1992; US-826935.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
                                                                                                    Gusterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä.
                                                                                                                         Spence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505
                                                                                   LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 36.9%;
Local Similarity 46.5%;
nes 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 3
R41941 standard; Protein;
R41941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1994 (first entry)
                                                                                                        Crompton MR,
                                                                              (WELL ) WELLCOME FOUND L7
Barker KT, Crompton MR,
Mitchell PJ, Page MJ, SE
WPI, 95-066901/09.
N-PSDB; Q81189.
08-JUL-1994; G01479.
09-JUL-1993; GB-014233.
11-MAR-1994; GB-004817.
(CANC-) CANCER RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpcfkalrerlssf 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | :|||:| :: 470 RPSFATLREKLHAI
                                                                                                                                                                                                                                                                                                                                                                      tumor metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pTK gene LpTK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9315201-A.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
```

φ

m

```
505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; R39705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9314193-A
                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESOLT

OTHER STATE

OTHER STAT
Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFTALYDFTARCGGELSVRRGDRLCALEE-GGGYIFARRLSGQPSAGLVPI-THV-AK- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 irsnkfsiksdvwsfgillyeiitygkmpysgmtgaqviqmlaqnyrlpqpsncpqqfyn 464
                                                  Claim 3; Fig 5; 60pp; English.

Claim 3; Fig 5; 60pp; English.

Claim 3; Fig 5; 60pp; English.

PTK genes were identified using two sets of degenerative

Oligonuclectide primers: a first set which amplifies all pTK DNA
segments (049743-44), and a second set which amplifies highly
conserved sequences present in the catalytic domain of the c-kit
subgroup of pTKs (049745-46). The pTK genes identified are described
in 049747-57 and R41897-02.

The LpTKs are expressed in lymphocytic cells, as well as
megakaryocytic cells. The partial and full-length LpTK2 gene
sequences are given in 049749 and 049754 respectively. The
protein sequence corresp. to 049749 is claimed (claim 7) and
stated as given in the specification, however is missing from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 hyfvalfdygartaedlsfragdklgvldtlhegwwfarhlekrrdgssgqlggyipsny 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yrikrldeggffltrrrifstlnefvshytktsdglcvklgkpclkiqvpapfdlsyktv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaedrslqaepwffgaigrsdaekqllysenktgsfliresesqkgefslsvldgavvkh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dqweidrnsiqllkrlgsgqfgevweglwnnttpvavktlkpgsmdpndflreaqimknl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhpkliqlyavctledpiyiitelmrhgslqeylqndtgskihltgqvdmaaqvasgmay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lesrnyihrdlaarnvlvgehniykvadfglarvfkvdnediyesrheiklpvkwtapea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEQRVVHRDLAARNVLVDDGLACKVADFGLARLLK-D--DIYSPSSSSKIPVKWTAPEA
                    New protein tyrosine kinase genes and proteins encoded by genes are of human mega-karyocytic origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1332; DB 8; Length 505;
Pred. No. 1.25e-114;
96; Mismatches 135; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agonist antibodies which activate specific protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein tyrosine-kinase İpTK2.
Protein tyrosine-kinase; pTK; LpTK2; agonist; cell
differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||||| : | |||:| ||| ||
LMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R85929 standard; Protein; 505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imlecwnaepkerptfetlrwkl 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.3%;
Best Local Similarity 44.2%;
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1995.
04-APR-1995; U04228.
04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95-366160/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9527061-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DO PER PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE PRINCIPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANYRVESQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 hyfvalfdygartaedlsfragdklqvldtlhegwwfarhlekrrdgssqqlqgyipsny 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 irsnkfsiksdvwsfgillyeiitygkmpysgmtgaqviqmlaqnyrlpqpsncpqqfyn 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced monouclear cell adhesion and fibronectin prodn bisclosure; Page 64-66; Jlpp; English.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46687) is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to
kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation

Disclosure: Page 56-58; In3pps.

DNA probes based on protein tyrosine-kinase (pTK) sequences were use to screen cDNA libraries to identify novel pTK genes. A LepTK2 gene (T03097) was isolated from lymphocytic and megakaryocytic cell libraries. The encoded novel pTK, LpTK2 (R85929), shows homology to known pTKs, and can be used to design drugs that modulate pTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 vaedrslqaepwffgaigrsdaekqllysenktgsfliresesqkgefslsvlḋgavvkh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | || :: : | ::|| | |||||||| : |||:| |: :| |: :| | :| | DVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 rhpkliglyavctledpiyiitelmrhgslgeylqndtgskihltgqvdmaagvasgmay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 yrikrldeggffltrrrifstlnefvshytktsdglcvklgkpclkiqvpapfdlsyktv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 lesrnyihrdlaarnvlvgehniykvadfglarvfkvdnediyesrheiklpvkwtapea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dqweidrnsiqllkrlgsgqfgevweglwnnttpvavktlkpgsmdpndflreaqimknl
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                     Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken pp60 c-src protein.
Endothelial, tyrosine Kinase protein; pp60 c-src;
Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                     Score 1332; DB 14;
Pred. No. 1.25e-114;
96; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warren SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madri JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||||| : | |||:| || ||
458 LMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 imlecwnaepkerptfetlrwkl 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jr 5
R39705 standard; Protein; 533
R39705;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.3%;
Best Local Similarity 44.2%;
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bell L, Luthringer DJ, WPI; 93-243209/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1993.
05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
```

536 AA;

Seguence

g

```
Score 1326; DB 8; Length 533;
Pred. No. 4.84e-114;
92; Mismatches 133; Indels 14; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                             fvalydyesrtetdlsfkkgerlqivnntegdwwlahslttgqt-gyipsnyva-ps-ds 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: : | |||:| |||||| | ||: |||| : ||:|| ||:| ||:|| ||:| ||:|| ||:| ||:|| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVSMAADGSLYLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC---MPQKAP-RQDVWER 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQ 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.
                                                                                                                                                                                                                                                                                                                                                                                                                   preslrlevklgggcfgevwmgtwngttrvaiktlkpgnmspeaflgeagvmkklrhekl 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 vqlyavvse-epiyivteymskgslldflkgemgkylrlpqlvdmaaqiasgmayvermn 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 IRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ksdvwsfgilltelttkgrvpypgmvnrevldqvergyrmpcppecpeslhdlmcqcwrr 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn bisclosure; Page 75-77; 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46688) is used to transform endothelial have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as comment angloplasty, heart bypass surgery, vessel graft and stent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 iqaeewyfgkitrreserlllnpenprgtflvresettkgayclsvsdfdnakglnvkhy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kirkldsggfyitsrtqfsslqqlvayyskhadglchrltnvcptskpqtgglakdawei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yvhrdlraanilvgenlvckvadfglarliedneytarggakfpikwtapeaalygrfti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c-src;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madri JA, Warren SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pp60 c-src protein:
Endothelial; tyrosine kinase protein; pp60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r 6
R39706 standard; Protein; 536
R39706;
                                                                                                                                                                                                                                             36.18;
44.78;
                                                                                                                                                                                                                                   Query Match 36.1%;
Best Local Similarity 44.7%;
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bell L, Luthringer DJ, WPI; 93-243209/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 dpeerptfeylg 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||:| |:
466 SPEERPSFATLR 477
                                                                                                                                                                            533 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapien.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1993
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8888888
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                  89 fvalydyesrtetdlsfkkgerlqivnntegdwwlahslstgqt-gyipsnyva-ps-ds 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
                                                                                                                                                                                                                                                                                                                                                                                                 206 kirkldsggfyitsrtgfnslgglvayyskhadglchrlttvcptskpgtgglakdawei 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 preslrlevklgggcfgevwmgtwngttrvaiktlkpgtmspeaflgeagvmkklrhekl 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||||::| :|| :|| :|| :|| ::|| ::|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|
                                                                                                                                                                                                                                                                 146 iqaeewyfgkitrreserlllnaenprgtflvresettkgayclsvsdfdnakglnvkhy 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 RVSMAADGSLYLQKGRLFPGLEELLTYY-KANWKLION-PLLQP-CMPOKAP-RQDVWER 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 vqlyavvse-epiyivteymskgslldflkgetgkylrlpqlvdmaaqiasgmayvermn 384
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      385 yvhrdlraanilvgenlvckvadfglarliedneytarggakfpikwtapeaalygrfti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 ksdvwsfgilitelttkgrvpypgmvnrevldgvergyrmpcppecpeslhdlmcgcwrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multi-cloning site
Claim 1; Fig 4.2; 15pp; Japanese.
The sequence consists of the N-terminal amino acids of the beta-
galactosidase gene fused with the lck gene. It is produced by
E.coli transformed with a recombinant vector (see Q13983). It is
useful for producing an antibody specifically immunoreactive with
recognise lck gene-derived polypeptide in T cells. The antibody may
sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 PHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R14201 standard; Protein; 417 AA.
R14201;
13-DEC-1991 (first entry)
(Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1189; DB 3; Length 417;
Pred. No. 1.17e-100;
81; Mismatches 118; Indels 15;
          Length 536;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "beta-galactosidase fragment"
                                                                      90; Mismatches 135;
   Score 1315; DB 8; I
Pred. No. 5.77e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27..417
/note= "lck gene polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
35.8%;
Local Similarity 44.7%;
hes 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1991.
28-DEC-1989; 338268.
28-DEC-1989; JP-338268.
(TOKU ) TOKUYAMA SODA KK.
WPI; 91-300980/41.
N-PSDB; Q14201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%;
Local Similarity 45.1%;
les 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 epeerptfeylq 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 SPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multi-cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J03201994-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 17
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
therapy Disclosure; Fig 5B; 40pp; English. Disclosure; Fig 5B; 40pp; English. The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes. Arg is expressed as two transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A and B (014937) and it is assumed that they are joined
                                                                                                                         138 gkpwwedewevpretlklverlgaggfgrcgw-gtttgttkvavkslkggsmsagrlpae 196
                                                                                                                                                                                                                                                                                                               apeainygtftiksdvwsfgillteivthgripypgmtnpeviqnlergyzmvrpdncpe 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pnlfvalydfvasgdntlsitkgeklrvlgyngngewse-vrskngggwypsnyit-pv- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QAKVC-HYRVSMAADGSLYLQKGRL-FPGLEELLTYYKA-NWKLIQNPLLQPCMPQKA 217
                                                                                                                                                                                                       iaegmafieernyihrdlraanilvsdtlsckiadfglarliedneytaregakfpikwt 315
                                                                                                                                                                                                                                                                                                                                    PQLFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITHVAKASP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nslekhswyhgpvsrsaae-yllsslin-gsflvresesspgqlsislryegrvyhyrik 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttadgkvyvtaesrfstlaelvhhhstvadglvttlhypapkcnkptvygvspihdkwem 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the arg second exon.
The amino acid sequence is represented as found in the specification.
Sequence 1146 AA;
                   rvpssnslnslepepwffknlsrkdaerqllapgnthgsfliresestagsfslsvrdfd
                                                                                                                                                                                        anlmkqlqhqrlvrlyavvtq-epiyiiteymengslvdflktpsgikltinklldmaaq
                                                               qnqgevvkhykirnldnggfyi-spritfpglhelasaitpiasdglctrlsrpcqtqkp
                                                                                                                                                                                                                                                                     Score 1114; DB 3; Length 1146;
Pred. No. 2.39e-93;
96; Mismatches 160; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1991.
22-OCT-1991; 559029.
23-OCT-1991; US-559029.
30-JUL-1990; US-559029.
(USSH) NAT INST OF HEALTH.
Kruh G, Arronson SA, King CR;
WRI; 91-353425/48.
NP-PSDB; Q14936.
Novel human gene related to abl proto-oncogene - designated "Abelson Related Gene", arg, useful for tumour diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R15156;
12-FEB-1992 (first entry)
Abelson Related Gene, A transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
Homo sapiens.
US755929-A.
                                                                                                                                                                                                                                                                                                                                                                                 elyglmrlcwkerpedrptfdylrsvledf 405
                                                                                                                                                                                                                                                                                                                                                                                                  |:| || || : ||:||:| : EVYVLMLECWRSSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 8
R15156 standard; Protein; 1146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.3%;
Local Similarity 38.7%;
Local Similarity 38.7%;
Les 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
 19
                                                                                            163
                                                                                                                                                                                        197
                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                   334
                                                                                                                                                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                             79
                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                  316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                ò
                                                          g
                                                                                          ö
                                                                                                                      g
                                                                                                                                                        ŏ
                                                                                                                                                                                       ద
                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Disclosure; Fig 5D: 40pp; English.

The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes. Arg is expressed as two transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A (Q14936) and B and it is assumed that they are joined to the arg second exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 pnlfvalydfvasgdntlsitkgeklrvlgyngngewse-vrsknaggwvpsnylt-pv- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 ttadgkvyvtaesrfstlaelvhhhstvadglvttlhypapkcnkptvygvspihdkwem 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 ertditmkhklrgghyrevyvgvwkkysltvavktlkedtmeveeflkeaavmkeikhpn 343
                                                                          367
                                                                                                               344
                                                                                                                                                  368 nfihrdlaarnclygenhvvkvadfglsrlmtgdtytahagakfpikwtapeslayntfs 427
                                                                                                                                                                                       404
                                                                                                                                                                                                                            428 iksdvwafgvllweiatygmspypgidlsqvydllekgyrmegpegcppkvyelmracwk 487
                                                                                                                                                                                                                                                 226 PHSEFALGRKLGEGYFGEVWEGLWLG-SLPVAIKVIKSANWKLTDLAKEIOTLKGLRHER 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 lvgllalctleppfyivteympyrnlldylrgcnrekvtavvllymatgissameylekk 403
248 drtditmkhklggggygevyvgvwkkysltvavktlkedtmeveeflkeaavmkeikhpn 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid sequence is represented as found in the specification Sequence 1182 AA;
                                                                                                             285 LIRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQ
                                                                                                                                                                         :||||||||| : ||||||| 345 RVVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 POLFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGOPSAGLVPITHVAKASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 nslekhswyhapvsrsaae-yllsslin-gsflvresesspgqls1s1ryegrvyhyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lvgllgvctleppfyivteympygnlldylrecnreevtavvllymatgissameylekk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.2%; Score 1072; DB 3; Length 1182; Best Local Similarity 37.8%; Pred. No. 2.92e-89; Matches 166; Conservative 97; Mismatches 163; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1991.
22-OCT-1991; 559029.
30-JUL-1990; US-559029.
Kruh G, Arronson SA, King CR;
WPI; 91-353425/48.
NPISB; 014937.
Novel human gene related to abl proto-oncogene - designated Abelson Related Gene", arg, useful for tumour dlagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                  R15157,
12-FEB-1992 '(first entry)
Abelson Related Gene, B transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                               n 9
R15157 standard; Protein; 1182
                                                                                                                                                                                                                                                                                                      488 wspadrpsfaethgafetm 506
                                                                                                                                                                                                                                                                                                                                         465 SSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
US7559029-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy
                                                                          308
                                                                        g
                                                                                                                                                  8
                                                                                                                                                                                       δ
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                   δ
                                                                                                               à
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

ø

```
Three-dimensional conformation of enzyme-affectors - using computer modelling design of specific affectors - using computer modelling design of specific affector complex computer modelling design of enzyme-affector complex Example; Pages 51-52; 115pp; English.

Example; Pages 51-52; 115pp; English.

CC The inventors provide a crystal structure of cAMP-dependent protein kinase (CAPK) with its catalytic subunit intact. The crystals contain a bound inhibitor peptide (PRI(5-24)) which comprises a fragment of the heat stable protein kinase inhibitors (PRI). PRI(5-24) includes the consensus feature common to all peptide substrates and inhibitors of CAPK. In addition it contains other features that convey unique high affinity binding characteristics. From an analysis of PRI(5-24) a template is derived from which all other protein kinases can be modelled and from which other inhibitors can be designed. For example, to design specific inhibitors of a first protein kinases comprises comprises obtaining the cresidues present in most protein kinases complex, generating a model of the protein kinase corresp. to points of contact for CAPK, and of the protein complex, examining the amino acids in the first contact for CAPK and PRI(5-24), and designing an inhibitor of the first protein kinase. In the example, the inventors use this methodology to design an inhibitor for pp60(c-src) which is the protein residues are incorporated into the appropriate position virues. The invariant residues in p60(c-src) which is protein kinases. Once the template is in place and the catalytic protein kinases. Once the template is in place and the catalytic interaction when the protein the example of the invariant residues present in most contains the correspondent of the invariant residues are incorporated into the appropriate position in the catalytic interaction when the protein residues are incorporated into the appropriate position in the catalytic interaction when the protein protein kinases. Once the template is in place and the catalytic 
                                                                                                                      nfihrdlaapnclvgenhvvkvadfglsrlmtadtytahagakfpikwtapeslayntfs 463
                                           345 RVVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFS 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iksdvwafgvllweiatygmspypgidlsgvydllekgyrmegpegcppkvyelmracwk
                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is possible to visualise the catalytic site. The site can additionally be refined using the complementary target phosphorylation site for pp66(c-src) (se 873200). Residues are altered using computer modelling until a fit is achieved for
                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1993 (first entry) Sequence of pp60(c-src) which is the proto-oncogene homologue the src protein kinase from Rous Sarcoma Virus. Inhibitor peptide; cellular protein kinase; proto-oncogene; src protein kinase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Invariant residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                         T 10
R32299 standard; peptide; 259 AA.
                                                                                                                                                                                       wspadrpsfaethqafetm 542
                                                                                                                                                                                                                                   465 SSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pp60(c-src) on the template.
Sequence 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sowadski JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-1993.
22-JUL-1992; U06137.
22-JUL-1991; US-735614.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     R32299;
07-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knighton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9302209-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
404
                                                                                              464
                                                                                                                                                                                          524
                                                                                                                                                                                                                                                                                                       RESULT
                                                                                         셤
                                                                                                                                                                                       셤
                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                         ò
```

Length 259;

Score 962; DB 6; Pred. No. 1.40e-78;

26.2%;

Similarity

Query Match Best Local (

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 lshpklvqlygvcleqapiclvfefmehgclsdylrtqrg-lfaaetllgm-cldvcegm 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 SDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSV--RA---QAKVC--H 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 yhiketndnpkryyvaekyvfdsipllinyhqhnggglvtrlrypvcfgrqkapvtaglr 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 ygkwvidpseltfvqeigsgqfglvhlgywlnkdkvaiktiregamseedfieeaevmmk 412
                                                                                                            292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 ialydyqtndpqelalrrneeyclld-sse-ihwwrvqdrnghegyvpssylvekspnnl 234
                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 926; DB 17; Length 620;
Pred. No. 4.29e-75;
94; Mismatches 161; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic tyrosine kinase BMX and related DNA - useful to stimulate haematopoietic cell growth.
Disclosure; Page 23-25; 40pp; English.
Cytoplasmic tyrosine kinase ITK (R94535) is selectively expressed at certain stages of T-cell development. The sequences of ITK and 2 other members of a newly identified non-receptor tyrosine kinase family, BTK (R94534) and TEC (R94536), and of the Drosophila Src28C tyrosine kinase (R94538), were compared with that of novel cytoplasmic tyrosine kinase BMX (see also R94533). Close homology was found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 QDVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANWKLTDLAKEIQTLKG
                                                                    5 levklgggcfgevwmgtwngttrvalktlkpgtmspeaflgeagvmkklrheklvglyav
                                                                                                                                                                                                              65 vse-epiyivteymskgslldflkgetgkylrlpglvdmaaqlasgmaybermnyvhrdl
                                                                                                                                                                                                                                                                                                                                                                                           412 FGVLLHEVFTYGOCPYEGMTNHETLOOIMRGYRLPRPAACPAEVYVLMLECWRSSPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 etyewynksisrdkaekllldtgke-gafmvrdsrta-gtytvsvftkavvsennpcikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 YRVSMAADGSL-YLQKGR-LFPGLEELLTYYKANWKLIQNPLLQP-CM-PQKAP-----R
                                                                                                                                                                                                                                                                                                                                                       124 raanilvgenlvckvadfglarliedneytarggakfpikwtapeaalygrftiksdvws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fgilltelttkgrvpypgmvnrevldqvergyrmpcppecpeslhdlhcqcwrkepeerp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUJ-1996 (first entry)
ITK tyrosine kinase.
Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
cell growth; cell proliferation; tumour; diagnosis; therapy; ITK.
   74; Indels
   40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-0CT-1995; F10555.
07-0CT-1994; US-320432.
(UYHE-) UNIV HELSINKI LICENSING LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .r. 11
R94535 standard; Protein; 620
R94535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.2%;
larity 37.3%;
Conservative
131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 96-209856/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 tfeylg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9611275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                     ò
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC DDA NAME OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
```

US-09-099-053-2-01.rag

```
WPI; 96-209856/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Src28C
                                                                                               436
                                                                                                                                                                                                                         495
                                                                                                                                                                                                                                                                                                                                                   554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
                          ò
                                                                                            g
                                                                                                                                                              ò
                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Nitralo K;

NR VATION K;

NR VATION K;

NR VATION K;

NR VATION K;

NR VATION K;

NR VATORIANIC VYROSINE Kinase BMX and related DNA - useful to stimulate haematopoietic cell growth.

PS Disclosure; Page 21-23; 40pp; English.

CC Vatoplasmic tyrosine kinase BTK (R04534) is selectively expressed cc at certain stages of B-cell development. The sequences of BTK cc and 2 other members of a newly identified non-receptor tyrosine cc kinase family, ITK (R04535) and TEC (R04538), were compared with that of novel cytoplasmic tyrosine kinase BMX (see also R04533).

CC Drosophila STC2RC tyrosine kinase BMX (see also R04533).

CC close homology was found.
                                399 NYRVFSQKSDVWSFGVLLHEVFIXGQCPYEGMINHEILQQIMRGYRLPRPAACPAEVYVL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --egyipsnyvteae-dsiemyewyskhmtrsqaeq11kqegke-ggfivrdsska-gky 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLSV--RA--QAK-VC-HYRVSMAADGSLYLQKGRLFPGLEELLTYYKANWK-LI-Q-N-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 plppepaaapvstselkkvvalydympmnandlqlrkgdeyfileesnlpwwrardkngg 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 tvsvfakstgdpggvirhyvvcstpgsgyylaekhlfstipelinyhqhnsaglisrlky 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 PVPTLPAEPCSPFPQL - FLALYDFTARCGGELSVRRGDRLCALEEGG-GYIFARRLSGQ 96
471 ayleeacvihrdlaarnclvgenqvikvsdfgmtrfvlddqytsstgtkfpvkwaspevf
                                                                                                                             sfsryssksdvwsfgvlmwevfsegkipyenrsnsevvedistgfrlykprlasthvygi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIK tyrosine kinase.
Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
cell growth; cell proliferation; tumour; dagnosis; therapy; BIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 24.6%; Score 904; DB 17; Length 659; Best Local Similarity 37.0%; Pred. No. 5.76e-73; Matches 168; Conservative 100; Mismatches 162; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region contains the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.219 // Tabel - N-terminal region contains // note - "the N-terminal region contains pleckstrin homology region consisting of a 7-strand antiparallel beta-sheet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551
/label- Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label- ATP-binding_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-0CT-1994; US-320432.
(UYHE-) UNIV HELSINKI LICENSING LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                    591 mnhcwkerpedrpafsrllrqlaei 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= SH2_domain
                                                                                                                                                                                                                                                                                                               459 MLECWRSSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            R94534 standard; Protein; 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407..644
/label= T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408..430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-1996.
09-OCT-1995; FI0555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9611275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R94534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                          531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                           SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTANDER SULTAN
                                                                                                                                                                                                                                                g
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                              ò
                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
```

```
,
     435
                                                                                                  484
                                                                                                                                                                                                  553
                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                   442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAGLVPITHVAKASPETLSDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSES-SLGGY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 slhtkvpqshvkhyhikqnarceyylsekhccetipdlinyhrhnsaglacrlksspcdr 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nvgyipsnyvqaeallgleryewyvgymsrqraesll-kqgdkegcfvvrksstkglytl 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic tyrosine kinase BMX and related DNA - useful to stimulate haematopoietic cell growth.

Disclosure; Page 28-29; 40pp; English.

The anino acid sequence (R94538) of Drosophila Src28C tyrosine kinase was compared with the sequences of 3 members of a newly-identified non-receptor tyrosine kinase family, BTK (R94535), and TEC (R94536), and with novel human cytoplasmic tyrosine kinase BMX (see also R94533), Close homology was found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
pvsqqnknapstaglgygsweidpkdltflkelgtgqfgvvkygkwrgqydvaikmikeg
                               324 DPPLLGFAC-QVAEGMSYLEEQRVVHRDLAARNUVDDGLACKVADFGLARLLKDDIYSP
                                                                                                                                                                                                                                                                                                                                                   383 SSSSKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pvpptaglshdkweihpiglmlmeelgsgqfgvvrrgkwrgsidtavkmmkegtmseddf
                                                                                                  smsedefieeakvmmnlsheklvqlygvctkqrpifiiteymangcllnylremrhr-fq
                                                                                                                                                                                                  tqqllem-ckdvceameyleskqflhrdlaarnclvndqgvvkvsdfglsryvlddeyts
                                                                                                                                                                                                                                                                                                  svgskfpvrwsppevlmyskfssksdiwafgvlmweiyslgkmpyerftnsetaehiagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila Src28C tyrosine kinase.
Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
cell growth; cell proliferation; tumour; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 900; DB 17; Length 441
Pred. No. 1.40e-72;
77; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186..425
/label= Tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | : | | : | | | | 443 YRLPRPAACPAEVYVLMLECWRSSPEERPSFATL 476
                                                                                                                                                                                                                                                                                                                                                                                                       614 lrlyrphlasekvytimyscwhekaderptfkil 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187..209 /
/label- ATP-binding_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-1996.
09-0CT-1995; F10555.
07-0CT-1994; US-320432.
(UYHE-) UNIV HELSINKI LICENSING LTD OX.
Alitalo K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
Key
Location/Qualifiers
domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65...155
/label- SH2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R94538 standard; Protein; 441
R94538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5%;
Local Similarity 37.3%;
nes 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
```

œ

```
433 laekl 437
                                                                                                                                                                                                                                                                         476 LREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q84888
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9506113-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakano S;
                                                                                                                                                                                                                                                                                                                                                             R71133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                         g
                                                              ò
                                                                                                g
                                                                                                                                   ò
                                                                                                                                                                    셤
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                  341
                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                              gkisggeavggl-gpped-glflvresarhpgdyvlcvsfgrdvihyrv-lhrdghltid
              222 ieeakvmtklqhpnlvqlygvctkhrpiyivteymkhgsllnylrrhektlignmgllld
                                                                                mciqvskgmtylerhnyihrdlaarnclvgsenvvkvadfglaryvlddqytssggtkfp
                                                                                                  342 ikwappevlnytrfssksdvwaygvlmweiftcgkmpygrlkntevvervqrgiilekpk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 gelafrkgdvvtileacenkswyrvkhhtsggegllaagalrerealsadpklslmpwfh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSLYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eavffcnlmdmvehyskdkgaictklvrpkrkhgtksaeeelaragwllnlqhltlgaqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 KGRLFPGLEELLTYYKANWKLIONPLLOP-CMP-OKAPRODV----WERPHSEFALGRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%; Score 894; DB 13; Length 466; larity 39.8%; Pred. No. 5.34e-72; Conservative 78; Mismatches 155; Indels 2:
                                                                                                                                                                                                                                                                                                                                                        27-001-1995 (first entry)
N-terminal truncated cytoplsmic tyrosine kinase.
cytoplasmic; tyrosine kinase; blood; cell differentiation;
screening; anticancer agent; SH3; src homology domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "tyrosine kinase domain"
                                                                                                                                                                                                                    402 scakelydvmklcwshgpeerpafrvlmdql 432
                                                                                                                                                                                                                                       ACPAEVYVLMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "SH2 domain"
                                                                                                                                                                                                                                                                                                                           Ä.
                                                                                                                                                                                                                                                                                                                R71132 standard; Protein; 466
R71132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1994; JO1411.
25-AUG-1993; JP-210403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81..155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
192..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9506113-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakano S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                        THE SULPTION OF THE SULPTION OF THE SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTION OF SULPTI
                                            ò
                                                                            qq
                                                                                                                ò
                                                                                                                                                g
                                                                                                                                                                                  ò
                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activative for use as cancer therapy claim 1; Page 41-44; 58pp; English.

A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are usful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. Sequence 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 894; DB 13; Length 507;
Pred. No. 5.34e-72;
78; Mismatches 155; Indels 23; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
GEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAVCSGGE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GELSVRRGDRLCALE -- EGGG-YIFARRLSGQPSA-GLVPITHVAKASPET-LSDQPWYF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gkisggeavqql-qpped-glflvresarhpgdyvlcvsfgrdvihyrv-lhrdghltid 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gegefgavlqgeylgq-kvavknikc-dvtaqafldetavmtkmghenlvrllgvilh-q 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gelafrkgdvvtileacenkswyrvkhhtsgqegllaagalrerealsadpklslmpwfh 124
                                                                                                                                                                         373 lwevísygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaeparrppfrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glyivmehvskgnlvnflrtr-gralvntagllgfslhvaegmeyleskklvhrdlaarn
                                                                                                                                                                                                                                                                                                                                      317 ilvsedlvakvsdfglakaerkgl----dssrlpvkwtapealkhgkftsksdvwsfgvl
                                                                                                                                                                                                                                                                                                                                                                                                               ::| | ::: | ::| | : | :|| : | ::| ::: | ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eavffcnlmdmvehyskdkgaictklvrpkrkhgtksaeeelaragwllnlqhltlgagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytoplasmic; tyrosine kinase; blood; cell differentiat: screening; anticancer agent; SH3; src homology domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "tyrosine kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "SH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AGG-1994; JO1411.
25-AUG-1993; JP-210403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.4%;
Best Local Similarity 39.8%;
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplsmic tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 15
R71133 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "S
233..478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95-106842/14.
```

```
පු
 ò
```

413	
khgkftsksdvwsfgvl	=======================================
-dssrlpvkwtapeal	=======================================
aerkgl	
akvsdfglakaerk	:: = :: ::
358 ilvsedlvakvsdfg]	- - -
358	

qq δχ QQ δy

³⁵⁶ VLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWSFGVL 415

⁴⁷⁴ laekl 478 Dp

^{| |||} 476 LREKL 480

Search completed: Thu May 20 12:17:45 1999 Job time: 226 secs.

		(TM)
'		
 		 _ <u> </u>
 -		//
 		 - -
' 	 >	' <u>-</u>
 	ブ 	<u>_</u> _

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:18:07 1999; MasPar time 28.76 Seconds 635.602 Million cell-updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (1-488) from US09099053.pep (1 of 6) 3671 1 MEPFLRRRLAFLSFFWDKIW......ERPSFAILREKLHAIHRCHP 488 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

116695 seqs, 37453910 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

Database:

Mean 49.350; Variance 96.105; scale 0.513 pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	0.00e+00	0.00e+00	1.20e-271	1.19e-260	5.25e-260	6.69e-253	6.89e-250	1.13e-249	1.85e-249	1.35e-248	8.20e-249	5.94e-248	3.62e-248	3.62e-248	2.63e-247	3.12e-246	1.16e-246	1.16e-246	1.38e-245	1.38e-245	1.38e-245	9.99e-245	2.31e-242
	14	kina		kina	kina	kina	kina	kina		kina														
	Description	protein-tyrosine	srm - mouse	protein-tyrosine					p56-tck - mouse															protein-tyrosine
2	Δ !																							
	a	A56040	I56322	S24553	S24550	A39939	S49016	TVHUHC	I48845	A23639	I49552	TVHUFR	I38396	OKHULK	B34104	A34104	TVHAST	TVCHS	TVFVS1	JQ1321	TVFVS2	TVFVPR	TVMSHC	S20808
	DB	7	7	7	7	7	~	-	~	~	7	н	~	Н	7	~	Н	Н	Н	~	Н	Н	П	~
	Length	496	496	506	505	507	451	505	509	509	512	529	505	509	532	532	509	533	568	503	557	587	503	526
æ	Query	80.0	79.9	o,	37.9	7	36.9	36.5	ė	9	36.4	9	36.3	o.	36.3	36.2	36.1	36.1	36.1	36.0	36.0	36.0	35.9	35.6
	Score	2938	2932	1442	1391	1388	1355	1341	1340	1339	1335	1336	1332	1333	1333	1329	1324	1326	1326	1321	1321	1321	1317	1306
	Result No.		7	m	4	Ŋ	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

180 SGSLYLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPCIPQIPLVQDEWERPRSEFVFGRK 239

g

(4 (4	44 11	00	υ'n.	50	17	206	protein-tyrosine protein-tyrosine	kina kina	.02e-24 .02e-24	
0 00	27 8	302	35.5	537 541 525	777	92 YS	59(Xfyn) - Xiph rotein-tyrosine		57e	
1110	000	900	200	522	7 7 7	· ·	protein-tyrosine protein-tyrosine	kina	.39e-24 .75e-24	
ייייייייייייייייייייייייייייייייייייייי		$\sigma \sigma$		52	00	0	protein-tyrosine protein-tyrosine	kina kina	.39e-24 .26e-24	
מין ניי	. 4 	დდ		52	7	_	protein-tyrosine protein-tyrosine	kina Kina	.26e-24 .87e-23	
(T) (T)		ω ω	. n	53 54	7.7		protein-tyrosine protein-tyrosine	kina kina	.80e-23	
(*) (*	۲ « ۱ د	α α		S S S	7 -		protein-tyrosine	kina	.32e-23	
1 (1) 4	600	000	4.	24.2	(1)		protein-tyrosine	kina	.32e-23	
4	- H	ဆေ		5 4 4	7 (7		pp62v protein - 1 pp62v protein - 1	sno	.44e-23 .32e-23	
44	2 6	7	4 4	53	71 0		protein-tyrosine	kina	.46e-23	
'বিব	7 4 5	9 9	44	55 A	121	A43610 TVHUSC	protein-tyrosine		.04e-23	
						ALIGNMENTS				
RESULT		П	A56	040	#	s complet				
TITLE	. 63		, O	tein	0	kinas	2.7.1.112) Srm,	nonrece	eptor type	
ORGANISM DATE	MSI		# fo 01-	formal_nam	0) # 0	Mus musculus # sequence_revis	common_name house ion 01-Dec-1995 #	mouse text_c	hange	
ACCES	ACCESSIONS		A56	12-Jun-1 156040 156040	ת					
# .		Ø	Koh R	Kohmura, N. R.; Taked	da,	Yagi, T.; Tom N.; Chiba, J	oka, Y.; Oyanagi, ; Ikawa, Y.; Aiza	M.; Ko wa, S.	ominami,	
## ##	ourna itle	н	MO1	. cel	re Bi	ol. (19 ceptor	6915-6925 e kinase, Srm: cl	Вu	and	
#	cce	ion	A56	arget 040	g	sruptio				
	## ## ## #re	tus ecul idue	_typ	prel e mRNA 1-49	H # 1	ary label KOH				
GENET	##cr ICS	J-SSC	efere		C)	186;	072; PID:d1005873	; PID:	9529073	
#map. CLASSIF	85	sition TION	# 12	perfami	ly ,	igned s	or Tyr-speci	ic pr	otein	
KEYWORDS	RDS		ATP	kinases; protein TP; phosphotransf	Pr.	kınase erase	оду; ѕнз пошо	тоду		
FEATORE 62-1 232-	11			doma doma	9.9	homology # ein kinase	label SH3\ homology #label	/N I		
240 SUMMAR	- Z		#1e	egi 49	g.c	otein kinas olecular-we	ATP-binding moti ght 55593 #check	f sum 30	T	
Que: Best Matc	ry Ma : Loc :hes	ch 1 Si 384	milar ; Co	80 Jarity 78 Conservat	.08 .48 ive	; Score 2938; ; Pred. No. 0 54; Mismat	DB 2; Length 4 .00e+00; ches 46; Indels	96; 6;	Gaps 4;	
qq	1		LRKRLTFL	3F.	KIW	AD-ESEEDIP	PEQAAAVEPC	SFPAPR	RARL 59	
Qy	1 1	MEPFLE	RRLA	- E	WDKIWE	EPDHGTP	GSLDPNTDPVPTLPAEPC	S-PFPQ	L 55	
qq	60	FRALYDE	<u> </u>	EEL	SGGI	SVSGGDRLYALKEEGDYIFAORL	SGPPSTGLVPVT	F	EPP 119	
ογ	26 1	FLALYDF		ARCGGELSV	RRGI	SVRRGDRLCALEEGGGYIF	SGQPSAGLV	AKAS	PETL 115	
qq	20	SDQPWYFS	<u> </u>	SRAQAQQLLLSPA:	<u> </u>	NAPGAFLIRP	SESSIGGYSLSVRAQAKVCHYR	H	17	
οy	9	SDOPWI	5	SRIOAQO	ij Lij	NEPGAFLIRP	SLGGY	≥:	SMAA 175	
i	100	TOTOTO	000	KULUCE		T TOMOT TAKEMENT	endange out to to contract	744444	000 40.	

N

```
4;
                                                                 295
                                                                                           359
                                                                                                                      355
                                                                                                                                               VLVGDDLTCKVADFGLARLLKDDVYSPSSGSKIPVKWTAPEAANYRVFSQKSDVWSFGIL 419
                                                                                                                                                                                                                235
                                        299
                                                                                                                                                                                                   LYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEERPTFAI 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRALYDFTARCAEELSVSRGDRLYALKEEGDYIFAQRLSGPPSTGLVPVTYLAKATPEPP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDQPWYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGYSLSVRAQAKVCHYRICMAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSLYLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPCIPQIPLVQDEWERPRSEFVLRKK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTKENEALKSLRHERLIRLHAICSLG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEPFLRKRLTFLSFFWDKIWPAD-ESEEDIPRIQGHDDNPVPEQAAVEPCSFPAPRARL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                              #formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
EPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHRDLAARN
                                                                                                         LGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLIKEIEALKSLRHERLIRLHAICSLG
                                                                                                                                                                                                                                                                                                                                                                                                                               Kawachi, Y.; Nakauchi, H.; Otsuka, F.
J. Invest. Dermatol. (1995) 21:533-538
Identification of a novel CDNA clone encoding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN\
#region protein kinase APP-binding motif
#length 496 #molecular weight 55731 #checksum 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues_______1-496 ##label RES
##cross-references GB:D49427; NID:9684971; PID:9684972
FICATION #superfamily unassigned Ser/Thr or Tyr-specific
Kinases, protein kinase homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2932; DB 2; Length 49
Pred. No. 0.00e+00;
54; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine kinase in murine skin.
                                                                                                                                                                                                                                                                                                                                      #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.9%;
1 Similarity 78.2%;
383; Conserved
                                                                                                                                                                                                                                                                                                                                                                                          12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                    monse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                       489
                                                                                                                                                                                                                                                                     156322
                                                                                                                                                                                                                                                                                                                                                    Srm
                                                                                                                                                                                                                                                       LREKLNAINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                       ~
                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                              journal
                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62-111
232-491
240-248
                                     240
                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
            176
                                                               236
                                                                                          300
                                                                                                                    296
                                                                                                                                                                        356
                                                                                                                                                                                                  420
                                                                                                                                                                                                                           416
                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                               476
                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
                                                                                                                                                                                                                                                                                                                                                 TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                            DATE
                                 g
                                                               ò
                                                                                       g
                                                                                                                                            g
                                                                                                                                                                      ۵y
                                                                                                                                                                                                 g
                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                 ò
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
    freshwater sponge

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                              355
                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYMEKPQTAGLSKQANEEWEIEKKQIKLLRGLGAGQFGEVWEGLWNGTTSVAVKTLKPGT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                               $24553  #type complete protein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sprotein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sprotein-tyrosine kinase 4  #formal_name Spongilla lacustris 07.may-1993 #sequence_revision 07-may-1993 #text_change 08-Sep-1997
                420 LYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEERPTFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHRDLAARN
                                                          360 VLVGDDLTCKVADFGLARLLKDDVYSPSSGSKIPVKWTAPEAANYRVFSQKSDVWSFGIL
                                                                              :|: | | :|: : : | ||| 35 DPNIDPVPILPAEPCSPFPQLFLALYDFTARCGGELSVRRGDRLCALE-EGGGGYIFARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 EPKPKPPPQVPPAQDVKYP-IYVGKYDYDSRTDDDLSFKKGDLMYIISTDEGDWWFARSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTAGKEGYIPSNYVA-EY-KSLDAEEWFFGQVKRVDAEKQLMMPFNNLGSFLIRDSDTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFSLSVRDIDRVRHYRIKKLENGTYFVTR-RLTFQSIQELVAYYTQQADGLCVNLKGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 MSIEEFLEEASIMKQLRHPKLIQLYAVCTKEEPIYIVTELMKHGSLLEYL-RGDGRSLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 39.3%; Score 1442; DB 2; Length 506;
Similarity 43.6%; Pred. No. 1.20e-271;
197; Conservative 100; Mismatches 140; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                           September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN
#ragion protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 506 #molecular-weight 57561 #checksun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1 1-506 ##label RAU
##cross-references EMBL:X61604; NID:910155; PID:910156
                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                           Raulf, F. submitted t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                      |||||:||:|
476 LREKLHAIHR 485
                                                                                                                                                                                       LREKLNAINR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                        $24553
                                                                                                                                                                                                                                                                                                                              ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                           #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 1
                                                                                                                                                                                                                                                                  m
                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122-214
238-496
246-254
268
                             296
                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 1
                                                                                                                                                                                                                                                                                                                                                                                            ACCESSIONS
300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARY
                                                                                                                                                                                                                                                                  RESULT
                           δý
                                                     g
                                                                                         δ
                                                                                                                     d
                                                                                                                                                       δŽ
                                                                                                                                                                                  g
                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

325

ŏ

3

ò

```
PRPAACPAEVYVLMLECWRSSPEERPSFATLR
                                                 S
                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                          ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125-222
241-499
446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                                                                                                                                                                                                                 #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66-114
                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARY
å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
8

    freshwater sponge

              453
                                  385 SSKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHFTLQQIMRGYR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDFSLSVKDQDRVRHYRVRRLEDGSLFVTRRSTFQILHELVDHYKIETDGLCCKLLYPCL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 QAEKPQTAGLLRQANEEWEIEKTQIKLLRRLGAGQFGEVWEGLWNGTTSVAVKTLKPGTM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 ----PQKAP--RQ--DVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANM 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIAGKEGYIPSNYVA-EY-KSLDAEEWFLGKIKRVEAEKMLNQSFNQVGSFLIRDSETTP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 SGQPSAGLVPITHVAKASPETLSDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 GGYSLSVRAQAKVCHYRVSMAADGSLYLQKGRLFPGLEELLTYYKANWKLIQNPLLQPCM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 SVEEFLQEASIMKRLRHPKLIQLYAVCTKEEPIYIVTELMKYGSLLEYLRGEDG-VLKIE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLVDVAAAQVASGMSYLEQQNYIHRDLAARNILVGEHGICKVADFGLARVIDEEIYEAHTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 PLLGFACQVAEGMSYLEEQRVVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKFPIKWTAPEAAMYNRFTIKSDVWSFGVVLYEIITYGRFPYPGMTNPEVLEKIQQNYRM 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRL 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 EPKPKPPPQVPPAQDVKYP-IYVGKYDYDSRTDDDLSFKKGDLMYIISTDEGDWWFARSK 97
                                                                                                                                                                                                                                     src-type tyrosine kinase 1
#formal_name Spongilla lacustris
07-May-1993 #sequence_revision 07-May-1993 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
              394 GAKFPIKWTAPEAAMYSRFTIKSDVWSFGIVLYËVITYGRFPYPGMTNAQVLEQIQOSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #checksum 3389
                                                                                                                                                                                                                                                                                                                                                   Raulf, F.
submitted to the EMBL Data Library, September 1991
S24550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif\
#active_site Lys #status predicted
#length 505 #molecular-weight 57693 #checksum 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-505 ##label RAU
##cross-references EMBL:X61601; NID:g10149; PID:g10150
                                                                                                                                                                                    S24550  #type complete
protein-tyrosine kinase (EC 2.7.1.112) 1
  (Spongilla lacustris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1391; DB 2; L
Pred. No. 1.19e-260;
95; Mismatches 147;
                                                                                     485
                                                                                                       PCPANCPKQFHDIMLDCWREDPASRPTFETLQ 486
                                                                                  454 MPRPMGCPEKLYAIMMDCWREDPASRPTFETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%;
43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 197; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
                                                                                                                                                                                                                                           ALTERNATE_NAMES ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                       *submission
                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                     #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61-111
122-214
238-496
246-254
                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                     RESULT
ENTRY
                                                                                                                                                                                                        TITLE
              유
                                               ö
                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

à

ö ద ò ò

ö

```
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:8778-8782
#title Additional member of the protein-tyrosine kinase family: the src-and lck-related protooncogene c-tkl.
#cross-references MUID:88097370
#accession A39939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mature
                                              - chicken
T-cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCSPLQDKLVVALYDYEPTHDGDLGLKQGEKLRVLEESGEWWRAQSLTTGQ-EGLIPHNF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNLQHPRLVRLYAVVTK-EPIYIITEYMEKGSLVDFLKTSEGIKLSINKLLDMAAQIAEG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GB:J03579; NID:g212712; PID:g212713
FICATION #superfamily protein-tyrosine Kinase src; protein kinase homology; SH2 homology; SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3 homology SH3
                                                                                                                                                antigen associated protein tki
#formal_name Gallus gallus #common_name chicken
06-Mar-1992 #sequence_revision 05-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence extracted from NCBI backbone (NCBIN:88831 NCBIP:88833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chow, L.M.; Ratcliffe, M.J.; Veillette, A. Mol. Cell. Biol. (1992) 12:1226-1233 tkl is the avian homolog of the mammalian lck tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||: : | :|||||: : |:|:::| :|| ||:|
PCSPFPQ-LFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 VAMVN--SLEPEPWFFKNLSRKNAEARLLASGNTHGSFLIRESETSKGSYSLSVRDFDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGETVKHYKIRNMDNGGYYI-SPRVTFSSLHELVEYYSSSSDGLCTRLGKPCRTQKPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 QA-KVCHYRVSMAADGSLYLQKGRL-FPGLEELLTYYKANWKLJQNPLLQPCMPQKA--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WWQDEWEVPRESLKLVEKLGAGQFGEVWMGFYNGHTKVAIKNLKQGSMSPSAFLAEANLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-QDVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif.
#modified_site myristylated amino end (Gly) (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #checksum 4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1388; DB 2; Length 507;
Pred. No. 5.25e-260;
93; Mismatches 136; Indels 15;
                                                                                                       protein (tkl);
A39939 #type complete
protein-tyrosine kinase (EC 2.7.1.112)
kinase-related transforming protein (tk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form) #status predicted #length 507 #molecular-weight 58011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references GB:M85043
##experimental_source thymus, spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52-507 ##label STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-88 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase cross-references MUID:92186854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.8%;
Best Local Similarity 45.3%;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                     A42126; A39939
A42126
                                                                                                                                                                                                                                                                                                      07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A39939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                       ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
```

.. = =

```
#description catalyzes the phosphorylation of a peptidyl tyrosine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
#title
                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal
                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                                                                                                           ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                             #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #title
                                                                                                                                                                                                                        TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION
                                                                                                                                                                                          RESULT
                                                                                                                                                                                                            ENTRY
                                                                                                                                                                                                                                                           DATE
                                                                  δλ
                                                                                                      음
                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                        Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, T.; Lowe, P.N.; Page, M.J.; Gusterson, B.A.; Crompton, M.R. Oncogene (1994) 9:2383-2390 Cloning and characterisation of cDNAs encoding a novel non-receptor tyrosine kinase, brk, expressed in human breast tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                    410 INYGTFTIKSDVWSFGILLTEIVTYGRIPYPGMINPEVIQNLERGYRMPQPDNCPQELYE 469
                                                                                                                    398 ANYRVESQKSDVWSFGVLLHEVFTYGQCPYEGMTNHFTLQQIMRGYRLPRPAACPAEVYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 KGLRHERLIRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 FLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVP-ITHVAKASPET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 VESEPWFFGCISRSEAVRRLQAEGNATGAFLIRVSEKPSADYVLSVRDTQAVRHYKIWRR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : :||:|: : ||::| : | : | |||||| || : : | |||| | ||::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 YVGLWDFKSRTDEELSFRAGDVFHVARKEEQWWWATLLDEAGGAVAQGYVPHNYLAERET 72
                                                                                                                                                                                                                                                                         S49016 #type complete
protein-tyrosine kinase (EC 2.7.1.112) brk - human
#formal_name Homo sapiens #common_name man
07-May-1995 #sequence_revision 21-Jul-1995 #text_change
                                 MAFIEAKNYIHRDLRAANILVSEALCCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGRLHLNEAVSFLSLPELVNYHRAQ-SLSHGLRLAAPCRKHEPEPLPHWDDWERPREEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 TLCRKLGSGYFGEVFEGLWKDRVQVAIKVISRDNLLHQQMLQSEIQAMKKLRHKHILALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AVVSVGDPVYIITELMAKGSLLELLRDSDEKVLPVSELLDIAWQVAEGMCYLESQNYIHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 451 #molecular-weight 51834 #checksum 5817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-451 ##label MIT
##cross-references EMBL:X78549; NID:g515025; PID:g515026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1355; DB 2; I
Pred. No. 6.69e-253;
                                                                                                                                                                                          LAMACWKEQPEERPTFEYMKSVLEDF 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ne GDB:BRK
##cross-references GDB:378058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.9%;
larity 46.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                            24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78-170
189-448
197-205
                                 350
                                                                                                                                                                     470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
                                                                                                                                                                                                                                                                                                                                                                                                                                             #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
15-67
                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                         DATE
                             g
                                                                 ŏ
                                                                                                g
                                                                                                                                   ò
                                                                                                                                                                 q
                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Diaz, M.O.; Rowley, J.D.
Mol. Cell. Biol. (1987) 7:2267-2275
Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and is expressed in hemopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H. Gene (1992) 113:275-280

The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase (PTK) encoding gene (HCK) confirms conservation of exon-intron structure among human PTKs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8913-8917
Putative tyrosine kinases expressed in K-562 human leukemia
                                                        371 WSFGILLHEMFSRGQVPYPGMSNHEAFLRVDAGYRMPCPLECPPSVHKLMLTCWCRDPEQ 430
                                                                               350 DLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M. Mol. Cell. Biol. (1987) 7:2276-2285
Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho,
                                                                                                                                                                                                                                                                                                                                              TVHUHC #type complete protein-tyrosine kinase (EC 2.7.1.112) hck - human protein-tyrosine kinase (EC 2.7.1.112) hck - human #formal_name Homo sapiens #common_name man 31_bec-1989 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #map_position 20q11-20q12
#introns 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A27811; A27812; JC1149; C38268; S31103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references GDB:119303; OMIM:142370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##residues 157-505 ##label HRA
##cross-references EMBL:X59741
SNCE A38268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362-417 ##label PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-505 ##label QUI
##cross-references GB:M16591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #cross-references MUID:87257942
#accession A27811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the src family. #cross-references MUID:92241680 #accession JC1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #cross-references MUID:87257943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:91062389
#accession C38268
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-May-1998
                                                                                                                                                                                                         || | :|||:| ::
470 RPSFATLREKLHAI 483
                                                                                                                                                                     431 RPCFKALRERLSSF 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDB: HCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A27811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A27812
```

I48845

US-09-099-053-2-01.rpr

```
#accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                            KEYWORDS
                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Voronova, A.F.; Sefton, B.M.
#journal Nature (1986) 319:662-685
#title Expression of a new tyrosine protein Kinase is stimulated by retrovitus promoter insertion.
#cross-references MUID:86146842
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.5%; Score 1341; DB 1; Length 505;
Best Local Similarity 43.3%; Pred. No. 6.89e-250;
Matches 189; Conservative 106; Mismatches 127; Indels 14; Gaps 10;
                                                                                                                                                                           #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site palmitate (Cys) (covalent) #status
                                                                                                                                         #product protein-tyrosine kinase hck #status predicted
#label MAT\
                                                              myristylation; phosphoprotein; phosphotransferase;
thiolester bond; transforming protein; tyrosine-specific
protein kinase
             *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; blocked amino end; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 VALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATR-KEGYIPSNYVARV--DSLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||: | :||:: ||:: ||:: ||:: :||
57 LALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITHVAKASPETLS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TEEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESLKLEKKLGAGQFGEVWMATYNKHTKVAVKTMKPGSMSVEAFLAEANVMKTLQHDKLVK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 SEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHAVVIK-EPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQRNYI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVWSFGILLMEIVTYGRIPYPGMSNPEVIRALERGYRMPRPENCPEELYNIMMRCWKNRP 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148845 #type complete
p56-tck - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision,02-Jul-1996 #text_change
03-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTLDNGGFYISPRSTFSTLQELVDHYKKGNDGLCQK-LSVPCMSSKPQKPWEKDAWEIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 HRDLRAANILVSASLVCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKS
                                                                                                                                                                                                                                                                                                                                                                                   #checksum 7314
                                                                                                                                                                                                                                                                                                                                                 (by
                                                                                                                                                                                                                                                                                                                                          #binding_site phosphate (Tyr) (covalent)
autophosphorylation) #status predicted
th 505 #molecular-weight 57312 #checksu
                                                                                                                                                                                                                                                                                                                              #active_site Lys #status predicted\
                                                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EERPTFEYIQSVLDDF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                   #length 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I48845
               CLASSIFICATION
                                                                                                                                                                             64-112
123-220
239-497
247-255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                        FEATURE
2-505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M. Cell (1985) 43:393-404
A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma
                                                                                                                                                                                                                                                                                                                                                     Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                                   57 PASPLQDNLVIALHSYEPSHDGDLGFERGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 VAKAN--SLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 ANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYV 457
                                                                   ##cross-references EMBL:X03533; NID:954813; PID:954814
FICATION #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||: : | :|| : : |:|: :|::| ||::|
PCSPFPO-LFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHDLVRHYTNASDGLCTKLSRPCQTQKPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 QAKVC-HYRVSMAADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPCMPQKA--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPDAFLAEANLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQLQHPRLVRLYAVVTQ-EPIYIITEYMENGSLVDFLKTPSGIKLNVNKLLDMAAQIAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAFIEEQNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYH
                                                                                                                                                                                    #domain SH3 homology #label SH3\
#domain protein Kinase homology #label KIN\
#red_don protein Kinase ATP-binding motif
#length 509 #molecular-weight 57942 #checksum 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A23639 #type complete protein-tyrosine kinase (EC 2.7.1.112), lymphocyte lck protein the musculus #common_name house mouse #formal_name Mus musculus #common_name house mouse
                                                                                                                                                                                                                                                                                                   Score 1340; DB 2; Length 509;
Pred. No. 1.13e-249;
91; Mismatches 142; Indels 15;
##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. (1987) 7:4407-4413
Two lck transcripts containing different 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||: ||: ||: ||:||:|
LMLECWRSSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMLCWKERPEDRPTFDYLRSVLDDF 497
                                           1-509 ##label RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-509 ##label MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:86079521
#accession A23639
                                                                                                                                                                                                                                                                                                     Query Match 36.5%;
Best Local Similarity 44.4%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A23639; I57629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A23639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATE_NAMES
                                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                    68-116
243-501
251-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
```

untranslated

ø

```
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION
                                                                                                                                                                                                                                                                                  ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                            #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123-215
239-501
247-255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383
                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                      #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56-112
                                                                                                                                                                                                                                                                                                                                                                                                              #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                    GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAKAN -- SLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSIGNE_LYPE DANA
##TOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 KQLQHPRLVRLYAVVTQ-EPIYIITEYMENGSLVDFLKTPSGIKLNVNKLLDMAAQIAEG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAFIEEQNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 INYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYH 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149552 #type complete
protein-tyrosine kinase (EC 2.7.1.112) bsk/iyk - mouse
intestinal tyrosine kinase
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oberg-Welsh, C.; Welsh, M. Gene (1995) 152:239-242 Cloning of BSK, a murine FRK homologue with a specific pattern of tissue distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHDLVRHYTNASDGLCTKLSRPCQTQKPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 WWEDEWEVPRETLKLVERLGAGGFGEVWMGYYNGHTKVAVKSLKQGSMSPVPFLAEANLM
                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 509 #molecular-weight 57952 #checksum 3251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1339; DB 2; Length 509;
Pred. No. 1.85e-249;
91; Mismatches 142; Indels 15;
                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession 149552
##status translated from GB/EMBL/DDBJ
##molecule_type mRNA
regions are present in t cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMMLCWKERPEDRPTFDYLRSVLDDF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:88142832
#accession 157629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%;
Local Similarity 44.4%;
les 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149552; 148608
149552
                                                                                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATE_NAMES
                                                                                                                                                                           CLASSIFICATION
                                                                         #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                            243-501
251-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                               FEATURE
68-116
                                                                                                                                                                                                                                                                                                                                                       127-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 KHEIKLPVKWTAPEAIRTNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; intestine; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change
                                                                                               Ziemiecki, A.
Biochem. Biophys. Res. Commun. (1995) 209:582-589
iyk, a novel intracellular protein tyrosine kinase
differentially expressed in the mouse mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 PEAPRSQEPERSHGQYFVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 TGLGQQLQGYIPSNYVAEDRSLQAEPWFFGAIKRADAEKQLLYSENQTGAFLIRESESQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 GGYSLSVRAQAKVCHYRVSMAADGSLYLQKGRLFPGLEELLTYYKANWK-L-I--QNP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 KIQVPTPFDLSYKTADQWEIDRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 - LQPCMPQKAP-R-QDVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 DPNDFLREAQIMKSLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 QQVDMAAQVASGMAYLESQNYIHRDLAARNVLVGEHNIYKVADFGLARVFKVDNEDIYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFSLSVLDEGVVKHYRIRRLDEGGFFLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPCL
                                                                               ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 512 #molecular-weight 58891 #checksum 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 36.4%; Score 1335; DB 2; Length 512; Local Similarity 43.2%; Pred. No. 1.35e-248; nes 198; Conservative 102; Mismatches 140; Indels 18;
                      ##cross-references GB:L36132; NID:9556287; PID:9777773
NCE I48608
.thors Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres,
                                                                                                                                                                                                                                                                                                                                               ##residues
##cross-references EMBL:248757; NID:9736263; PID:9736264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVHUFR #type complete
protein-tyrosine kinase (EC 2.7.1.112) fgr
kinase-related transforming protein (fgr)
#formal_name Homo saplens #common_name man
31_Dec-1988 #sequence_revision 30-Sep-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-May-1998
A27676; A28353; A24842; A45930; S24306
A27676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 YRLPQPSNCPQQFYSIMLECWNVEPKQRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translated from GB/EMBL/DDBJ
1-512 ##label RES
                                                                                                                                                                                               intestine.
#cross-references MUID:95251656
#accession 148608
                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSIONS
REFERENCE
```

16;

Length 529;

^

```
81 LFIALYDYEARTEDDLTFTKGEKFHILNNTEGDWWEARSLSS-GKTGCIPSNYVA-PV-D 137
                                                                                                                                                                      138 SIQAEEWYFGKIGRKDAERQLLSPGNPQGAFLIRESETTKGAYSLSIRDWDQTRGDHVKH 197
                                                                                                                                                                                                                                                                                                                                                                                       EISRSSITLERRIGTGCFGDVWLGTWNGSTKVAVKTLKPGTMSPKAFLEEAQVMKLLRHD 316
                                                                                                                                                                                                                                                    198 YKIRKLDMGGYYI-TTRVQFNSVQELVQHYMEVNDGLCNLLIAPCTIMKPQTLGLAKDAW
      #active_site Lys #status predicted
#length 529 #molecular-weight 59478 #checksum 2467
                                                               Score 1336; DB 1; Length 52
Pred. No. 8.20e-249;
95; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:355675
#map_position 4q35-4q35
CLASSIFICATION #superfamily prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##status preliminary
##molecule_type mRNA
                                                               Query Match 36.4%;
Best Local Similarity 45.9%;
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-Apr-1998
138396
138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLDPEERPIFEYLQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 RSSPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB: FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
FEATURE
49-105
232-494
240-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
      291
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                    ò
                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                           Primary structure of the human fgr proto-oncogene product p55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                         K.; Sukegawa, J.; Yamamoto, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalyzes the phosphorylation of a peptidyl tyrosine residue by \ensuremath{\mathsf{AIP}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site palmitate (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; autophosphorylation; blocked amino end; lipoprotein;
myristylation; phosphoprotein; phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Patel, M.; Leevers, S.J.; Brickell, P.M.
#journal Oncogene (1990) 5:201-206
#title Structure of the complete human c-fgr proto-oncogene and identification of multiple transcriptional start sites.
#cross-references WID:90206622
#accession S24306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thiolester bond; transforming protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brickell, P.M.; Patel, M.
Br. J. Cancer (1988) 58:704-709
Structure and expression of c-fgr protooncogene mRNA in Epstein-Barr virus converted cell lines.
A45930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                            ##molecule_type mRNA
##molecule_type mRNA
##residues 1.529 ##label REA
##residues 1.529 ##label REA
##rcross-references GB:M19722; GB:J03429; NID:g182573; PID:g182574
A28353 A28353 A28353 Inoue, K.; Ikawa, S.; Semba, K.; Sukegawa, J.; Yamamot
                                                                                                                                                                                                                         #journal Oncogene (1987) 1:301-304
#title v-fgr oncogene from a human B lymphocyte cell line,
    Rao, C.D.; Miki, T.; Cheah,
                                                                                                                                                                                                                                                                                                                                                                                                                      Nishizawa, M.; Semba, K.; Yoshida, M.C.; Yamamoto,
Sasaki, M.; Toyoshima, K.
Mol. Cell. Biol. (1986) 6:511-517
Structure, expression, and chromosomal location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##nolecule_type_DNA
##residues 111-416 ##label REB
##cross-references GB:M12724; NID:g182581; PID:g553286
ENCE A45930
Katamine, S.; Notario, V.; Rao, C.D.;
M.S.C.; Tronick, S.R.; Robbins, K.C.
Mol. Cell. Biol. (1988) 8:259-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proto-oncogene; thiolester bond; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "yeue GDB:FGR ##cross-references GDB:120615; OMIM:164940 #map_bosition 1p36.2-1p36.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-177;524-529 ##label BRI
##cross-references GB:M27454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation not shown
                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-143 ##label INO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-142 ##label PAT ##cross-references EMBL:X52207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c-fgr gene.
#cross-references MUID:87064334
#accession A24842
                                                                                                  *cross-references MUID:88094395
                                                                                    (c-fgr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                        A24842
                                                                                                                                                                                                                                                                                                                                              A28353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                              *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                         #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal
#title
  authors
                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84-133
144-241
261-519
269-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title
                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,6
```

```
463
                                                                         317 KLVQLYAVVSE-EPIYIVTEFMCHGSLLDFLKNPEGQDLRLPQLVDMAAQVAEGMAYMER 375
                                                                                                                                   343
                                                                                                                                                                                                                                                                                            TIKSDVWSFGILLTELITKGRIPYPGMNKREVLEQVEQGYHMPCPPGCPASLYEAMEQTW 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.
#journal Gene (1994) 138:247-251
#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.
#cross-references WUD:94171047
#accession 138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change
376 MNYIHRDLRAANILVGERLACKIADFGLARLIKDDEYNPCQGSKFPIKWTAPEAALFGRF
                                                                                                                                                                                                                  344 QRVVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVF
                                                                                                                                                                                                                                                                                                                          #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 505 #molecular-weight 58254 #checksum 9379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138396 #type complete
protein-tyrosine kinase (EC 2.7.1.112) FRK - human
FYN-related kinase (FRK)
#formal_name Homo sapiens #common_name man
15-Mar-1996 #sequence_revision 15-Mar-1996 #text_cf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain SH3 homology #label SH3/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.3%; Score 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

```
S07822

Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.;
Ziegler, S.F.; Wilson, C.B.
J. Cell. Blochem. (1988) 38:117-126
Structure and expression of lck transcripts in human lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koya, Y.; Caccia, N.; Toyonaqa, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.

Eur. J. Immunol. (1986) 16:1643-1646
A human T cell-specific CDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine
                                                                                                                                                                                                                                                                                                                                   ANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAAACPĀĒVYV 457
                                                                                                                                                                                                 54 QLFLALYDFTARCGGELSVRRGDRLCALEE-GGGYIFARRLSGQPSAGLVPI-THV-AK- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 DQWEIDRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKNL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDTGSKIHLTQQVDMAAQVASGMAY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 HYFVALFDYQARTAEDLSFRAGDKLQVLDTLHEGWWFARHLEKRRDGSSQQLQGYIPSNY 104
                                                                                                                                                                                                                                                                                    105 VAEDRSLQAEPWFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 YRIKRLDEGGFFLTRRRIFSTLNEFVSHYTKTSDGLCVKLGKPCLKIQVPAPFDLSYKTV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 LESRNYIHRDLAARNVLVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 IRSNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQQFYN 464
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKHULK

#type complete
protein-tyrosine kinase (EC 2.7.1.112) lck - human
kinase-related transforming protein (lck)
#formal_name Homo sapiens #common_name man
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.;
Fischer, S.; Benarous, R.
Gene (1989) 84:105-113
Structure of the human lck gene: differences in genomic
organisation within src.related genes affect only
N-terminal exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-may-1998
JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||: :|::| : |:|:|:|:|:|:|:|:|:|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Pred. No. 5.94e-248;
96; Mismatches 135; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues 1-86,'P',88-509 ##label PER
##cross-references EMBL:X13529; NID:g34294; PID:g34295
BNCE S07200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-509 ##label ROU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||| : | |||:| ||| ||
LMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 IMLECWNAEPKERPTFETLRWKL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references EMBL:X14053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:89123626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #cross-references MUID:90108697
Best Local Similarity 44.2%;
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JQ0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S07822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J00152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.
Miyamoto, N.G.; Mak, T.W.
Mol. Cell. Biol. (1989) 9:2173-2180
Structure of the two promoters of the human lck gene:
differential accumulation of two classes of lck transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #product protein-tyrosine kinase lck #status predicted
#!abal MAT\
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GDB:119360; OMIM:153390
#map_cosition 1935-1234.3
#introns 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
#journal Mol. Cell. Biol. (1988) 8:3058-3064
#title Structure of the murine lck gene and its rearrangement in murine lymphoma cell line.
#cross-references MUID:89096891
                                                                                                                                                                                                                                                                    #journal Rosen, N. (1987) 1:357-374
#title Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines. #cross-references WUID:88217332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; blocked amino end; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-35,'vR' ##label RES
##cross-references GB:M21510; NID:G187031; PID:G553522
##cross-references GB:M21510; NID:G187031; PID:G553522
T Protein tyrosine kinases play important roles in the control cell growth and differentiation.
                                                                                                                                                                                                                                               Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.; Linna, T.J.

#journal Biochim. Biophys. Acta (1986) 888:286-295

#title Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).

#cross-references MID:87000726

#accession S07143
#cross-references MUID:87133831
#accession S07200
#molecule_type mRNA
##residues 1-205, ASAITPI', 212-257, 'RCGW', 262, 'TTT', 266,'T'
268-281, 'AGRLP', 287-503, 'STA' ##label KOG
##cross-references EMBL:X05027; NID:936807; PID:936808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myristylation; phosphoprotein; phosphotransferase;
thiolester bond; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
##residues 'A',376-509 ##label TRE
##cross-references EMBL:X04476; NID:935779; PID:935780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 368-471,'H',473-509 ##label VEI
##cross-references EMBL:X06369; NID:g34288; PID:g34289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-35 ##label TAK
##cross-references GB:M26692; NID:g341523; PID:g349702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:89313764
#accession A32797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDB: LCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157636
                                                                                                                                                                                                             S01879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68-116
127-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
2-509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

```
501 DPEERPTFEYLQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||:| |:
SPEERPSFATLR 477
                                                           laevis
                                                                                                                                                                         ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                               ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSIONS
REFERENCE
#authors
        #journal
#title
                                                                                                                                                                                                                                                                                                                #introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87-136
147-244
264-522
272-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466
                                                                                                                                                                                                                                                                                    #gene
                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                     GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
#domain protein kinase_homology #label KIN\
#region protein kinase_ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site palmitate (Cys) (covalent) #status
predicted\
#binding_site palmitate (Tys) (covalent) #status
#active_site Lys #status predicted\
#binding_site phosphate (Tyr) (covalent) (by
#binding_site phosphate (Tyr) (covalent)
#binding_site phosphate (Tyr) (covalent)
#predicted\
#binding_site phosphate (Tyr) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frog
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 PASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase-related transforming protein (src); kinase-related transforming protein (src) 2 ** transforming protein (src) 2 ** fransforming protein (src) 2 ** fransforming protein (src) 30 ** fransforming (src) 30 ** fransforming (src) 30 ** fransforming (src) 30 ** fransforming (src) 30 ** fransforming (src) 40 ** fransform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 PCSPFPQ-LFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 VAKAN--SLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQKP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 ANYRVESQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 INYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 QAKVC-HYRVSMAADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPCMPQKA--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-532 ##label STE
##cross-references GB:M23422; GB:J04822; NID:g214796; PID:g214797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPDAFLAEANLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQLQHQRLVRLYAVVTQ-EPIYIITEYMENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 MAFIEERNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA
                                                                                                                                                                                                                                                                                                       #length 509 #molecular-weight 58000 #checksum 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B., Blol. Chem. (1989) 264:10649-10653
The two Xenopus laevis SRC genes are co-expressed a produces functional pp(60src).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
                                                                                                                                                                                                                                                                                                                                                                                                               Indels 15;
                                                                                                                                                                                                                                                                                                                                                             Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **status preliminary; not compared with conceptual ##molecule_type mRNA ##resident
                                                                                                                                                                                                                                                                                                                                                          Score 1333; DB 1; L
Pred. No. 3.62e-248;
91; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 LMRLCWKERPEDRPTFDYLRSVLEDF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcross-references MUID:89278134
                                                                                                                                                                                                                                                                                                                                                          36.3%;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B34104; I51563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IS1563
Steele, R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession
  243-501
251-259
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ournal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                          SUMMARY
                                                                                                           3,5
                                                                                                                                                                273
                                                                                                                                                                                                                                                  505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
src
464/1
*superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; autophosphorylation; phosphoprotein; phosphotransferase;
tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A34104 #type complete protein-tyrosine kinase (EC 2.7.1.112) src 1 - African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase-related transforming protein (src); kinase-related transforming protein (src) 1 transforming protein (src) 30.00 trans_name Xenopus laevis #common_name African clawed frog 30.00 trans_1990 #sequence_revision 30.00 trans_1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440
                       expressed in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMN 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 FVALYDYESRTETDLSFRKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA-PS-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 IQAEEWYLGKITRREAERLLLSLENPRGTFLVRESETTKGAYCLSVSDYDASRGLNVKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTAVCPTAKPQTQGLSKDAWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 PRDSLRLELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 532 #molecular-weight 59736 #checksum 7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A34104
Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. (1989) 264:10649-10653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1333; DB 2; Length 532;
Pred. No. 3.62e-248;
90; Mismatches 133; Indels 14;
                                                                                                                           translated from GB/EMBL/DDBJ
                                                                                                                                                                     Nucleic Acids Res. (1985) 13:1747-1761
Two divergent cellular src genes are e
                                                                                                                           preliminary;
                                                                 #cross-references MUID:85215578
#accession I51563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.3%;
Best Local Similarity 45.1%;
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-Mar-1998
A34104; I51564
```

```
80/1 **superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps 10;
                                                                                                                                                                                                         Steele, R.E.; Chosn, R.; Ral, B.B.A.; Winokur, S.T.; Unger,
                                                                                                                 ##status
##molocule_type mRND
##molocule_type mRND
##residues
##residues
##residues
##cross-references GB:M24704; GB:J04822; NID:g214804; PID:g214805
                                                                                                                                                                                                                            T.F. #journal Oncogene (1992) 7:2345-2350 #title Structural organization of a src gene from xenopus laevis. #cross-references WUID:93064714 #accession 151564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA-PS-DS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 IQAEEWYLGKITRREAERLLLSLENPRGTFLVRESETTKGAYCLSVSDYDANRGLNVKHY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRDSLRLELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMN 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *LILLE The two Xenopus laevis SRC genes are co-expressed and #cross-references MUID:89278134 #accession A3410A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTAVCPTAKPQTQGLSRDAWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 532 #molecular-weight 59856 #checksum 7110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1329; DB 2; Length 532;
Pred. No. 2.63e-247;
92; Mismatches 132; Indels 14;
                                                                                                                                                                                                                                                                                      ##scatus preliminary; translated from GB/EMBL/DDBJ##molecule_type DNA ##residues 1-112 ##...
                                                                                                                                                                                                                                                                                                                                                    ##residues 1-113 ##label ST2
##cross-references GB:M33646; NID:g214808; PID:g214810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%;
ilarity 44.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 DPEERPTFEYLQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 SPEERPSFAILR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 194; Conser
                                                                                                                                                                                          I51564
                                                                                                                                                                                                                                                                                                                                                                                                           #introns
CLASSIFICATION
                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87-136
147-244
264-522
272-280
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322
                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                          GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

Search completed: Thu May 20 12:21:21 1999 Job time : 194 secs.

US-09-099-053-2-01.rsp

* * *	
* *	(TM)
******	·
* * *	

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:21:39 1999; MasPar time 21.11 Seconds 653.617 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-09-099-053-2 (1-488) from US09099053.pep (1 of 6) 3671 1 MEPFLRRLAFLSFFWDKIW......ERPSFATLREKLHAIHRCHP 488 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 50.552; Variance 83.305; scale 0.607 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7	Fred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	2.70e-294	8.39e-295	1.56e-293	1.62e-292	9.02e-293	9.02e-293	9.35e-292	1.74e-290	5.40e-291	5.40e-291	1.00e-289	1.00e-289	1.00e-289	1.04e-288	3.34e-288	3.34e-288	3.70e-285	6.64e-285	1.15e-285
, , , , , ,	Description	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN
í	TT CT	SRM_MOUSE	SRK4_SPOLA	SRK1_SPOLA	LCK_CHICK	LCK_MOUSE	HCK_HUMAN	FGR_HUMAN	FRK_HUMAN	LCK_HUMAN	SRC2_XENLA	SRC1_XENLA	STK_HYDAT	SRC_CHICK	SRC_AVISS	HCK_RAT	SRC_AVIST	SRC_AVIS2	HCK_MOUSE	SRC_AVISR	SRC_HUMAN	BLK_HUMAN	FYN_XIPHE	YES_CHICK
í	£ ;	٦	Н	Н	Н	Н	Н	Н	Н	Н	٦	Н	Н	Н	Н	Н	H	Н	Н	1	Н	Н	Н	Н
4	watch Length UB	496	206	505	507	508	526	529	505	508	531	531	509	532	568	503	557	587	524	526	535	504	536	541
Query	Match	79.9	39.3	37.9	37.8	36.5	36.5	36.4	36.3	36.3	36.3	36.2	36.1	36.1	36.1	36.0	36.0	36.0	35.9	35.8	35.8	35.5	35.5	35.5
	score	2932	1442	1391	1388	1339	1341	1336	1332	1333	1333	1329	1324	1326	1326	1321	1321	1321	1317	1315	1315	1303	1302	1305
Result		Н	2	m	4	Ŋ	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

																			•	:	
2.14e-284	1.19e-284	3.83e-284	2.21e-283	1.27e-282	4.23e-281	2.44e-280	7.83e-280	1.40e-279	7.83e-280	4.66e-278	8.89e-276	8.89e-276	9.17e-275	5.12e-275	5.12e-275	9.75e-273	5.44e-273	3.13e-272	5.78e-271	1.97e-268	7.06e-264
TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	NEURONAL PROTO-ONCOGEN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS
SRC_RSVH1	FYN_MOUSE	YES_XIPHE	SRC_RSVP	SRC_RSVSR	YES_XENLA	YES_HUMAN	FYN_XENLA	FYN_HUMAN	YES_MOUSE	YES_AVISY	LYN_RAT	SRCN_MOUSE	BLK_MOUSE	LYN_MOUSE	FYN_CHICK	SRC_RSVPA	YES_CANFA	FGR_MOUSE	YRK_CHICK	LYN_HUMAN	SRK2_SPOLA
Н	н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	 1	щ	ч	П
526	533	544	526	526	537	543	536	536	541	528	511	540	498	511	533	523	539	517	532	511	362
35.4	35.4	35.4	35.3	35.2	35.1	35.0	34.9	34.9	34.9	34.7	34.5	34.5	34.4	34.4	34.4	34.2	34.2	34.1	34.0	33.7	33.2
1300	1301	1299	1296	1293	1287	1284	1282	1281	1282	1275	1266	1266	1262	1263	1263	1254	1255	1252	1247	1237	1219
24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SULT 1 SRM_MOUS Q62270; 01-NOV-1 01-NOV-1 TYROSINE	O) S EI E	CC EMBL; D49427; G684972; DR EMBL; D26186; G529073; DR MGD; MGI:101865; SRMS. DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
SRMS OR SRM. MUS MUSCULUS (MOUSE). BUKARYCHZ, METAZOA; CHORDATA; VERTEBRATA; MAWMALIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.		EXP. DERMATOL. 21:533-538(1995). [2] SEQUENCE FROM N.A. TISSUE-LONG; MEDLINE: 95021220. KOHNURA N., TAGI T., TOMOOKA Y., OYANAGI M., KOMINAMI R., TAKEDA N., CHIBA J., IKAWA Y., AIZAWA S.; "A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption."; "A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption.";
SRMS OR SRM. SURS OR SRM. MUS MUSCILUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURNAE; MUS. [1] SEQUENCE FROM N.A. STRAIN-C57BL/6; TISSUE=THYMUS; MEDLINE; 973666; TISSUE=THYMUS; KAWACHI Y., NAKAUCHI H., OTSUKA F.; "ISOLation of a cDNA encoding a tyrosine kinase expr	[1] SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=THYMUS; MEDLINE; 97369678. KAWACHI Y., NARAUCHI H., OISUKA F.; "ISSOLATION Of a CDNA encoding a tyrosine kinase expressed in	KOHMURA N., TAGI I., TOMOOKA Y., OYANAGI M., KOMINAMI R., TAKEDA N., CHIBA J., IKAWA Y., AIZAWA S.; "A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption."; "A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption."; MOL. CELL. BIOL. 14.6915-6925(1994)!- CARLALYIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY!- SIMILARITY: CONTAINS 1 SH3 DOMAIN!- SIMILARITY: CONTAINS 1 SH3 DOMAIN. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the ERBE outstatite the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
SRMS ON SRM. MUS MUSCULUS (MOUSE). EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; MAMMALIA; EUTHERIA; EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS. [1] SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=THYMUS; MEDLINE; 9735968. KAWACHI Y., NARAUCHI H., OTSUKA F.; "ISOLATION Of a CDNA encoding a tyrosine kinase expressed in skin."; EXP. DERMATOL. 21:533-538(1995). [2] SEQUENCE FROM N.A. TISSUE-LUNG; MEDLINE; 95021220.	11 SEQUENCE FROM N.A. STRAIN=CS7BL/6; TISSUE=THYMUS; MEDLINE; 9739678. KAWACHI Y., NAKAUCHI H., OTSUKA F.; KAWACHI Y., OTSUKA F.; ISOJALION Of a CDNA encoding a tyrosine kinase expressed in Skin."; EXP. DERMATOL. 21:533-538(1995). [2] SEQUENCE FROM N.A. TISSUE=LUNC. 95021220.	AGISTROPARTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE! CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE! SIMILARITY: TO CHTER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN BELONGS TO THE SRC SUBFAMILY! SIMILARITY: CONTAINS 1 SH2 DOMAIN! SIMILARITY: CONTAINS 1 SH3 DOMAIN! SIMILARITY: THE CATALITY IN T
SERMS OR STAN. MUSA GUNGELUS. EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MUS. [1] SEQUENCE FROM N.A. STRAIN-CSTSLA[6]; TISSUE-THYMUS; MEDLINE; 97369678. KAWACHI Y., NARAUCHI H., OTSUKA F.; "Isolation of a cDNa encoding a tyrosine kinase expressed in murin. EXP. DERMINCL. 21:533-538(1995). [2] [2] EXP. DERMINCL. 21:533-538(1995). [3] EXP. DENMINA N.A. TISSUE-LUNG; MEDLINE; 95021220. KOMMINA N., YAGIT I., TOMOOKA Y., OYANAGI M., KOMINAMI R., TAKEDA N CHIRA J., IKAMA Y., AIZAMA S.; A novel nonreceptor tyrosine kinase, SIM: cloning and targeted	SEQUENCE FROM N.A. STRAIN=C57BL/6: TISSUE=THYMUS; MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. MEDLINE; 9736678. [2] [2] [2] [2] [2] [3] [4] [5] [5] [6] [6] [7] [7] [8] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	This SWISS-PROT entry is copyright. It is produced through a collaboral between the Swiss institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
SRMS OR SRM. MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; RODENTIA; SCIUROGNATHI; MURIDA [1] SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=THYMUS; MEDLINE; 97389678. KAMACHI Y., NACHI H., OTSUK "ISOlation of a CDNA encoding skin.", EXP. DERMATOL. 21:533-538(1995 [2] SEQUENCE FROM N.A. TISSUE=LUNG; MEDLINE; 9502120. KOHMURA N., YAGI T., TOMOOKA Y CHIBA J., IKAWA Y., AIZAWA S.; A novel noireceptor tyrosine disruption."; A novel noireceptor TYPOSHAE -! CATALYTIC ACTIVITY: ATP + -! SIMILARITY: CONTAINS 1 SH3 -! SIMILARITY: CONTAINS 1 SH3 -! SIMILARITY: CONTAINS 1 SH3	II SEQUENCE FROM N.A. STRAIN—C57BL/6; TISSUE—THYMUS; MEDLINE; 97369678. KAWACHI Y., NAKAUCHI H., OTSUK "ISOLAtion of a CDNA encoding skin."; CONTACT OF A	

```
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325
g
                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                     4;
                                                                                      SH2.
PROTEIN KINASE.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
R -> G (IN REF. 2).
LRK -> FGR (IN REF. 2).
N -> I (IN REF. 2).
W+> FD44DEF6 CRC32;
                                                                                                                                                                                                                                                             235
                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                               60 FRALYDFTARCAEELSVSRGDRLYALKEEGDY-FFAQRESGPPSTGLVPVTYLAKATPEPP 119
                                                                                                                                                                                                                                                                                      SDQPWYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGYSLSVRAQAKVCHYRICMAP 179
                                                                                                                                                                                                                                                                                                                                                                                       EPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHRDLAARN 359
                                                                                                                                                                                                                                                                                                                                                                                                                       VLVGDDLTCKVADFGLARLLKDDVYSPSSGSKIPVKWTAPEAANYRVFSQKSDVWSFGIL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEERPTFAI 479
                                                                                                                                                                                                                             1 MEPFLRKRLTFLSFFWDKIWPAD-ESEEDIPRIQGHDDNPVPEQAAAVEPCSFPAPRARL 59
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                               SGSLYLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPCIPQIPLVQDEWERPRSEFVLRKK
                                                                                                                                                                                                                                                                                                                                LGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTKENEALKSLRHERLIRLHAICSLG
                                                                                                                                                                                                                                                                                                                                                               TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.

55 116 SH3.
                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EURARYOTA, METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
                                                                                                                                                                                   Score 2932; DB 1; Length 496; Pred. No. 0.00e+00;
                                                                                                                                                                                                   54; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 2

SRK4_SPOLA STANDARD; PRT; 506 AA.

501-NOV-1995 (REL. 32, CREATED)

01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

01-NOV-1995 (REL. 32, LAST SANOTATION UPDATE)

TYROSINE-PROTEIN KINASE SRK4 (EC 2.7.1.112).
PS00109; PROTEIN_KINASE_IYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                                                                    Μ.
M
                                                                                                                                                                                   Query Match 79.9%;
Best Local Similarity 78.2%;
                               PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P11362; 1FGI.
                                                                                                                                                                  55731
                                                                                                                                                                                                   383; Conservative
                                                                                        1124
2344
2540
2562
3854
3854
236
236
236
236
2496
2496
2496
2496
2496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LREKLNAINR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREKLHAIHR 485
      PROSITE; P
PROSITE; P
PROSITE; P
                                                                                       DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
CONFLICT
                                                                                                                                                          CONFLICT
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                      296
                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                       356
                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1D SR AC P44 DT 011 DT 011 DT 011 DE T1 SGN SF CO S SI OC EE
g
                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                    음
                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 39.3%; Score 1442; DB 1; Length 506;
Local Similarity 43.6%; Pred. No. 0.00e+00;
Nes 197; Conservative 100; Mismatches 140; Indels 15; Gaps 10;
                                                                               MEDLINE; 92334872.

OTTILIE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;

OTTILIE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;

ONTILIE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;

Spongilla lacustris.";

ONCOGENE 7:1625-1630(1992).

-:-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

PROTEIN TYROSINE PHOSPHATE.

PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| || :: | :| || || SGQPSAGLVPITHVAKASPETLSDQPWYPSGVSRTQAQQLLLSPPNEPGAFLIRPSESSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 DTAGKEGYIPSNYVA-EY-KSLDAEEWFFGQVKRVDAEKQLMMPFNNLGSFLIRDSDTTP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 MSIEBFLEEASIMKQLRHPKLIQLYAVCTKEEPIYIVTELMKHGSLLEYL-RGDGRSLKL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 PDLVDMCSQVASGMSYLEQQNYIHRDLAARNILVGEHKICKVADFGLARVIDEEIYEAKL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M----PQKA--PRO--DVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSAN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 EPKPKPPPQVPPAQDVKYP-IYVGKYDYDSRTDDDLSFKKGDLMYIISTDEGDWWFARSK 97
                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : :: | :| || :| || :| || || 265 MKLTDLAKEIQTLKGLRHERLIRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVMEKPQTAGLSKQANEEWEIEKKQIKLLRGLGAGQFGEVWEGLWNGTTSVAVKTLKPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00069; pkinase; 1.
HSSP; P0023; TPPK.
TRANSFERASE; TROSSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
7; 807A71D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH2.
PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61604; G10156; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 493 PF
246 254 AT
268 268 AT
359 359 BY
506 AA; 57561 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00017; SH2;
PFAM; PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                    SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

```
kinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                 LCK_CHICK
P42683;
                                                        156
                                                                                                                                                                                                                                                                                                                                         g
                           ò
                                                       g
                                                                                   ò
                                                                                                             ద
                                                                                                                                          ò
                                                                                                                                                                      g
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>α</del>
                                                                                                                                                                                                                                                                                                                        OTTILE S., RAULE F., BARNEKOW A., HANNIG G., SCHARTL M.;
"Multiple src-related kinase genes, srkl-4, in the fresh water sponge
Spongilla lacustris."
Spongilla lacustris."
-1.625-1630(1992).
-1. CATALXTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
GAKFPIKWTAPEAAMYSRFTIKSDVWSFGIVLYEVITYGRFPYPGMTNAQVLEQIQOSYR 453
                          385 SSKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- ALTERNATIVE PRODUCTS: SRK1 AND SRK4 MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 13;
                                                                                                                                                                                                                                       SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EUKARYOTA: METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1391; DB 1; Length 505; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred No. 0.00e+00;
95; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3AE3DF34 CRC32;
                                                                                                                                                                   01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
101-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRK1 (EC 2.7.1.112).
                                                                                                                                          505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X61601; G10150; --.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TXR; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50001; SH2; 1.
PROSITE: PS50002; SH3; 1.
PRAM; PF00017; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000523; ZPTK.
                                                       MPRPMGCPEKLYAIMMDCWREDPASRPTFETL 485
                                                                       SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 SH2 DOMAIN. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 A1
258 A1
268 A1
359 B3
57693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 43.6%;
nes 197; Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
246
268
268
359
359
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             MEDLINE; 92334872
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFERASE;
                                                                                                                          LT 3
SRK1_SPOLA
P42686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
 394
                                                       454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>:</u>.
                                                                                                                          g
                           å
                                                     g
                                                                                 ö
```

39

g S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                          94 SGQPSAGLVPITHVAKASPETLSDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSL 153
                                                                                                                     386 SKIPVKWTAPPAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHFTLQQIMRGYRL 445
                                                                                                                                                                                    216 QAEKPQTAGLLRQANEEWEIEKTQIKLLRRLGAGQFGEVWEGLWNGTTSVAVKTLKPGTM 275
                                                                                                                                                                                                                                  214 ----PQKAP--RQ--DVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANM 265
                                                                                                                                                                                                                                                                               276 SVEEFLQEASIMKRLRHPKLIQLYAVCTKEEPIYIVTELMKYGSLLEYLRGEDG-VLKIE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 AKFPIKWTAPEAAMYNRFTIKSDVWSFGVVLYEIITYGRFPYPGMTNPEVLEKIQQNYRM 454
98 DTAGKEGYIPSNYVA-EY-KSLDAEEWFLGKIKRVEAEKMLNQSFNQVGSFLIRDSETTP 155
                                                                                                                                                                                                                                                                                                                                                                        335 QLVDVAAQVASGMSYLEQQNYIHRDLAARNILVGEHGICKVADFGLARVIDEEIYEAHTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN TYROSINE PHOSPHATE.
ENZYME REGULATION: REGULATED BY PHOSPHORYLATION ON TYR-348.
SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 88097370.
STREBHARDT K., MULLINS J.I., BRUCK C., RUEBSAMEN-WAIGMANN H.;
"Additional member of the protein-tyrosine kinase family: the src-
and lck-related proteonocyene c-tkl.";
PROC. NATL. ACAD. SCI. U.S.A. 84:8778-8782(1987).
-:- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
-:- CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     GDFSLSVKDQDRVRHYRVRRLEDGSLFVTRRSTFQ1LHELVDHYK1ETDGLCCKLLYPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE; 92186854.
CHOW L., RATCLIFFE M., VEILLETTE A.;
"tki is the avian homolog of the mammalian lck tyrosine protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVI
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 PCPANCPKQFHDIMLDCWREDPASRPTFETLQ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. CELL. BIOL. 12:1226-1233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 46-507 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-88 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE KINASE C-TKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALLUS GALLUS (CHICKEN)
```

```
MUTAGENESIS
                                                                                                                                                                                                                                                                                   MEDLINE;
10;
                                                                                                    TRANSFERASE;
                                                                                                                                                                                                                                                                  PCSPLQDKLVVALYDYEPTHDGDLGLKQGEKLRVLEESGEWWRAQSLTTGQ-EGLIPHNF 113
                                                                                                                                                                                                                                                                          230
                                                                                                                                                                                                                                                                                                                                       290
                                                                                                                                                                                                                                                                                                                                                                                           349
                                                                                                                                                                                                                                                                                                 114 VAMVN--SLEPEPEFKFKNLSRKNAEARLLASGNTHGSFLIRESETSKGSYSLSVRDFDQN 171
                                                                                                                                                                                                                                                                                                                                                                            277
                                                                                                                                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                                                                                                                                         MAFIEAKNYIHRDLRAANILVSEALCCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                 410 INYGTFTIKSDVWSFGILLTEIVTYGRIPYPGMTNPEVIQNLERGYRMPQPDNCPQELYE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). PHOSPHORYLATION.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                               QGETVKHYKIRNMDNGGYYI-SPRVTFSSLHELVEYYSSSSDGLCTRLGKPCRTQKPQKP
                                                                                                                                                                                                                                                                                                                                                            WWQDEWEVPRESLKLVEKLGAGOFGEVWMGFYNGHTKVAIKNLKQGSMSPSAFLAEANLM
                                                                                                                                                                                                                                                                                                                                                                      291 KNLOHPRLVRLYAVVTK-EPIYIITEYMEKGSLVDFLKTSEGIKLSINKLLDMAAQIAEG
                                                                                                                                                                                                                                   Score 1388; DB 1; Length 507;
Pred. No. 0.00e+00;
93; Mismatches 136; Indels 15;
                                                                                  PFAM, PF00069; pkinase; 1.
HSSP, P0629; 3LCK.
PROTO-ONCOGENE: TROSINE-PROPEIN KINASE; PHOSPHORYLATION; TRAN
ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; PALMITATE;
                                                                                                                                 MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                              SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                    06C5A291 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCK_MOUSE STANDARD; PRT; 508 AA. P06240; O61794; O61795; O62320; O1-JAH (REL. 06, CREATED) 01-FBB-1994 (REL. 28, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
             EMBL; M85043; G212533; -.
EMBL; J03579; G212713; ALT_INIT.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
an email to license@isb-sib.ch)
                                                                                                                          PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 LMMQCWKEQPEERPTFEYMKSVLEDF 495
                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                   37.8%;
                                                                                                                                                                                                                                           Best Local Similarity 45.3%;
Matches 202; Conservative
                                                                                                                                                                                                                    58008
                                                                    ; SH2; 1.
                                                                                                                                                       1119
222
496
257
271
                                                                                                                                                                                             362
392
503
                                                                                                                                                                                                            503
507 AA;
                                                                                                                                                       59
125
243
249
                                                                                                                                                                                             362
                                                                   PFAM; PF00017
PFAM; PF00018
                                                                                                                  LIPOPROTEIN.
                                                                                                                         INIT_MET
LIPID
LIPID
LIPID
                                                                                                                                                                                             ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
send
                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                         350
                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                             231
                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                                                                                                                                                                                                                                                                                                                         338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
ID LC
AC PO
DT 01
DT 01
g
                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                               ò
```

```
VORONOVA A.F., ADLER H.T., SEFTON B.M.;
"Two lok transcripts containing different 5' untranslated regions are present in T cells.";
                                                                                                                                                                                                                                                                                                                is rearranged and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERLMUTTER R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GARVIN A.M., PAWAR S., MARTH J.D., PERLMUTTER R.M.;
"Structure of the murine lck gene and its rearrangement in a murine
lymphoma cell line.";
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (P56-LCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITE: 91133805.
CARRERA A.C., ALEXANDROV K., ROBERTS T.M.;
The conserved lysine of the catalytic domain of protein kinases is actively involved in the phosphotransfer reaction and not required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J., SHAW A.S., LUBLIN D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF LYS-272.

MEDLINE; 91163633.

MEDLINE; 91163633.

**BRARAM N., MICELI M.C., PARNES J.C., VEILLETTE A.;

**Enhancement of T-cell responsiveness by the lymphocyte-specific tyrosine protein kinase p561ck.";

NATURE 350:62-66(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE, 93059694.

HURLEY T.R., AMREIN K.E., SEFTON B.M.;

"Creation and characterization of temperature-sensitive mutants the lck tyrosine protein kinase.";

J. VIROL. 66:7406-7413(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cells:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ģ
                                                     LCK OR LSK-T.
MUS MUSCULUS (MOUSE).
EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91219495.
ABRAHAM K.M., LEVIN S.D., MARTH J.D., FORBUSH K.A., PERLMUTTE
"Thymic tumorigenesis induced by overexpression of p56lck.";
PROC. NATL. ACAD. SCI. U.S.A. 88:3977-3981(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIINE; 86146842.
VORONOVA A.F., SEFTON B.M.;
"Expression of a new tyrosine protein kinase is stimulated retrovirus promoter insertion.";
NATURE 319:682-685(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translational basis for virus host-range restriction."; PROC. NATL. ACAD. SCI. U.S.A. 85:4257-4261(1988).
                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 86079521.
MARTH J.D., PEET R., KREBS E.G., PERLMUTTER R.M.;
"A lymphocyte-specific protein-tyrosine kinase gene i
overexpressed in the murine T cell lymphoma LSTRA.";
CELL 43:393-404(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMREIN K.E., SEFTON B.M.; "Avian reovirus mRNAs are nonfunctional in infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for anchoring ATP.";
PROC. NATL. ACAD. SCI. U.S.A. 90:442-446(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94019312.
SHENOY-SCARIA A.M., TIMSON L.K., KWONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOL. CELL. BIOL. 7:4407-4413(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. CELL. BIOL. 8:3058-3064(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-10 FROM N.A. MEDLINE; 88142832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-34 FROM N.A. MEDLINE; 89096891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF TYR-504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF TYR-504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89096891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88248001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALMITOYLATION
```

S

```
273
274
275
504
282
508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCK_HUMAN
P08631;
 MUTAGEN
MUTAGEN
MUTAGEN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
   SO FIT SO
                                                                                                                                                                            셤
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@liber.ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE;
                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                             CD4 OR CD8.
-!- INSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.
-!- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-) (BY SIMILARITY). PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
PROTEIN TYROSING PREGULATION ON TYR-504.
-!- ENZYME REGULATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
                                                                 MEDLINE: 95071286.

KOEGL M., ZLATKINE P., LEY S.C., COURTNEIDGE S.A., MAGEE A.I.;
"Palmitoylation of multiple Src-family kinases at a homologous N-terminal motif.".

BIOCHEM. J. 303:749-753(1994).

-I-FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH2 DOMAIN; SH3 DOMAIN; PALMITATE
"Palmitylation of an amino-terminal cysteine motif of proteir tyrosine kinases p561c% and p59fyn mediates interaction with aglycosyl-phosphatidylinositol-anchored proteins."; MoL. CELL. BIOL. 13:6385-6392(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K->N: REDUCED ACTIVITY.
V->L: REDUCED ACTIVITY.
A->S: REDUCED ACTIVITY.
V->A: REDUCED ACTIVITY.
K->R: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X03533; G54814; -...
EMBL; M12056; G198764; -...
EMBL; X03533; E7690; ALT_SEQ.
EMBL; X03533; E7690; ALT_SEQ.
EMBL; M21511; G554186; ALT_SEQ.
EMBL; M18098; G198767; -...
PIR; A23639; A23639.
MGD; MGI:96756; LCK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1...
PROSITE; PS50011; PROTEIN_KINASE_ATP; 1...
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1...
PROSITE; PS50011; SH21; 1...
PROSITE; PS50001; SH2; 1...
PROSITE; PS50002; SH3; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
.
.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITATE.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTO-ONCOGENE; TYROSINE-PRC
ATP-BINDING; MYRISTYLATION;
LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P06239; 1LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1120
2223
2497
3463
3633
363
270
270
272
                                                                                                                                                                                                                                                           T-CELL ONTOGENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2244
2244
2250
2250
2270
2270
2270
                                                                                                                                                    DEVELOPMENT
                                                           PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
MOD_RES
MOD_RES
MOTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPID
```

```
Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 87257942.
QUINTRELL N., LEBO R., VARWUS H., BISHOP J.M., PETTENATI M.J.,
QUINTRELL N., LEBO R., VARWUS H., BISHOP J.M., PETTENATI M.J.,
LE BEAU M.M., DIAZ M.O., ROWLEY J.D.;
"Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and is expressed in hemopolatic cells.";
MOL. CELL. BIOL. 7:2267-2275(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 22-526 FROM N.A.
MEDLINE; 87257943.
ZIEGLER S.F., MARTH J.D., LEWIS D.B., PERLMUTTER R.M.;
"Novel protein tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin.";
                                                                                                                                                                                                                                                                                                                                        163 QAKVC-HYRVSMAADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPCMPQKA--P 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 PASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 114
                                                                                                                                                                                                                                                                                                                                                                                                                115 VAKAN--SLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 WWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPVPFLAEANLM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 INYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYH 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHDLVRHYTNASDGLCTKLSRPCQTQKPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 KQLQHPRLVRLYAVVIQ-EPIYIITEYMENGSLVDFLKTPSGIKLNVNKLLDMAAQIAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 MAFIEEQNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
1XPOSINE-PROPEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK)
(HEMOPOIETIC CELL KINASE).
                                                                                                                                                                                                                           Pred. No. 2.70e-294;
91; Mismatches 142; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                  Length 508;
S->N: REDUCED ACTIVITY.
L->M: REDUCED ACTIVITY.
K->Y: REDUCED ACTIVITY.
Y->F: CAUSES THYMIC TUMORS.
VP -> DA (IN REF. 2).
W; 70423550 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION
                                                                                                                                                                                                  Score 1339; DB 1; Pred. No. 2.70e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 LAMICWKERPEDRPTFDYLRSVLDDF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOL. CELL. BIOL. 7:2276-2285(1987).
        273 S-
274 L-
275 K-
504 Y-
283 VF
57821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 22-526 FROM N.A.
                                                                                                                                                                                                Query Match 36.5%;
Best Local Similarity 44.4%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN)
```

```
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HE COC OS REE BLANKER REE COC OS REE REE COC OS REE REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE COC OS REE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOMERINS for HIV-1 Nof ";

BIOCHEMISTRY 37:14683-14691(1998).

-!- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE DEGRANULATION PROCESS OF NEUTROPHILS.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- SUBCELLOLAR LOCATION: D60-HCK AND P59-HCK ARE ASSOCIATED WITH MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTY IN CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                               HORITA D.A., BALDISSERI D.M., ZHANG W., ALTIERI A.S., SMITHGALL T.E., GMENTENE W.H., BYRD R.A.; "Solution structure of the human Hck SH3 domain and identification of its ligand binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE
                      LOCK P., RALPH S., STANLEY E., BOULET I., RAMSAY R., DUNN A.R.;
"Two isoforms of murine hck, generated by utilization of alternative translational initiation codons, exhibit different patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYELOID AND B-LYMPHOID LINEAGES.
ALTERNATIVE.PRODUCTS: THE P60-HCK AND P59-HCK ARE PRODUCED BY USE OF ALTERNATIVE INITIATION SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZHANG W., SMITHGALL T.E., GMEINER W.H.; "Sequential assignment and secondary structure determination for Src homology 2 domain of hematopoietic cellular kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98453315.
AROLD S., O'BRIEN R., FRANKEN P., STRUB M.P., HOH F., DUMAS C., LADBURY J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RT loop flexibility enhances the specificity of Src family
                                                                                                                                                                                           MEDLINE; 97177106.
SIGHERI F., MORREFI I., KURIYAN J.;
"Crystal structure of the Src family tyrosine kinase Hck.";
NATURE 385:602-609(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
                                                                                                                         MOL. CELL. BIOL. 11:4363-4370(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. MOL. BIOL. 278:253-265(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS LETT. 406:131-135(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 139-245.
                                                                                                                                                                                                                                                                                              [5]
STRUCTURE BY NMR OF 78-138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M16591; G306832; -. EMBL; M16592; G306833; -.
                                                                                                  subcellular localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A27812; TVHUHC.
2HCK; 20-AUG-97.
3HCK; 15-OCT-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5HCK, 17-JUN-98
1AD5, 15-MAY-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1BU1; 11-NOV-98
                                                                                                                                                                                                                                                                                                                                              MEDLINE; 98239731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97263487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>-</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 VALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATR-KEGYIPSNYVARV--DSLE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 SMAADGSLYLQKGRLFPGLEELLTYYK-ANWKLIQNPLLQPCMPQKA--PRQ-DVWERPH 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TEEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 RTLDNGGFYISPRSTFSTLQELVDHYKKGNDGLCQK-LSVPCMSSKPQKPWEKDAWEIPR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 ESLKLEKKLGAGQFGEVWMATYNKHTKVAVKTMKPGSMSVEAFLAEANVMKTLQHDKLVK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 LHAVVIK-EPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQRNYI 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 LHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 HRDLRAANILVSASLVCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 DVWSFGILLMEIVTYGRIPYPGMSNPEVIRALERGYRMPRPENCPEELYNIMMRCWKNRP 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR)
(C-FGR).
              PROSITE; PS50002; SH3; 1.
PFAM; PF00015; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
TRANSFERASE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; ATP-BINDING; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 106; Mismatches 127; Indels 14;
                                                                                                                                         TYROSINE-PROTEIN KINASE P60-HCK.
TYROSINE-RROTEIN KINASE P59-HCK.
MYRISTATE (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALLA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                             Length 526;
                                                                                                                                                                                                                                                                                                                                          S -> C (IN G306833).
F9B6EE42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                             Score 1341; DB 1; I
Pred. No. 8.39e-295;
                                                                                                                                                                                                                                SH2.
PROTEIN KINASE.
ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:
-:
-:
-:
-:
-:
                                                                                                                                                                                                                                                                                                                                                                                            Match 16.5%;
Local Similarity 43.3%;
Les 189; Conservative 1
                                                                                                                                                                                         23
138
241
241
276
290
381
411
411
59583 b
SH2; 1.
SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 EERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 EERPTFEYIQSVLDDF 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMAN)
                                                                                                                                                                                                                                                                                                    381
411
24
526 AA;
PS50001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGR OR SRC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGR_HUMAN
P09769;
                                                                                                                                                                                             LIPID
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                           CHAIN
                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

283

435 403

US-09-099-053-2-01.rsp

```
SEQUENCE FROM N.A.
MEDLINE; 95210166.
CANCE W.G., CRAVEN R.J., BERGMAN M., XU L.H., ALITALO K., LIU E.T.;
CANCE W.G., CRAVEN R.J., BERGMAN M., XU L.H., ALITALO K., LIU E.T.;
"Rak, a novel nuclear tyrosine kinase expressed in epithelial cells.";
CELL GROWTH DIFFER. 5:1347-1355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIQAEEWYFGKIGRKDAERQLLSPGNPQGAFLIRESETTKGAYSLSIRDWDQTRGDHVKH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRK_HUMAN STANDARD; PRT; 505 AA.
P42665; Q13128;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE_PROTEIN KINASE FRK (EC 2.7.1.112) (NUCLEAR TYROSINE PROTEIN
                          YRVSMAADGSLYLOKGRL-FPGLEELLTYYKANWKLIQNPLLOPC--M-PQK-APRQDVW
                                                                                                                                                                                                376 MNYIHRDLRAANILVGERLACKIADFGLARLIKDDEYNPCQGSKFPIKWTAPEAALFGRF
                                                                                                                                                                                                                                                                                                                                                                   344 QRVVHRDLAARNVLVDDGLACKVADFGLARLLKDDIXSPSSSSKIPVKWTAPEAANYRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                436 TIKSDVWSFGILLTELITKGRIPYPGMNKREVLEQVEQGYHMPCPPGCPASLYEAMEQTW
                                                                                     YKIRKLDMGGYYI-TTRVQFNSVQELVQHYMEVNDGLCNLLIAPCTIMKPQTLGLAKDAW
                                                                                                                                                                      EISRSSITLERRLGTGCFGDVWLGTWNGSTKVAVKTLKPGTMSPKAFLEEAQVMKLLRHD
                                                                                                                                                                                                                                                            KLVQLYAVVSE-EPIXIVTEFMCHGSLLDFLKNPEGQDLRLPQLVDMAAQVAEGMAYMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94171047.
LEE J., WANG Z., LUOH S.-M., WOOD W.I., SCADDEN D.T.;
"Cloning of FRK, a novel human intracellular SRC-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Novel protein Kinases expressed in human breast cancer.";
"Novel protein Kinases expressed in human breast cancer.";
INT. J. CANCER 54:571-577(1993)
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLUIAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- TISSUE SPECIFICITY: RESTRICTED TO CELLS LINES DERIVED FOR LYMPHOLD, BRAIN, BREAST, COLON AND BLADDER ORIGIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CADMAIN. BELONGS TO THE SRC SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
MEDLINE; 93293373.
CANCE W.G., CRAVEN R.J., WEINER T.M., LIU E.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLDPEERPTFEYLQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||||||:| |:
RSSPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE 138:247-251(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LYMPHOID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINASE RAK).
                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  НОМО
                                                                                     198
                                                                                                                                                                        257
                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                 8
                                                                                                                               9
                                                                                                                                                                    g
                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 12;
             KATAMINE S., NOTARIO V., RAO C.D., MIKIT., CHEAH M.S.C.,
TRONICK S.R., ROBBINS K.C.;
"Primary structure of the human fgr proto-oncogene product p55c-fgr.";
MOL. CELL. BIOL. 8:259-266(1988).
                                                                                                                                                                                                                                                                                                                                        INOUE K., IKAWA S., SEMBA K., SUKEGAWA J., YAMAMOTO T., TOYOSHIMA K.; "Isolation and sequencing of cDNA clones homologous to the v-fgr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 LFIALYDYEARTEDDLTFTKGEKFHILNNTEGDWWEARSLSS-GKTGCIPSNYVA-PV-D 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
B2B2227E CRC32;
                                                                                                                                                                                                             Structure, expression, and chromosomal location of the human c-fgr
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROPEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFERASE, TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE, ATP-BINDING; PHOSPHORYLATION; SH2 DOMAIN.

77 138 SH3.

DOMAIN 144 241 SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Mismatches 124; Indels 16;
                                                                                                                                                                    NISHIZAWA M., SEMBA K., YOSHIDA M.C., YAMAMOTO T., SASAKI M:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 529;
                                                                                                                                                                                                                                                                                                                                                                                  oncogene from a human B İymphocyte cell line, IM-9.";
ONCOGENE 1:301-304(1987).
-!- CATALXIIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1336; DB 1; I
Pred. No. 1.56e-293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                       CELL. BIOL. 6:511-517(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G553286; --
G553286; JOINED.
G553286; JOINED.
G553286; JOINED.
G553286; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59478 MW;
                                                                                                                          SEQUENCE OF 111-416 FROM N.A. MEDLINE; 87064334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M, PF00017; SH2; 1.
1; PF00018; SH3; 1.
1; PF00069; Pkinase; 1.
3; P66241; ISHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M19722; G182574; -.
EMBL; M12724; G553286; -.
EMBL; M12719; G553286; JOINI
EMBL; M12710; G553286; JOINI
EMBL; M12721; G553286; JOINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.4%;
45.9%;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-143 FROM N.A. MEDLINE; 88262220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
516
277
291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A27676; TVHUFR.
PIR; A28353; A28353.
MIM; 164940; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291
382
412
424
529 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 199; Conser
MEDLINE; 88094395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M12723;
                                                                                                                                                                                            LOYOSHIMA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAM; PF00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
```

EMBL;

PFAM; PFAM; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot

55 LFLALYDFTARCGGELSVRRGDRLCALEEGGGYIF-ARRLSGQPSAGLVPITHVAKASPE 113

g ö

DERIVED FROM TISSUES

ORIGIN. IN THE CATALYTIC

ω

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee1sb-sib.ch).
                                                                                                                                                                                                                                      SH3.
SH2.
SH2.
SH2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
G -> R.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                       HYFVALFDYQARTAEDLSFRAGDKLQVLDTLHEGWWFARHLEKRRDGSSQQLQGYIPSNY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                    224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 ANYRVESQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 VAEDRSLQAEPWFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 IRSNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQQFYN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 YRIKRLDEGGFFLTRRRIFSTLNEFVSHYTKTSDGLCVKLGKPCLKIQVPAPFDLSYKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQWEIDRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDTGSKIHLTQQVDMAAQVASGMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESRNY IHRDLAARNVLVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels 16;
                                                                                                                                                                                                                                                                                                                                                                       Score 1332; ...DB-1; .Length..505; ...
Pred. No. 1.62e-292;
96; Mismatches 135; Indels 16;
                                                                                                                                                                                                                                                                                                                                     -> A (IN REF. 2)
C4226A83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508
                                                                                                    PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; S42; 1.
PROSITE; PS50002; S43; 1.
PROSITE; PS50017; S42; 1.
PFAM; PF00017; S43; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||||| : | |||:| ||| || 1|
LMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMLECWNAEPKERPTFETLRWKL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                               58254 MW;
                                                                                                                                                                                                                             SH3 DOMAIN; PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.3%;
Best Local Similarity 44.2%;
Matches 196; Conservative
                                                                                                                                                                                         PF00069; pkinase; 1.
P00523; 2PTK.
                                                                                 EMBL; U00803; G392888; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCK_HUMAN STANDARD
P06239; P07100;
01-03AN-1988 (REL. 06, C
01-FEB-1994 (REL. 28, L
15-JUL-1998 (REL. 36, L
                                                                                                                                                                                                                                                               491
248
262
354
387
1122
                                                                                              EMBL; U22322; G732528;
                                                                                                                                                                                                                                                                                                                                     115
505 AA;
                                                                                                                                                                                                                  TRANSFERASE;
                                                                                                                                                                                                                                                                                                   ACT_SITE
MOD_RES
VARIANT
                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                           NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     φ
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                      HSSP:
                                                                                                                                                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465
                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
ID LC
AC PC
DT 01
DT 01
           g
                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     φ
```

LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

```
"Structure of the human lck gene: differences in genomic organisation within src-related genes affect only N-terminal exons."; GENE 84:105-113(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEILLETTE A., FOSS F.M., SAUSVILLE E.A., BOLEN J.B., ROSEN N.; "Expression of the lock tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines."; ONCOGENE RES. 1:357-374 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                                                                                                                            KOGA Y., CACCIA N., TOYONAGA B., SPOLSKI R., YANAGI Y., YOSHIKAI Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE; 89313764.
TAKADERA T., LEUNG S., GERNONE A., KOGA Y., TAKIHARA Y.,
MIYAMOTO N.G., MAK T.W.;
"Structure of the two promoters of the human lck gene: differential
accumulation of two classes of lck transcripts in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (P56-LCK) (LSK) (T CELL-SPECIFIC PROTEIN-TYROSINE KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
MEDLINE; 95173978.
MIKOL V., BAUMANN G., KELLER T.H., MANNING U.M., ZURINI M.G.M.;
"The crystal structures of the SH2 domain of p561ck complexed with two phosphonopeptides suggest a gated peptide binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human T lymphocytes express a protein-tyrosine kinase homologous \mathfrak{p}\mathsf{SGLSTRA}.";
                                                                                                                                                                                                                                                                                                                       "A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine kinases."; EUR. J. IMMUNOL. 16:1643-1646(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94203291.
ECK M.J., ATWEELL S.K., SHOELSON S.E., HARRISON S.C.;
"Structure of the regulatory domains of the Src-family tyrosine
                                                                                                                                                                                        'Structure and expression of lck transcripts in human lymphoid
                                                                                                                 SEQUENCE FROM N.A.
MEDLINE: 89123626.
PERLMUTTER R.M., MARTH J.D., LEWIS D.B., PEET R., ZIEGLER S.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89096891.
GARVIN A.M., PAWAR S., MARTH J.D., PERLMUTTER R.;
"Structure of the murine lck gene and its rearrangement in a
Lymphoma cell line.";
                                                                   CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                ROUER E., VAN HUYNH T., DE SOUZA S.L., LANG M.C., FISCHER S.,
BENAROUS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TREVILLYAN J.M., LIN Y., CHEN S.J., PHILLIPS C.A., CANNA C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOCHIM. BIOPHYS. ACTA 888:286-295(1986).
                                                                                   HOMINIDAE; HOMO
                                                                                                                                                                                                                         CELL. BIOCHEM. 38:117-126(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL. BIOL. 8:3058-3064(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. CELL. BIOL. 9:2173-2180(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 367-508 FROM N.A. MEDLINE; 88217332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 374-508 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [6]
SEQUENCE OF 1~34 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NATURE 368:764-769(1994).
                                                                   EUKARYOTA; METAZOA; CH
PRIMATES; CATARRHINI;
                                                   SAPIENS (HUMAN)
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 87133831.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87000726
                                                                                                                                                                      WILSON C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINNA T.J.;
                                                                                                                                                                                                                                                                                                           MAK T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Тутрнота
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase
                                                   HOMO
```

σ

```
functional pp6Osrc.";
J. BIOL. CHEM. 264:10649-10653(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 LMLECWRSSPEERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 LMRLCWKERPEDRPTFDYLRSVLEDF 496
                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 438-491 FROM N.A.
TISSUE-ERYTHROCYTE;
                                                                                                                                                                                       36.3%;
                                                                                                                                                              57869
                                                                                                                                                                                                   Local Similarity 44.4%;
les 198; Conservative
  5043
2043
2043
2043
2043
2044
2044
508
 363
504
208
34
86
2057
2057
2057
207
208
374
508
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
 ACT_SITE
MOD_RES
MOD_RES
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
  0.44444444444
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107: PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109: PROTEIN_KINASE_TYR; 1.
PROSITE; PS00101: PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001: SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM; PF00011: SH2; 1.
PFAM; PF001018: SH3; 1.
PFAM; PF001018: SH3; 1.
PFAM; PF001069; pkinase; 1.
PROTEONCOCENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE; LIPOPROTEIN; 3D-SIRUCTURE.
                                                                                                                                 YAMAGUCHI H., HENDRICKSON W.A.;
"Structural basis for activation of human lymphocyte kinase Lck upon tyrosine phosphorylation.";
NATURE 384:484-489(1996).
                                                                                                                                                                                  -: FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
-:- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-:- ENZYME REGULATION: REGULATED BY PHOSPHORYLATION ON TYR-504.
-:- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
                                  MEDLINE; 96177765.
TIONG L., WARREN T.C., KING J., BETAGERI R., ROSE J., JAKES S.;
"Crystal structures of the human p561ck SH2 domain in complex with
two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";
J. Mol. BIOL. 256:601-610(1996).
                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
MYRISTATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
SIMILARITY).
                       X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225
                                                                                                            X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARI
ATP (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X13529; G34295; -...
EMBL; M3681; G187034; -...
EMBL; X04476; G35780; -...
EMBL; X14055; G825687; -...
EMBL; X14054; G825687; -...
EMBL; X14054; G825687; JOINED.
EMBL; X05369; G34289; -...
EMBL; X05027; G36808; -...
EMBL; M21510; G553522; ALT_TERM.
EMBL; M21510; G553522; ALT_TERM.
MOL. BIOL. 246:344-355(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
223
497
258
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB: 3LCK; 03-DEC-97.
PDB: 1CWD; 07-DEC-96.
PDB: 1LKW; 07-DEC-96.
PDB: 1LKK; 08-MAR-96.
PDB: 1LKL; 08-MAR-96.
MIM; 153390; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ0152; OKHULK.
1LCJ; 15-OCT-95.
1LCK; 15-OCT-95.
                                                                                                                         MEDLINE; 97100952
                                                                                                                                                                                                                                                 CD4 OR CD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
DOMAIN
DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB;
```

```
350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 VAKAN--SLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 MAFIEERNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 INYGTETIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 PASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQKP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 WWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPDAFLAEANLM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY). PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE; 89278134.
STEELE R.E., UNGER T.F., MARDIS M.J., FERO J.B.;
"The two Xenopus laevis SRC genes are co-expressed and each produces
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 KQLQHQRLVRLYAVVTQ-EPIYIITEYMENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG
                                          P -> R (IN G187034).

I -> R (IN G187034).

Q -> P (IN REF. 1).

VRHYINA -> ASAIPPIA (IN REF. 2).

G -> A (IN G187034).

EVWMGYYNGH -> RCGWGTITGT (IN REF.
                                                                                                                                                                                                                                                                                                                                                     Score 1333; DB 1; Length 508;
Pred. No. 9.02e-293;
91; Mismatches 142; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRC2_XENLA STANDARD; PRT; 531 AA.
P13116;
U-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-2 (EC 2.7.1.112) (P60-SRC-2).
                                                                                                                                                                                              PDAFL -> AGRLP (IN REF. 2).

T -> A (IN REF. 5).

L -> H (IN REF. 4).

OYODOP -> STA (IN REF. 2).

#; 10E545CE CRC32;
```

```
TRANSFERASE; A)
MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194;
                                                                                                Query Match
440
                                                                 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                        g
                                                               Ω
                      ò
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifixed and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVALYDYESRTETDLSFRKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA-PS-DS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQ 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 IQAEEWYLGKITRREAERLLLSLENPRGTFLVRESETTKGAYCLSVSDYDASRGLNVKHY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTAVCPTAKPQTQGLSKDAWEI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRDSLRLELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 IRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY). C6ABE595 CRC32;
                    are expressed in Xenopus laevis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                               PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
TRANSFERASE; AIP-BINDING; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
                                                               SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOWAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVSMAADGSLYLOKGRLFPGLEELLTYYKANWKLIONPLLQPC---MPQKAP-RQDVWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1333; DB 1; Length 531;
Pred. No. 9.02e-293;
90; Mismatches 133; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
MYRISTATE (BY SIMILARITY).
SH3.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                   "Two divergent cellular src genes are expressed in Xenc
NUCLEIC ACIDS RES. 13:1747-1761(1985).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                            PROSITE; B34104:
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                      SH3 DOMAIN; SH2 DOMAIN
                                                                                                                                                                                                             EMBL; M23422; G214797; -.
EMBL; M30858; G555569; -.
EMBL; M30857; G555569; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59605 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 36.3%;
Local Similarity 45.1%;
nes 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       140
243
279
293
414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
531 AA;
MEDLINE; 85215578
                                                                                                                                                                                                                                                                                                                                                                        MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                            LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
            STEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Óζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA-PS-DS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BYS IMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
AB0705D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        each produces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00523; 2PTK.
TRANSFERASE; ATP-BINDING; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE; 05.70134.

MEDINE; 05.70134.

The two Xenopus laevis SRC genes are co-expressed and each produce functional pefoster.

"The two Xenopus laevis SRC genes are co-expressed and each produce functional pefoster."

"I BIOL. CHEM. 264:10649-10653(1989).

-! CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-! STALLARITY: CONTAINS 1 SH2 DOMAIN.

-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.

-! SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                              406 KSDVWSFGVLLHEVFTYGQCPYEGMTNHFTLQQIMRGYRLPRPAACPAEVYVLMLECWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1329; DB 1; Length 531;
Pred. No. 9.35e-292;
92; Mismatches 132; Indels 14;
                                                                                                                                                                                                                                                                                                                                                    01-7BA-1990 (REL. 13, CREATED)
01-FBB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-ROV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-1 (EC 2.7.1.112) (P60-SRC-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE (BY SIMILARITY).
SH3.
SH2.
SH2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                               531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_IXR; PROSITE; PS50011; PROTEIN_KINASE_DOM: PROSITE; PS50001; SH2; 1. PROSITE; PS50002; SH3; 1. PROSITE; PS00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 DOMAIN; SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%;
larity 44.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M24704; G214805; -. PIR; A34104; A34104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59725
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                  500 DPEERPTFEYLQ 511
                                                                                                                                                                          SPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414
531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89278134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
```

```
HSSP; P00523; 1PRL.
                                                                              DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469
                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                         439
                                                                                                                                                                                                                                                                                                                                                                                                 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOL. CELL. BIOL. 9:4141-4151(1989).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          simple
                                       ::: |::|::|::|::||::|| ::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:
                                                                                                                                                                                                                                                                                          PRDSLRLELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL
                                                                                                                                                                                                                         PHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERL
                                                                                                                                                                                                                                                                     VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMN
                                                                                                                                                                                                                                                                                                                                                                               KSDVWSFGILLIELTIKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRK
          IQAEEWYLGKITRREAERLLLSLENPRGTFLVRESETTKGAYCLSVSDYDANRGLNVKHY
                                                                                               KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTAVCPTAKPQTQGLSRDAWEI
                                                                                                                                                                                                                                                                                                                                                     380 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS)
EUKARYOTA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; ANTHOMEDUSAE;
HYDRIDAE; HYDRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOSCH T.C.G., UNGER T.F., FISHER D.A., STEELE R.E.; "Structure and expression of STK, a src-related gene in metazoan Hydra attenuata."; MOL. CELL. BIOL. 9:4141-4151(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE STK (EC 2.7.1.112) (P57-STK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00107; PROTEIN_KINASE_ATP; PROSITE: PS00109; PROTEIN_KINASE_TYR; PROSITE: PS500011; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M25245; G159274; -. PIR; A34094; TVHAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPEERPTFEYLQ 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00017; SH2;
PFAM; PF00018; SH3;
PFAM; PF00069; pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 90066418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 12
STK_HYDAT
P17713;
                                                                                                                                                                                                                                                                     321
               141
                                                                                               201
                                                                                                                                                                                  261
                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                              346
                                                                                                                                                                                                                                                                                                                                                                                                                                        440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466
                                                        ò
                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                         ò
                                                                                                                                                                              g
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                              òχ
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | |||| | ||||| |:| : ||:| : | ::| EFALGRKIGEGYFGEVWEGLWLGSLPVAIKVIKSANWKLTDLAKEIQTLKGLRHERLIRL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 IFVALYDYEARISEDLSFKKGERLQIINTADGDWWYARSLITN-SEGYIPSTYVAPEKSY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 VWSFGILMAEIVTKGRIPYPGMTNAQTIAEVEKGYRMPIMPGCPEPLYNIMLQTWNKDPE 478
                                                                                SH2.
PROTEIN KINASE.
AIP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
2B724CE9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRC_CHICK STANDARD; PRT; 532 AA.
P00523; Q91345; Q92013;
21-JU1-1986 (REL. 01, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the cellular gene homologous to the RSV for generating the transforming virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                 E-AEE-WYFGDVKRAEAEKRLMVRGLPSGTFLIRKAETAVGNFSLSVRDGDSVKHYRVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDLAARNILVGENYICKVADFGLARLIEDDEYTAHEGAKFPIKWTAPEAALYNRFTIKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDTGGYFITTRAPFNSLYELVQHYTKDADGLV-CALTLPCPKDKPVTGGIAKDAWEIPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLRLNRKLGAGQFGEVWAGVWNNTTQVAVKTLKPGTMSPASFLDEAGVMKKLRHKHLVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 YAICSDREPIYIVTEYMSGGSLLDYLSKGEGVNLQLPTLIDMAAQVASGMAFLEAQGYIH
    PROTO-ONCOGENE; PHOSPHORYLATION; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                     Length 509;
                                                                                                                                                                                                                                                   Score 1324; DB 1; L. Pred. No. 1.74e-290; 90; Mismatches 144;
TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; TRANSFERASE; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                             56885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 83155664.
TAKENA T., HANAFUSA H.;
"Structure and sequence of th
src gene and the mechanism fc
CELL 32:881-890(1983).
                                                                                                                                                                                                                                                36.1%;
ilarity 43.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
REVISION TO 525.
TAKEYA T., HANAFUSA H.;
CELL 34:319-319(1983).
                                                120
120
120
120
120
130
130
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 NRPIFDYLQGVL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||:| |: |
ERPSFATLREKL 480
                                                                                  126
240
246
246
268
360
390
390
390
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 188; Conser
```

```
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1326; DB 1,
NO. 5.40e-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2.
PROTEIN KINASE.
PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION.
65406BF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                       بنبن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYRISTATE
                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -: - - - - - - - - - ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .ch 36.1%;
1 Similarity 44.7%;
193; Conservative
                                                                                                           EMBL; V00402; G63354; -.
EMBL; S43604; E75862; -.
EMBL; S43616; E75867; -.
EMBL; S43587; E75861; -.
EMBL; S43609; E75863; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280
294
385
415
                                                                                                                                                                                                                                                                                    07-FEB-95.
07-FEB-95.
27-JAN-97.
                                                                                                                                                                                                                                                              07-FEB-95.
07-FEB-95.
                                                                                                                                                                                                            31-MAY-94.
24-DEC-97.
                                                                                                                                                                                                                                      08-MAR-96
                                                                                                                                                                                                  1SRL; 31-MAY-94
                                                                                                                                                                                                                                                08-MAR-96
                                                                                                                                                                                                                                                                                                                          27-JAN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
147
266
11
272
294
385
415
526
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                     A00630; TVCHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE.
                                                                                                                                                                                                                                    10WE;
10WF;
1PRL;
1PRM;
                                                                                                                                                                                                                                                                                     1RLP;
1RLQ;
1NLO;
                                                                                                                                                                                                            1SRM;
2PTK;
                                                                                                                                                                                                                                                                                                                          1NLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
LIPID
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
MOD_RES
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262
                                                                                                                                                                                                                                                             PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                              PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 86151652.
COOPER JA., GOULD K.L., CARTWRIGHT C.A., HUNTER T.;
"TY527 is phosphorylated in pp60c-src: implications for regulation.";
SCIENCE 231:1431-1434(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98070614.
WILLIAMS J.C., WEIJLAND A., GONFLONI S., THOMPSON A.,
COURNWEIDGE S.A., SUPERIL-FURGA G., WIRRENGA R.K.;
The 2.35 A crystal structure of the inactivated form of chicken Src:
a dynamic molecule with multiple regulatory interactions.";
J. MOL. BIOL. 274:757-775(1997).
                                                                                                                                                                                                                                                                                                                                       normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS
                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACCITAINTY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
BNZYME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE
PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE
ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE
C-TERMINAL END OR BY OTHER MUTATIONS.
POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.
SIMILARITY: CONTAINS I SH2 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                     ņ
                                                                                                                                    cyclic AMP-
                                                                                                                                                                                                                                                                                                                                       its
                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93279385.
YU H., ROSEN M.K., SCHREIBER S.L.;
"IH and 15N assignments and secondary structure of the Src SH3
          DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; Analysis of cDNAs of the proto-oncogene c-src: heterogeneity exons and possible mechanism for the genesis of the 3' end of v-src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95063992.
FENG S., CHEN J.K., YU H., SIMON J.A., SCHREIBER S.L.;
"Two binding orientations for peptides to the Src SH3 domain:
development of a general model for SH3-ligand interactions:";
SCIENCE 266:1241-1247(1994).
                                                                                                                                                                                                         GOULD K.L., WOODGETT J.R., COOPER J.A., BUSS J.E., SHALLOWAY HUNTER T.;
                                                                                                                                                                                                                                    "Protein kinase C phosphorylates pp60src at a novel site."; CELL 42:849-857(1985).
                                                                                                                                                                                                                                                                                              SMART J.E., OPPERMANN H., CZERNILOFSKY A.P., PURCHIO A.F., ERIKSON R.L., BISHOP J.M.;
Characterization of sites for tyrosine phosphorylation in transforming protein of Rous sarcoma virus (pp60v-src) and cellular homologue (pp60c-src).";
                                                                                              ATP-BINDING SITE.
MEDLINE; 84270751.
KAMPS M.P., TAYLOR S.S., SEFTON B.M.;
"Direct evidence that oncogenic tyrosine kinases and dependent protein kinase have homologous ATP-binding NATURE 310:589-592(1984).
                                                                                                                                                                                                                                                                                                                                                 cellular homologue (pp60c-src).";
PROC. NATL. ACAD. SCI. U.S.A. 78:6013-6017(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532
                                                                        MOL. CELL. BIOL. 11:4165-4176(1991).
                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION AT TYR-526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 76-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 80-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS LETT. 324:87-92(1993).
                                                                                                                                                                                                                                                                         PHOSPHORYLATION AT TYR-415
SEQUENCE OF 1-18 FROM N.A. MEDLINE; 91304409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND MACROPHAGES
                                                                                                                                                                                                 MEDLINE; 86028181.
                                                                                                                                                                                                                                                                                      MEDLINE; 82082387
                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10]
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Gaps 10; 322 VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN 380 85 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA-PS-DS 141 201 PRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGNMSPEAFLQEAQVMKKLRHEKL 321 56 FLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQPSAGLVPITHVAKASPET 114 202 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEI 261 142 IQAEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHY PEAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
TYROSINE-PROTEIN KINASE; 1.
TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; PHOSPHORYLATION;
TRANSFERASE; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN; Pred. No. 5.40e-291; 92; Mismatches 133; Indels 14; Length 532; PKC). (AUTO-)

g ŏ P P δy g ò

```
megakaryocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKANO Y
                                                                              170
                                                                                                        263
                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                          셤
                       ò
                                                  В
                                                                            δλ
                                                                                                       g
                                                                                                                                 ŏ
                                                                                                                                                            g
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                  ğ
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 10;
                                                                                            PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 7F080552 CRC32;
                                                                                                                                                                                                                                                                                   TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                         IKAWA S., HAGINO YAMAGISHI K., KAWAI S., YAMAMOTO T., TOYOSHIMA K.; "Activation of the cellular src gene by transducing retrovirus."; MOL. CELL. BIOL. 6:2420-2428(1986).
-!- FUNCTION: THIS PHOSPHOPROFIEN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASES IN THE CATALYTIC
IRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQR
                                                                              KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRR
                                        346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSO
                         381 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI
                                                                                                                                                                                                                                                                                                                        AVIAN SARCOMA VIRUS (STRAIN S1).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN VITRO.

-:- CATALYITG ACTIVITY: AIP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
-:- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE C.
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
PROSITE: PS00107: PROTEIN_KINASE_ATP; 1.
PROSITE: PS00107: PROTEIN_KINASE_DOM; 1.
PROSITE: PS50001; SH3; 1.
PROSITE: PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONCOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1326; DB 1; I
Pred. No. 5.40e-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00523; 2PTK.
TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN;
                                                                                                                                                                                                                                         01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                  568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYRISTATE.
SH3.
SH2.
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; FOCUSE; 1. PFAM; PF00017; SH2; 1. PFAM; PF00018; SH3; 1. PFAM; PF00069; pkinase; 1. HSSP: P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.4%;
Matches 192; Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
245
520
281
386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3 DOMAIN; SH2 DOMAIN
                                                                                                                                                           466 SPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 AA;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 87064539.
                                                                                                                                 DPEERPTFEYLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
2267
2273
2295
416
                                                                                                                                                                                                                SRC_AVISS
P14084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPID
                                                                                                                                                                                                                                                                                                             V-SRC
                                                                              441
                                                                                                                                 501
```

FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA-PS-DS 142

86

සු ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCK_RAT STANDARD; PRT; 503 AA.
P50545; Q64647;
P01-OCT-1996 (RREL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P56-HCK) (HEMOPOIETIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTAR; TISSUE-SPLEEN;
VIJAYA GOURI B.S., REMA V., KAMATKAR S., SWARUP G.;
VIJAYA GOURI B.S., REMA V., KAMATKAR S., SWARUP G.;
VIJAYA GOURI B.S., REMA V., KAMATKAR S., SWARUP G.;

Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and characterization of its gene product.";

J. BIOSCI. 19:117-129(1994)

-!- FUNDTION: MAY SERVE AS PART OF A SICNALING PATHWAY COUPLING THE FC CONTRIBUTE TO THE ACTIVITION OF THE RESPIRATORY BURST. MAY ALSO CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE DECANIZATION PROCESS OF NEUTROPHILS.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHARE.

-!- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES.
                                                                                                                                                                                            PRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL 322
                                                                                                                                                                                                                          346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIXSPSSSSKIPVKWTAPEAANYRVFSQ 405
                                                                                              262
                                                                                                                                                                                                                                                                                                                                                                                             382 YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRK 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOZAWA Y.;
                                                                                                                                           RVSMAADGSLYLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC---MPQKAP-RQDVWER 225
                                                                                                                                                                                                                                                                                            323 VRLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                           115 LSDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHY
IQAEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNARGLNVKHY
                                                                                                203 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OKANO Y., SUGIMOTO Y., FUKUOKA M., MATSUI A., NAGATA K.I., NOZ
"Identification of rat cDNA encoding hck tyrosine kinase from
medakarvocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. RES. COMMUN. 181:1137-1144(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 DPEERPTFEYLQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 SPEERPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92109719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
```

```
12;
                                     REMEL; S74141; G241437; ---
REMEL; M8366; G204576; ---
REMEL; M8366; G204576; ---
REMEL; M8366; G204576; ---
REMEL; M8366; G204576; ---
REMEL; M52345; G57582; ---
REMEL; PS00107; PROPERIN_KINASE_ATP; 1.
RPOSITE; PS00101; PROTEIN_KINASE_DOM; 1.
RPOSITE; PS50002; SH3; 1.
RPCSITE; PS50002; SH3; 1.
RPCAM; PF00017; SH2; 1.
RPCAM; PF00018; SH3; 1.
RPCAM; PF00018; SH3; 1.
RPCAM; PF00069; pkinase; 1.
RSSP; PO8631; ZHCX
RYSPERASE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; ATP-BINDING; WAYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; ALTERNATIVE INITIATION.
TRANSFERASE; TYROSINE-PROTEIN KINASE; RESPRINGE REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REMEMBER REME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
F -> V (IN REF. 2).
K -> R (IN REF. 2).
K -> T (IN REF. 2).
W, D94DE009 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 NWK-LIQNPLLQPCMPQKA--PRQ-DVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 GEWWKARSLATK-KEGYIPSNYVARVN--SLETEEWFFKGISRKDAERHLLAPGNMLGSF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GKDGLCQK-LSVPCVSPKPQKPWEKDAWEIPRESLQMEKKLGAGQFGEVMMATYNKHIKV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 AVKTMKPGSMSVEAFLAEANLMKTLQHDKLVKLHAVVSQ-EPIFIVTEFMAKGSLLDFLK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 SEEGSKQPLPKLIDFSAQISEGMAFIEQRNYIHRDLRAANILVSASLVCKIADFGLARII 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 EDNEYTAREGAKFPIKWTAPEAINFGSFTIKSDVWSFGILLMEIVTYGRIPYPGMSNPEV 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 PDPTSPKKLGPNS--INSLPPGFVEGSEDTIVVALYDYEAIHREDLSFQKGDQMVVLEES 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.0%; Score 1321; DB 1; Length 503; Best Local Similarity 41.2%; Pred. No. 1.00e-289; Matches 193; Conservative 114; Mismatches 144; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 IRALEHGYRMPRPDNCPEELYSIMIRCWKNRPEERPTFEYIQSVLDDF 491
                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3.
SH2.
PROTEIN KINASE.
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
205
306
503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NP_BIND
BINDING
BAT_SITE
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÓΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

Search completed: Thu May 20 12:22:23 1999 Job time: 44 secs.

************************** (MI) *******************

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu May 20 12:22:43 1999; MasPar time 45:53 Seconds 584.987 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-09-099-053-2 . (1-488) from US09099053.pep (1 of 6) 3671 . MEPFLRRRLAFLSFFWDKIW......ERPSFAILREKLHAIHRCHP 488 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 48.824; Variance 91.236; scale 0.535

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df					
Result No.	Score	Query Match	Query Match Length DB	DB	a	Description	Pred. No.
	1437	39.1	517		094879	DSRC41	2.786-282
7	1366	37.2	451	11	064434	SRC-RELATED INTESTINAL	2.47P-266
9	1355	36.9	451	4	013882	TYROSINE KINASE.	7.27e-264
4	1342	36.6	496	13	093411	NON-RECEPTOR PROTEIN I	6.00e-261
S	1335	36.4	206	11	062662	SRC RELATED TYROSINE K	2.23e-259
9	1335	36.4	512	11	061364	B-CELL SRC-HOMOLOGY TY	2.23e-259
7	1334	36.3	512	11	061745	B-CELL SRC-HOMOLOGY TY	3.73e-259
8	1321	36.0	533	13	098915	GENE C-SRC PRODUCING P	3.07e-256
თ	1321	36.0	533	13	090992	C-SRC.	3.07e-256
10	1315	35.8	587	14	064817	PROTEIN-TYROSINE KINAS	6.78e-255
11	1307	35.6	488	13	013064	LYN PROTEIN TYROSINE K.	4.21e-253
12	1306	35.6	526	11	060567	H-19 PROVIRAL SEQUENCE	7.05e-253
13	1304	35.5	512	4	012850	LYMPHOCYTE-SPECIFIC PR	1.98e-252
14	1300	35.4	505	4	016291	BLK-PROTEIN TYROSINE K	1.56e-251
15	1299	35.4	534	4	016248	P59FYN.	2.61e-251
16	1296	35.3	517	ហ	077050	SRC-TYPE PROTEIN TYROS	1.23e-250
17	1296	35.3	525	14	092806	P60 SRC.	1.23e-250
18	1291	35.2	526	14	207461	TYROSINE-PROTEIN KINAS	1.62e-249
19	1281	34.9	527	13	091952	C-SRC TYROSINE KINASE.	2.80e-247
20	1281	34.9	537	11	062844	PROTO-ONCOGENE FYN.	2.80e-247

2.80 1.067ee - 224 1.386ee - 224
PP62V. (SCHULDT-RUPPIN D STRA TSUP1 SRC (FRAGMENT). COMPLETE GENOME. SRC. TYGOSINE KINASE. FGR MRNA. GARDNER-RASHEED FELINE SRC TYROSINE KINASE. GARONER-RASHEED FELINE GAG-ONC PUSION PROTEIN. PROTO-ONCOGENE TYROSINE FLAGE. PL20 POLYPROTEIN. PROTO-ONCOGENE TYROSIN PROTEIN PROTEIN PROCESSA TYPE 2 PROTEIN FEC29. DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN DSRC29A TYPE 2 PROTEIN TYROSINE KINASE.
086362 086563 0964994 0954994 09685466 0885477 0885477 0885477 0871104 097113 092809 092809 092809 092809 092809 092809 092809 092809 092809 092809 092809 092809 092809 092809
44444444444444444444444444444444444444
545 546 526 526 527 523 523 523 641 1149 621 786 623 786 786 823 786 786 786 786 786 786 786 786 786 786
@@@@\\@\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
11288 128821 128821 1286020 128609 128609 128609 128609 128609 128609 13
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

ALIGNMENTS

					H	_					
					SC	109	26	167	157	227	
			λq s		Gaps	TR-	30P	0 X S	3 X S	LEK	
		Ä.	eyes		; 15;	SKK	RLS	RHNI	SLG	CVO.	
		BCT			17;	LAR	FAR	SES	SES	CKP.	-
		INS	phi		ngth 5. Indels	DWW	SGYI	IRD —	IRP	VNL	
	E)	DA; DRO	ros		Length 517; Indels 1	DTO.	EG-C	GAFI	GAFI	DGITC	-
	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	АРО	ē α C r) 1	д (; 1;	ILN.	ALE	NEH 	NEP(KDS!	
ڼړ	JPDA V UP	HEX A; E	nigo	GRC32;	28.7	HLE	RLC	LPE -	SPP	SHYS	-
AA A	CE (TA; RPH2	K.X.	S S	.786 ches	RKGE	RRGI	KKLI -	CLLI	SLVE	··
517	ED) SEQUENCE UPDATE) ANNOTATION UPDAT	HEA	SAIGO K.; in develo	A33DC5EA	Score 1437; DB 5; Pred. No. 2.78e-282; 92; Mismatches 141;	LSE	LSV	EAE	O A O	TLO	-
::	red) SEC	rrac (RAC	SA	300	NO Mis	DED:	GGE	KRI	SRT	TFR	-
PRT;	CREATED) LAST SEC LAST ANN	A ; E ;	g i.	d . **	core red 2;	DAR	TAR	FRK	FSG/	ARRJ	•
	02, C 02, L 09, L	565	SEQUENCE FROM N.A. STRAIN-CANTON S; MEDLINE; 96268448. MEDLINE; 96268448. "REQUIATION O S., KOJIMA T., SAIGO K.; "REQUIATION Of Cell-cell contacts in developing Drosophila Descell, a new. Glose rellative of vertehrate C-src".	DEV. 10:1645-1656(1996). D42125; D1008290; SE; FEBGN0004603; Src41. PF00018; SH3; 1. PF00018; SH3; 1. PF00069; pkinase; 1.		PVPQIPESETAGANVKIFVALYDYDARTDEDLSFRKGEHLEILNDTQGDWWLARSKKTR-	PYPTLP-AEPCSPFPQLFLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQP	SEGYIPSNYVAKIKSIEAEPWYFRKIKRIEAEKKLLLPENEHGAFLIRDSESRHNDYS	PWY	LSVRDGDTVKHYRIRQLDEGGFFIARRITFRILQELVEHYSKDSDGLCVNLCKPCVQIEK	:
.;		R (F THRC ACHY ILA.	KOČ 11 o	C45-1656(19 1008290; -1 04603; Src4 SH2; 1. SH3; 1. Pkinase; 1.	.18; .68; ive	FVAI	FLAI	EEAE	CSDC	DEGC	-
NAR	(TREMBLREL. (TREMBLREL. (TREMBLREL.	STE AR' BR	S.,	33. 1656 1. 1. 1. 596 3. 2. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3.	39 45 vat:	VKI)	POLI		PET)	ROLI	
IWI	MBL	OGA; OA; ROS	A. 8. DO: ell	645-165 1008290 104603; SH2; 1. SH3; 1. Pkinase AA; 59	ty ser	GAN	SPF	KLK	KAS	YRI	-
PRELIMINARY;	(TRE (TRE	SLAN STAZ IPTE	FROM N.A. INTON S; 96268448. F., ENDO on of cel	7.16000 7.7 S 1.7	Lari Con	SETA	AEPC	4YVA	[HVA	LVKH	_
_	7 0 0 0 0	A , , A	FROJ NTOJ 962(DEV. 10:: DEV. 10:: DEV. 10:: DE): PE00017; PE00018; PE00069; CE 517	imi. 8;	IPE	GT	IPSI	VPI	DGD	
	Q94879; 01-FEB-1997 01-FEB-1997 01-JAN-1999	DSRC41. DROSOPHILA MELANOGASTER (F BROSOPHILA METAZOA; ARTHRO PPERRGOTA; DIPTERA; BRACHY DROSOPHILIDAE; DROSOPHILA.	SEQUENCE FROM N.A. STRAIN-CANTON S; MEDLINE; 96268448. TARAHASHI F., ENDO TARAHASHI P., ENDO TARAHASHI A new. Clos.	GENES DEV. 10:1649-1656(1996 EMBL; D42125; D1008290; FLYBASE; FB90004603; Src41. PFAM; PF00017; SH2; 1. PFAM; PF00018; SH3; 1. PFAM; PF00069; pkinase; 1. SEQUENCE 517 AA; 59097 MW	ch 1 S 20	VPQ -	VPT	EGY 	AGL	SVR	-
T 094879	094879; 01-FEB- 01-FEB- 01-JAN-	DSRC41 DROSOP EUKARY PTERYG DROSOP	[1] SEQUENCE STRAIN-CA MEDLINE; TAKAHASHI "REGULATI "REGULATI	GENES GENES, FLYBAS PFAM; PFAM; SEQUEN	Mat Joca	51 F	40 F		98 S	168 I	-
LT 200	0100	DSI DR(PTI DRC	SEQ STR MED TAK TAK	SEL	Query Match 39.1%; Best Local Similarity 45.6%; Matches 208; Conservative	٠,	7	11	٥,	16	
RESULT ID Q	Z E E E	80000 80000	R R R R R R R R R R R R R R R R R R R	SCREEN	O B Be	οp	Οy	QQ	δy	QQ	
щн	~. பபப	40000				ц	U	ц	J	ם	

13;

228 PVTEGLSHRTRDQWEIDRTSLKFVRKLGSGQFGDVWEGLWNNTTPVAIKTLKSGTMDPKD 287 : : : | || | : | : | | | |

g

US-09-099-053-2-01.rspt

```
BRK OR PTK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 3
Q13882
Q13882;
                                                                                                                                                                                                                                                                                                                                                                                                         252
                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
                                73
                                                                                                                                                       133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCLANDER COORDER CONTRACT STANDER COORDER COOR
                                                                                δ
                                                                                                                                                 g
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
CMPQK-APR-QDVWERPHSEFALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTD 269
                                                                                                                                                                                                                                                                                                                                               388 IPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMINHETLQQIMRGYRLPR 447
                                                          288 FLAEAQIMKKLRHTKLIQLYAVCTVEEPIYIITELMKHGSLLEYLQAIAGKGRSLKMQTL 347
                                                                                                                       327
                                                                                                                                                                                    348 IDMAAQIAAGMAYLESQNYIHRDLAARNVLVGDGNIVKIADFGLARLIKEDEYEARVGAR 407
                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVP-ITHVAKASPET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 YVGLWDFKARTDEELSFQAGDLLHVTKKEELWWWATLLDAEGKALAEGYVPHNYLAEKET 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASIOURHIN V., SERFAS M.S., SIYANOVA E.Y., POLONSKAIA M., COSTIGAN V.J., LIU B., THOMASON A., TYNER A.L.; "A novel intracellular epithelial cell tyrosine kinase is expressed oncogene 10:349-357(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                             408 FPIKWTAPEAANYSKFSIKSDVWSFGILLTELVTYGRIPYPGMTNAEVLTQVEHGYRMPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC-RELATED INTESTINAL KIRASE (EC 2.7.1.112)
(PROTEIN-TYROSINE KINASE) (TYROSYLPROTEIN KINASE) (PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBU DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PROSENS PROSENS PROSENS PROSENS PROFES G847795; -. EMBL; U16805, G847795; -. EMBL; AF016645, G2738777; -. EMBL; AF016645, G2738777; -. EMBL; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00107; PROTEIN_KINASE_TYR; 1. PROSITE; PS000115, SH2; 1. PFAM; PF000118; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94268846.
SIYANOVA E.Y., SERFAS M.S., MAZO I.A., TYNER A.L.;
"Tyrosine kinase gene expression in the mouse small intestine.";
ONCOGENE 9:2053-2057(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.2%; Score 1366; DB 11;
Best Local Similarity 46.8%; Pred. No. 2.47e-266;
Matches 204; Conservative 74; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA; 51972 MW; 5A749D95 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PPNCEPRLYEIMLECWHKDPMRRPTFETLQWKLEDF 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-HSD: ICR AND BALB/C; TISSUE-INTESTINE;
MEDLINE; 95140424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TYROSINE)) (HYDROXYARYL-PROTEIN KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-HSD: ICR; TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-77 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C;
SIYANOVA E.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 2
064434
064434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
212
                                                                                                                       270
                                                                                                                                                                                                                                                 328
                                                                                                                                                                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT OF THE SULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                g
                                                                                                                    ò
                                                                                                                                                                                 g
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
LEE H., KIM M., LEE K.-H., KANG K.-N., LEE S.-T.;

"Exon-intron structure of the human PTK6 gene demonstrates that PTK6 constitutes a distinct family of non-receptor tyrosine kinase.";

MOL. CELLS 8:401-407(1998).

R EMBL, X78849; 6315026; -.

R EMBL, U61412; 63551753; JOINED.

R EMBL; U61408; 63551753; JOINED.

R EMBL; U61408; 63551753; JOINED.

R EMBL; U61409; 63551753; JOINED.

R EMBL; U61409; 63551753; JOINED.

R EMBL; U61410; 63551753; JOINED.

R EMBL; U61410; 63551753; JOINED.

R EMBL; U61410; 63551753; JOINED.

R EMBL; U61410; 63551753; JOINED.

R EMBL; U61411; 63551753; JOINED.

R EMBL; U61411; 63551753; JOINED.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                             251
                                                                                                                                                                                                                                        370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430
                           VESEPWFFGCISRSEAMHRLQAEDNSKGAFLIRVSQKPGADYVLSVRDAQAVRHYRIWKN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-receptor protein situ hybridization.";
                                                                                                                                   AVATAGDPVY I I TELMPKGNLLQLLRDSDEKALP I LELVDFASQVAEGMCYLESQNY I HR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEGRLHLNEAVSFSNLSELVDYHKTQ-SLSHGLQLSMPCWKHKTEPLPHWDDWERPREEF
                                                                                                                                                                                                             TLCKKLGAGYFGEVFEALWKGQVHVAVKVISRDNLLHQHTFQAEIQAMKKLRHKHILSLY
                                                                                                                                                                                                                                                                                                                                                                                                                             DLAARNVLVTENNLCKVGDFGLARLVKEDIY-LSHEHNVPYKWTAPEALSRGHYSIKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSFGVLLHEIFSRGOMPYPGMSNHETFLRVDAGYRMPCPLECPPNIHKLMLSCWSRDPKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94309916.
MITCHELL P.J., BARKER K.T., MARTINDALE J.E.;
"Cloning and characterisation of cDNAs encoding a novel
tyrosine kinase, brk, expressed in human breast tumours.
ONCOGENE 9:2383-2390(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARK S.H., LEE K.H., KIM H., LEE S.T.;
"Assignment of the human PTK6 gene encoding a tyrosine kinase to 20q13.3 by fluorescence in CYTOGENET. CELL GENET. 77:271-272(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL. 01, C
(TREMBLREL. 01, I
(TREMBLREL. 08, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 RPCFKDLCEKLTGITR 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 RPSFATLREKLHAIHR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BREAST CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01-NOV-1996 (TREMBLREL. 01-NOV-1998 (TREMBLREL. TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 97430836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 98419955.
```

က

```
LT 5
Q62662
Q62662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                           229
                                                                                                  289
                                                                                                                                         349
                                                                                                                                                                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
  172
                                       230
                                                                              290
                                                                                                                      350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                      RESULT
                                     g
                                                                                                                     셤
                                                                                                                                                            ద
                                                                                                                                                                                 ò
                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                 쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                  ò
                                                           ò
                                                                            d
                                                                                                 ò
                                                                                                                                         õ
                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                      ώ
ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                      349
                                                                                                                                                                                                                                                                                                                                   WSFGILLHEMFSRGQVPYPGMSNHEAFLRVDAGYRMPCPLECPPSVHKLMLTCWCRDPEQ 430
                                                                                                                                                                                                                                                                                                                                              VLLALYDYDGVHPGDLTFRKGDHLLLKKESGEW-WEACLISTGEEGFVPSNYVA-YF-NS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : ||| |:|| :|| :|||| |:|||| |:|| ||:|| ||:|| ||:|| ||:|| LSDQPMYFSGVSRTQAQQ-KVCHYRVSM 173
                                                                                                       FLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVP-ITHVAKASPET 114
                                                                                                                               VESEPWFFGCISRSEAVRRLQAEGNATGAFLIRVSEKPSADIVLSVRDTQAVRHYKIWRR 132
                                                                                                                                         191
                                                                                                                                                                                                             TLCRKLGSGYFGEVFEGLWKDRVQVAIKVISRDNLLHQQMLQSEIQAMKKLRHKHILALY 251
                                                                                                                                                                                                                               ALGRKIGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTD-LAKEIQTLKGLRHERLIRLH 289
                                                                                                                                                                                                                                                    AVVSVGDPVYIITELMAKGSLLELLRDSDEKVLPVSELLDIAWQVAEGMCYLESQNYIHR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NON-RECEPTOR PROTEIN TROSINE KINASE LALGO.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LESEEWYFKGMSRKEAERQLLSPVNKSGAFMIRDSETMKGCFSLSVRDSGDTVKHYKIRT 171
                                                                                       13 YVGLWDFKSRIDEELSFRAGDVFHVARKEEQWWWATLLDEAGGAVAQGYVPHNYLAERET 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                      Gaps
                                                                                                                                                                                 ::||||||: |:||:||:||:||:||:||:|| |:
LFLALYDFTARCGGELSVRRGDRLCALEEGGGYIFARRLSGQPSAGLVPITHVAKASPET
                                                                                                                                                                      AGGRLHLNEAVSFLSLPELVNYHRAQ-SLSHGLRLAAPCRKHEPEPLPHWDDWERPREEF
                                                                                                                                                                                                                                                                                             DLAARNILVGENTLCKVGDFGLARLIKEDVY-LSHDHNIPYKWTAPEALSRGHYSTKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. WEINSTEIN D.C., MARDEN J., CARNEVALI F., HEMMATI-BRIVANLOU A.; "FGF-mediated mesoderm induction involves the Src-family kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 496;
                                                  Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                    Indels
                                                Score 1355; DB 4; I
Pred. No. 7.27e-264;
73; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1342; DB 13;
Pred. No. 6.00e-261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99; Mismatches 135;
      PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 451 AA; 51834 MW; 4AC30408 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 36.6%;
Local Similarity 43.7%;
les 190; Conservative
                                                Query Match 36.9%;
Best Local Similarity 46.5%;
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      || | :|||:| ::
RPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                          RPCFKALRERLSSF 444
SH2;
SH3;
                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           LT 4
093411
093411;
                                                                                                                                                                                                                                                                                                                                                      410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                              470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                          26
                                                                                                                              73
                                                                                                                                                  115
                                                                                                                                                                      133
                                                                                                                                                                                                                               231
                                                                                                                                                                                                                                                     252
                                                                                                                                                                                                                                                                        290
                                                                                                                                                                                                                                                                                                               350
                                                                                                                                                                                                                                                                                                                                   371
                                                                                                                                                                                                                                                                                                                                                                          431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                            192
                                                                                                                                                                                                                                                                                            312
 San
                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                       g
                                                                                                           ö
                                                                                                                              셤
                                                                                                                                                  ò
                                                                                                                                                                    g
                                                                                                                                                                                        ò
                                                                                                                                                                                                           g
                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA;
                                                                                                                                                                                                    349
                                                                                                                                                                                                                                  409
                                                                                                                                                                                                                                                                                                                                                                                                                                               RDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSD 408
                                                                                                                                                                                                                                                                                                                                                                                                              410 VWSFGVLLTEIITYGRTPYPGMSNSEVITALERGYRMPCPSTCPKELYSIMLQCWQQDPE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PITHV-AK-ASPE-TLSDQPWYFSGVSRTOAQQLLLSPPNEPGAFLIRPSESSLGGYSLS 159
                             |:|: : | |:||:| |: || : || : ||:| |: |
PAEPCSPFPQLFLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQ-PSAGLV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQGYIPSNYVAEDRSLQAEPWFFGAIKRADAEKQLLYSENQTGAFLIRESESQKGDFSLS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           37 PPEANRSQGQYFVALFDYEARTAEDLSFHAGDKLQVLDTSHEGWWLARHLEKKGPGLGQQ
LDDGGFFIST-RIPFPSLPELVRHYQGKVDGLCQ-CLTIPCQTVRPEKPWEKDAWEIPRE
                                                                                                   SLSLQKKLGAGQFGDVWLAMYNGHTKVAVKTMKPGSMSPGAFLEEANLMKSLQHDRLVRL
                                                                                                                                                                                                                                                                                                             RDLRAANCLVSETLLCKIADFGLARVIEDSEYTAREGTKFPIKWTSLEAANYGSFTIKSD
                                                                                                                                                                                                       HAVVTQGEPIYIITEYMQKGSLLDFLKSEEGSDQPLIQLIDFSAQIAEGMWFIEQRNYIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUNITHA I., AVIGAN M.I.;
BIOCHIM. BIOPHYS. ACTA, GENE STRUCT. EXPR. 1221:348-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE, 9633034.

SUNITHA 1., AVIGAN M.1.;

SUNITHA 1., AVIGAN M.1.;

"The apical membranes of maturing gut columnar epithelial ce contain the enzymatically active form of a newly identified fyn-related tyroshe kinase.";

ONCOGENE 13:547-559(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHÖRDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC RELATED TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE;
AVIGAN M.I.;
SUBMITTED (MAY-1994) TO EMBL/GENBANK/DDBJ DATA BAN
EMBL; U09583; G939625; -.
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROMITE: PSO0107; PROTEIN_KINASE_ATP; 1.
PRAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; Pkinase; 1.
SEQUENCE 506 AA; 58166 MW; 8A3172C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 1335; DB 11; 43.4%; Pred. No. 2.23e-259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE; SUNITHA I., AVIGAN M.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERPSFATLREKLHAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 ORPTFEYLQSILEDF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 196; Conser
```

```
Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RODENTIA;
                                                                                                                                     372 KEIQTIKGIRHERLIRIHAVCSGGEPVYIVTELMRKGNIQAFIGTPEGRALRIPPLIGFA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REAQIMKSLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDGGSKIRLTQQVDMA 336
                                                                                                                                                                                                                                       456
                                                                                                                                                                                                                                                      97 TGLGQQLQGYIPSNYVAEDRSLQAEPWFFGAIKRADAEKQLLYSENQTGAFLIRESESQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 KIQVPTPFDLSYKTADQWEIDRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 PVPTLPAEPCSPFPQLFLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQPS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 95137395.

MEDLINE: 95137395.

OBERG-WELSH C., WELSH M.;

OBERG-WELSH C., WELSH M.;

Cloning of BSK, a murine FRK homologue with a specific pattern of tissue distribution.";

GENE 152:232-242(1995).

EMBL: 136132; G777773; -...

MGD: MGI:103265; FRK.

PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
                   VLDEGVVKHYRIRRLDEGGFFLTRRKTFSTLNEFVNYYTTTSDGLCVKLEKPCLKIQVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 PEAPRSQEPERSHGQYFVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDFSLSVLDEGVVKHYRIRRLDEGGFFLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPCL
                                                           PFDLSYKTVDQWEIDRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFL
                                                                                                                                                                                                                                       PVKWTAPEAIRTNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIHMLGQNYRLPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-CELL SRC-HOMOLOGY TYROSINE KINASE (PROTEIN TYROSINE KINASE).
FRK OR BSK.
MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA: EUTHERIA:
SCIUROGNATHI: MURIDAE; MURINAE: MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.4%; Score 1335; DB 11;
Best Local Similarity 43.2%; Pred. No. 2.23e-259;
Matches 198; Conservative 102; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                069; pkinase; 1.
512 AA; 58891 MW; DECF53C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      PRT; .. 512 AA-
                                                                                                                                                                                                                                                                                                               457 SNCPEQFYSIMMECWNVEPKQRPTFETLHWKL 488
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     LT 6
Q61364
Q61364;
                                                                                       214
157
                                                          217
                                                                                                                    277
                                                                                                                                                                                                                                      397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                        g
                                                                                                                    g
                                                                                                                                                ò
                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                       ò
                             Q
```

```
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336
                               396
                                                                                                                                                                                                                                                                 397 KHEIKLPVKWTAPEAIRTNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQN 456
                                                                                                                                                                                                                                                                                                          157 GDFSLSVLDEGVVKHYRIRRLDEGGFFLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPCL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|||| :: | ||| :: | :|:::| : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || : ::| || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 KIQVPTPFDLSYKTADQWEIHRNSIQLLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 QQVDMAAQVASGMAYLESQNYIHRDLAARNVLVGEHNIYKVADFGLARVFKVDNEDIYES 396
DPNDFLREAQIMKSLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TGLGQQLQGYIPSNYVAEDRSLQAEPWFFGAIKRADAEKQLLYSENQTGAFLIRESETQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALBAC; TISSUE-MAMMARY GLAND;
MEDLINE; 95251656.
THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
wiyk, a novel intracellular protein tyrosine kinase differentially
expressed in the mouse mammary gland and intestine.";
BIOCHEM BIOPHYS. RES. COMMUN. 209:582-589(1995).
EMBL; 248757; G73644; -.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                             337 QQVDMAAQVASGMAYLESQNYIHRDLAARNVLVGEHNIYKVADFGLARVFKVDNEDIYES
                                                                                                                                                                      277 DPNDFLREAQIMKSLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 PEAPRSQEPERSHGQYFVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-SCL SRC-HOWOLOGY TYROSINE KINASE (INTESTINAL TYROSINE KINASE)
FRK OR IYK.
MUS WUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1334; DB 11; Length 512;
Pred. No. 3.73e-259;
103; Mismatches 140; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||:|: || : | :||||| | :||: || || 43 YRLPRPAACPAEVYVLMLECWRSSPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                    457 YRLPQPSNCPQQFYSIMLECWNVEPKQRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169; pkinase; 1.
512 AA; 58928 MW; 808D1612 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.3%;
Best Local Similarity 43.0%;
Matches 197; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1
PFAM; PF00069; pkinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 7
Q61745
Q61745;
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                              δ
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

S

```
RVSMAADGSLYLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC----MPQKAP-RQDVWER 225
                                                                                                                                                                                                                                                                                                                                                                                                         HANAFUSA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                          27 9
090992
                                                                                                                                                                                                                                                                                090992;
                                                                                                                                                                                                                                                                                                                            C-SRC.
 170
                      263
                                           226
                                                                 323
                                                                                                             382
                                                                                                                                                        442
                                                                                                                                                                                                                        466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                          RESULT
                                                                                                           8
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                  g
                                           ŏ
                                                                 g
                                                                                       ò
                                                                                                                                  ö
                                                                                                                                                        8
                                                                                                                                                                             ò
                                                                                                                                                                                                   음
                                                                                                                                                                                                                          ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                       Src
 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSSKIPVKWTAPEAANYRVFSQKSDVWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 IQAEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHY 202
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE: 83155664.
TAKEYA T., HANAFUSA H.;
"Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
397 KHEIKLPVKWTAPEAIRTNKFSIKSDVWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQN
                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97008971.
WEIJLAND A., NEUBAUER G., COURTREIDGE S.A., MANN M., WIENERGA R.;
"The purification and characterization of the catalytic domain of
expressed in Schizosaccharomyces pombe. Comparison of
unphosphorylated and tyrosine phosphorylated species.";
EUR. J. BIOCHEM. 240:756-764(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA-PS-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.H.;
heterogeneity:
the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 14;
                                                                                                                                                                GENE C-SRC PRODUCING PROTEIN PP60-C-SRC.
THIS GENE IS HOMOLOGOUS TO THE ROUS SARCOMA VIRUS GENE V-SRC
                                                                                                                                                                                                           GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WEILAND A.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 484-533 FROM N.A.
MEDLINE; 91304409.
DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H
Analysis of cDNas of the proto-oncogene c-src: het
exons and possible mechanism for the genesis of the
v-src.";
MOL. CELL. BIOL. 11:4165-4176(1991).
EMBL; V00402; E281134;
EMBL; V00400; E1181088;
EMBL; S4359; E27011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1321; DB 13;
Pred. No. 3.07e-256;
92; Mismatches 134;
                                                       YRLPQPSNCPQQFYSIMLECWNVEPKQRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00069; pkinase; 1.
SEQUENCE 533 AA; 60010 MW; 0D446FF3 CRC32;
                                                                                                             ΑĄ
                                                                                                           533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00107; PROTEIN_KINASE_ATP;
PROSITE: PS00109; PROTEIN_KINASE_TYR;
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                  CREATED)
                                                                                                          PRT;
                                                                                                                                02,
02,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.4%;
Matches 192; Conservative
                                                                                                           PRELIMINARY;
                                                                                                                     Q98915; Q91343;
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                32:881-890(1983)
                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>..</u>
                                                                                                                                                                                                 C-SRC OR C-SCR.
                                                                                                                                                                                       (PP60C-SRC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                 T 8
098915
                                           457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                     ò
                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
10,
322
                                                                                                                                                                                              381
                                                                                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                                                                                                                                                                  441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA-PS-DS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 8315564.

TARETA T., HANAFUSA H.;

Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";

CELL 32:881-890(1983).

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; SH2: 1.

PPRAM; PF00017; SH2: 1.
                                                   VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN
                                                                                                                                                                                                                                                       ::| || | ||:||||| ||:|||| ||:||| ||: ||:|| |: ||:|||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQPSAGLVPITHVAKASPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 IQAEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLINVCPTSKPQTQGLAKDAWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVSMAADGSLYLQKGRLFPGLEELLTYYKANWKLIONPLLOPC---MPQKAP-RQDVWER
PRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL
                                                                                                                                                                                                                                                                                                                                                                                                  YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1321; DB 13; Length 533;
Pred. No. 3.07e-256;
92; Mismatches 134; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00069; pkinase; 1.
SEQUENCE 533 AA; 60038 MW; 8E987D6B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 44.4%;
nes 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 DPEERPTFEYLO
```

ဖ

```
Query Match
                                                                                                                                                                                                                                                                                                                                   013064;
                                                                                                                                                                                                                                                                                 T 11
013064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                        ò
                                                                                                                       g
                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                             ID DATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps 10;
                                                                                                                          441
                                                                                                                                                                FVALYDYESRTETDLSFKKGERLQIVNNFEGDWWLAHSLFFGGT-GYIPSNYWA+PS-DS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 KIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQAEEWYFGKTTRRESERLLLUNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 PRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSSEAFLQEAQVMKKLRHEKL 322
      381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE, 95016532.
YATSULA B.A., GERYK J., SVOBODA J., RYNDITCH A.V., CALOTHY G.,
DEZELEE P.;
"Origin and evolution of the c-src-transducing avian sarcoma virus
PR2257.";
J. GEN. VIROL. 75:2777-2781(1994).
VQLYAVVSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN
                                                           286 IRLHAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQR
                                                                                                                          YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI
                                                                                                                                                                                                                                                 KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1315; DB 14; Length 587;
Pred. No. 6.78e-255;
91; Mismatches 135; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65778 MW; A02F2A78 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L21974; G347052; -- PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match
Local Similarity 44.4%;
hes 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM: PF00017; SH2; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF00069; pkinase; 1.
TYROSINE-PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
PROTEIN-TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                           587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVIAN SARCOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=PR2257/16;
                                                                                                                                                                                                                                                                                                                                                                      DPEERPTFEYLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II 10
Q64817
Q64817;
                                                                                                                                                                                                                                                                                                                                                                                                                              466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                                                              442
                                                                                                                                                                                                                                                                                                                                                                   502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
OF THE SULT
                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    염
                                                  ŏ
                                                                                                                 용
                                                                                                                                                                               δy
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

```
11;
                     RTLDNGGYYI-SPRITFTSINEMIQHYQKQADGLCRK-LDKPCFSPKPQKPWDKDAWEIP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 TEEWFFKDLTRKDAERQLLAPGNNPGAFLIRESETSKGSYSLSIRDCDPQTGDVIKHYKI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 RESIKMVRKLGAGQFGEVWMGFYNNSTKVAVKTLKPGSMSVQAFMEEANLMKTLQHDKLV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 RLYAVVSKEEPIYIITEYMAKGSLLDFLKSDEGGKVILPKSIDFSAQIAEGMAYIEKKNY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 IHRDLRAANVLVSESLMCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIK 399
442 KSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRK 501
                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 IALYPYQGIHEDDLSFKKGEKLKVLEEHGEWWKAKSLSTK-KEGFIPSNYVARVN--TLE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMAADGSLYLQKGRL-FPGLEELLTYY-KANWKLIQNPLLQPCMPQKA--PRQ-DVWERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDVWSFGVLLYEIITFGKIPYPGMSNSDVMSALQRGYRMPRMENCPEELYDIMKQCWKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATA BANKS
                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FURANT Y., FUNDRIKI K., SATO K.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BA
EMBL, ABOO3358, D1020891. .
PROSITE: PSO0107: PROTEIN KINASE_ATP: 1.
PROSITE: PSO0109: PROTEIN_KINASE_TYR: 1.
PFAM: PF00017: SH2: 1.
PFAM: PF000018: SH3: 1.
PFAM: PF000018: SH3: 1.
PFAM: PF000018: SH3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.6%; Score 1307; DB 13; 42.8%; Pred. No. 4.21e-253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                             488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526
                                                                                                                                                                                                                                                                                                                                                                                     XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
1D 060567
AC 060567;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                     (TREMBLREL. 04,
(TREMBLREL. 04,
(TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                      LYN PROTEIN TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AEERPTFDYLQSVLDDF 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||:| : | :
467 PEERPSFATLREKLHAI 483
                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                |||||:| |:
466 SPEERPSFATLR 477
                                                                                      502 DPEERPTFEYLQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       01-JUL-1997
                                                                                                                                                                                                                                                                                          01-JUL-1997
01-NOV-1998
```

~

```
505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 LYQLMRLCWKERPEDRPTFDYLRSVLEDF 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                   Local Similarity
nes 199; Conserv
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
016291
016291;
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                  MESOCRICETUS AURATUS (GOLDEN HAMSTER).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVALYDYESWIEIDLSFKKGERLQIVNNIEGDWWLAHSLITGQI-GYIPSNYVA-PS-DS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KICKLYSGGFYITSRTQFGSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTQGLAKDAWEI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRESLRLEAKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 YVHRDIRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 VVHRDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQ 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 IQAEEWYFGKITRRESERLLLNPENPRGTFLVRKSETAKGAYCLSVSDFDNAKGPNVKHY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLYAVVSE-EPIYIVIEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 526;
                                                                                                                                                                                                                                              DATA BANKS
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
H-19 PROVIRAL SEQUENCE (LTR,V-3SCR1,LTR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE.
                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-MESENCHYMAL;
BODOR J., ROZKOT F.
SUBMITTED (MAY-1990) TO EMBL/GENBANK/DDBJ DATA BAN EMBL: X52822; G49657; -
PROSITE: PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE: PSO0109; PROTEIN_KINASE_TYR; 1.
PRAM: PF00018; SH2; 1.
PFAM: PF00018; SH2; 1.
PFAM: PF00069; pkinase; 1.
SEQUENCE 526 AA; 59061 MW; 0E2418FA_CRG32;...
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.6%; Score 1306; DB 11; Best Local Similarity 43.9%; Pred. No. 7.05e-253; Matches 191; Conservative 92; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIŠSUE-LEUKEMIA;
MEDLINE; 94187714.
WRIGHT D.D., SEFTON B.M., KAMPS M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ULT 13
Q12850 PRELIMINARY;
Q12850
01285-1996 (TREMBLREL. 01, C
01-NOV-1998 (TREMBLREL. 01, L
01-NOV-1998 (TREMBLREL. 08, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPEERPTFKYLQAQL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 SPEERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                  V-3SRC-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263
  DDR RED DR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

```
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and chromosomal localization of the human homologue of a B-lymphocyte specific protein tyrosine kinase (blk)."; OCCENE 10.47-486(1995).

EMBL: S76617, 694204, -.

PFAM; PF00017; SH2; 1.

PFAM; PF00018; SH3; 1.

SEQUENCE 505 As; 57756 MW; 8BCCFF4D CRC32;
"Oncogenic activation of the Lck protein accompanies translocation of the Lck gene in the human HSB2 T-cell leukemia.";
MOL. CELL. BIOL. 14:2429-2437(1994).
EMBL; U07365; G4609665; --
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PFAM; PF000118; SH3; 1.
PFAM; PF000118; SH3; 1.
PFAM; PF000118; SH3; 1.
PFAM; PF000118; SH3; 1.
SEQUENCE 512 AA; 58412 MW; 12B0BA65 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGEVVKHYKIRNLDNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQKP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 PASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQ-EGFIPFNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 VAKAN--SLEPPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 PEAINYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNLEVIONLERGYRMVRPDNCPEE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 NIMKQLQHQRLVRLYAVVTQ-EPIYIITEYMENGSLVDFLKTPSGIKLTINKLLDMAAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 AEGMVFIEERNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTA
                                                                                                                                                                                                                                                                                                                                                       Indels 18;
                                                                                                                                                                                                                                                                                                  Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 95148118.
DREBIN J.A., HARTZELL S.W., GRIFFIN C., CAMPBELL M.J.,
NIEDERHUBER J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
BLK-PROTEIN TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                35.5%; Score 1304; DB 4; Le
larity 44.3%; Pred. No. 1.98e-252;
Conservative 91; Mismatches 141;
```

```
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSLVT-GREGYVPSNFVARV--E 117
                                                                                                                                    169
                                                                                                                                                                                                                                                                                                           235
                                                                                                                                                                                                                                                                                                                                                            224
                                                                                                                                                                                                                                                                                                                                                                                                             236 IPRQSLRLVRKLGSGQFGEVWMGYYKNNMKVAIKTLKEGTMSPEAFLGEANVMKALQHER 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                               284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 LFVALYDYEARTEDDLSFHKGEKFQILNSSEGDWWEARSLTT-GETGYIPSNYVA-PV-D 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIQAEEWYFGKLGRKDAERQLLSFGNPRGTFLIRESETTRGAYSLSIRDWDDMKGDHVKH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVRLYAVVTK-EPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAYIERM 354
                                                         Gaps
                                                                                                                                                                                                          118 SLEMERWFFRSQGRKEAERQLLAPINKAGSFLIRESETNKGAFSLSVKDVTTQGELIKHY
                                                                                                                                                                                                                                    178 KIRCLDEGGYYI-SPRITFPSLQALVQHYSKKGDGLCQR-LTLPCVRPAPQNPWAQDEWE
                                                                                                                                                                                                                                                                                                                                       355 NSIHRDLRAANILVSEALCCKIADFGLARIIDSE-YTAQEGAKFPIKWTAPEAYHFGVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLERGYRMPRPDTCPPELYRGVIAECW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Mismatches 136; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 534;
  Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%; Score 1299; DB 4; Length 53 larity 43.4%; Pred. No. 2.61e-251; Conservative 94; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., MANDAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q16248;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01; LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
P59FYN.
Score 1300; DB 4; 1
Pred. No. 1.56e-251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 95123664.
RIGHEY K. SLOCOMBE P., PROUDFOOT K., WAHID
BEBBINGTON C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSRPEERPTFEFLOSVLEDF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%;
                                                      195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 188; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID DET THE REAL OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF
                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                         ò
                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
322
114 TLSDQPWYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-QA-K---VCH 168
                    262
                                                                               284
                                                                                                     381
                                                                                                                        344
                                                                                                                                             441
                                                                                                                                                         501
                                                                                                                                                                                              YKIRKLDNGGYYITTRAQFETLQQLVQHYSEKADGLCFNLTVIASSCTPQTSGLAKDAWE
                                   263 VARRSLCLEKKLGQGCFAEVWLGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDK
                                                                        LVQLYAVVSE-EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERM
                                                                                                                                                                                   IKSDVWSFG1LLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWK
                                                                                                                                             382 NYIHRDLRSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPERALYGRFT
                                                                                                                                                                                                                                         SSPEERPSFATLR 477
                                                                                                                                                                                                                            502 KDPEERPTFEYLQ 514
                                                                                                                       285
                                                                                                                                                                                    442
                                                                                                                                                                                                                                                465
                                        169
                    203
                                                                                                     323
 δy
               g
                                    ò
                                                        g
                                                                              QY
                                                                                                  g
                                                                                                                      οy
                                                                                                                                          g
                                                                                                                                                               ŏ
                                                                                                                                                                                  d
                                                                                                                                                                                                      οy
                                                                                                                                                                                                                           g
```

Search completed: Thu May 20 12:28:10 1999 Job time : $327\ \mathrm{secs.}$

US-09-099-053-2-02.rag

*****	. (MI)	*****
***************************************		**********************
******		*******
******		*******
******		*******
*****		******
******		*******
******		*******

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Thu May 20 12:31:26 1999; MasPar time 8.25 Seconds Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated

1 MEPFLRRRLAFLSFFWDKIW......PNTDPVPTLPAEPCSPFPQL >US-09-099-053-2 (1-55) from US09099053.pep (2 of 429 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-geneseq35 Database:

| Spart | 2.part | 3.part | 4.part | 5.part | 5.part | 7.part | 7.

Mean 26.823; Variance 102.975; scale 0.260 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description	Pred. No.
н	429	100.0	488	39.	W89248	Human SAD.	1.38e-34
7	82	19.8	563	18	R92128	Porphyromonas gingiva	8.95e+00
e	85	19.8	563	15	R79924	P. qindivalis cell su	8.95e+00
4	82	19.1	302	35	W72007	HSV-2 strain SB5 Cont	1.60e+01
Ŋ	82	19.1	302	36	W72168	HSV-2 strain SB5 Cont	1.60e+01
ø	82	19.1	302	36	W72148	HSV-2 strain SB5 Cont	1.60e+01
7	81	18.9	312	ഗ	R26079	E2 f	1.93e+01
æ	81	18.9	340	37	W81594	Protein encoded by hu	1.93e+01
σ	81	18.9	399	37	W81590	Protein encoded by hu	1.93e+01
10	79	18.4	249	35	W76166	Sed ID 57 from US5804	2.82e+01
11	79	18.4	249	27	. W31220	HIV-TAT protein trans	2.82e+01
12	79	18.4	249	24	W26460	Protein of the invent	2.82e+01
13	79	18.4	295	37	W68493	A truncated papilloma	2.82e+01
14	79	18.4	400	32	W57431	Bacillus agaradherens	2.82e+01
15	79	18.4	400	25	W23601	Bacillus agaradherens	2.82e+01
16	79	18.4	400	25	W22521	Bacillus agaradherens	2.82e+01
						•	

22222222222222222222222222222222222222	
Bovine papillomavirus Bovine papillomavirus Bovine papillomavirus Bovine papillomavirus Bovine papillomavirus Bovine papillomavirus Gorotein coupled hum G-protein coupled hum Cloned alkaline endog Human D4 dopamine rec Recombinant human D4 Sequence encoded by a D4 dopamine receptor. Human dopamine D4 rec Human dopamine D4 rec Human dopamine D4 rec Human dopamine D4 rec Human dopamine D4 rec	The asset of the property of t
	M48995 R89515 R895215 R48950 P94683 W7088096 W09873 W72169 W75095 R60520
17777777777777777777777777777777777777	733757 7337 7337 7337 7337 7337 7337 73
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	758 763 763 763 763 763 763
44444400000000000	
77777777777777777777777777777777777777	
11100000000000000000000000000000000000	

```
E Human SAD.

E WAR 1970; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; two type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; when developementative disease; neuronal survival; Alzheimer's disease; parkinson's disease; meuronal survival; Alzheimer's disease; No benchedgementative disease; neuronal survival; Alzheimer's disease; No benchedgementative disease; meuronal survival; Alzheimer's disease; No benchedgementative disease; No benchedgementative; .r. 1
W89248 standard; Protein; 488 AA.
W89248;
                                                                          10-MAR-1999 (first entry)
                                                                                                        Human SAD
```

comprises amino acids indicated

```
Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Esser KM, Leary JJ WPI; 98-286847/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V62131
                                         W09526404-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mamma1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Signal peptide encoded by nucleotides designated in the specification to encode the signal peptide, comprises amino acids indicated as -5 to +10"
                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotides designated
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide(s) derived from type II fimbrial protein of Porphyromonas gingivalis used in the diagnosis and treatment of periodontosis Example 1; Page 16-21; 22pp; Japanese. R92128 is the 72 kb subunit protein of Porphyromonas gingivalis which contains the type II fimbrial protein. Peptides derived from the type II fimbrial protein. Peptides derived from the priodontosis. The peptides may also be used in a vaccine for immunisation against the disease.
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                             17-ocr-1996 (first entry)
Porphyromonas gingivalis 72 kD subunit protein.
Periodontosis, gingivalis, type II fimbrial; vaccine; diagnosis; immunisation; epitope.
Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. gingivalis cell surface protein.
Cell surface polypeptide. P. gingivalis; Bacteroides gingivalis;
pCSP409: diagnosis; prevention; periodontal disease; vaccine; ds
Porphyromonas gingivalis strain OMZ409.
                                                                                                                                                                                                            1 mepflrrrlaflsffwdkiwpaggepdhgtpgsldpntdpvptlpaepcspfpgl 55
                                                                                                                                                                                                                                    1 MEPFLRRRLAFLSFFWDKIWPAGGEPDHGTPGSLDPNTDPVPTLPAEPCSPFPQL 55
                                                                                                                                                                     ö
                                                                                                                              Length 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 18; Length 563; Pred. No. 8.95e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mature protein encoded by nucleot
in the specification to encode the mature
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 lgfnwnplvpdpdpsnpenpnnpdpnpdepgtpvptdpegplpd 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 429; DB 39; Lapred. No. 1.38e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6..563
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T. 3
R79924 standard; Protein; 563 AA:
                                                                                                                                                                                                                                                                                                                     .T 2
R92128 standard; Protein; 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK.
(KYOW ) KYOWA MEDEX KK.
(MEIT ) MEITO SANGYO KK.
WPI; 96-167222/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%;
                                                                                                                         Ouery Match
Best Local Similarity 100.0%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1994; 204422.
05-AUG-1994; JP-204422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                  488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T18119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J08048695-A.
                                                                 proteins.
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R79924;
                                                                                                                                                                                                                                                                                                                                                              R92128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866668
                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                                                           NAME OF THE PART OF THE PROPERTY OF THE PARTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
Taim 10; Page 41; 748pp; English.

This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain sequence of the invention. This sequence was isolated from a HSV-2 strain SBS (deposited as ATCC VR-2546) DNA fragment designated Contig ID 101.

Based on homology, this sequence is a (X02138) 34K (Us10) protein.

The proteins can be used for the treatment tor prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the cell surface polypeptide of P. gingivalis. The DNA encoding this sequence was isolated on a 3.4 kb Kpil/Xhor P. gingivalis fragment which was combined with pBluescript to give pCSP409. This plasmid was used to transform E. coli, which upon culture produced the cell surface protein. The expressed protein can be used in the diagnosis and prevention of periodontal disease, e.g. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                               peptide - used
diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W72007;
07-DBC-1998 (first entry)
HSV-2 strain SB5 Coniig ID 101 ORF#1 protein.
HSV-2 strain SB5; immunological response induction; therapy;
antivital identification; viral protein inhibitor.
W09820016-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 35; Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85; DB 15; Length 563
Pred. No. 8.95e+00;
11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                           DNA coding for Porphyromonas gingivalis cell surface
for production of the peptide for the prevention and
periodontal disease
Claim 1; Page 16-22; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEBCHAM CORP.
Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ogawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 lgfnwnplvpdpdpsnpenpnnpdpnpdepgtpvptdpegplpd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.60e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                               H
                                                                                                                                                                                                                                                                                               Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82;
                                                                                                                                                                                                                                                                                            Hokkoku H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 4
W72007 standard; Protein; 302 AA.
                                                                                                      29-MAR-1994; JP-081074.
29-MAR-1994; JP-081074.
08-JUL-1994; JP-180815.
(KYOW) KYOWA HAKKO KKY.
(KYOW) KYOWA MEDEX CO LTD.
(MEIT ) MEITO SANGYO KK.
FUKUI M, Hasegawa M, Hokkoku Yamada K, Yasuda K;
WPI; 95-351324/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.9%;
Matches 18; Conservative
peptide, c
to 558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998.
31-OCT-1997; U20016.
09-JUN-1997; US-049018.
04-NOV-1996; US-030279.
```

```
312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inside the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9845438-Al.
                                                                                                                                                                                                                                                                                                                   WO9212728-A.
                                                                                                                                                                                                                                                                                                                                   06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W81594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рр
    8888888
                                                                                                                                                      g
                                                                                                                                                                               ö
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 12. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to induce an iso be used to induce an immunological response in a mammal sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 100; 748pp; English.
This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 3. Based on homology, this sequence is a virion protein US10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus type-2 sequences - useful in, e.g. preventic
and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                     Herpes simplex virus type-2 sequences - useful in, e.g. preventic
and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1998 (first entry)
HSV-2 strain SBS Contig ID 3 ORF#10 protein.
HSV-2 strain SBS; immunological response induction; therapy; antivitral identification; viral protein inhibitor.
Herpes simplex virus type 2.
                                                                                                        08-JAN-1999 (first entry)
HSV-2 strain SB5 Contig ID 12 ORF#10 protein.
HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
WO9820016-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%; Score 82; DB 36; Length 302; 42.9%; Pred. No. 1.60e+01; vative 9; Mismatches 9; Indels
                                                                                                                                                                                          11-0CT-1997; U20016.
09-UNU-1997; US-049018.
04-NOV-1996; US-030279.
(SMIK ) SMITHKLINE BEEGHAM CORP.
Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB,
ESSET KM, Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chan Ji, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB,
Esser KM, Leary JJ;
WPI: 98-286847/25.
N-PSDB; V62164.
65 raypgtrdphdphgcpgsldphgnpagpaglps-p-vpyapl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 raypgtrdphdphgcpgsldphgnpagpaglps-p-vpyapl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus type-2 sequences - useful in,
               Herpes simplex virus type-2 sequences - useful in,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. 6
W72148 standard; Protein; 302 AA.
                                                                    r 5
W72168 standard; Protein; 302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-1997; U20016.
09-UUN-1997; US-0490.8.
08-UNV-1995; US-0430.79.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                        Esser KM, Leary JJ;
WPI; 98-286847/25
N-PSDB; V62175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                              W72168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W72148;
                                                                                                                                                                                                                                                                                                                                             mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           татта1
                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
4
The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal. Sequence 302 AA;
                                                                                                                                                                                                                                                                                                  ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1999 (first entry)
Protein encoded by human UCP3sh gene reading frame 3.
Uncoupling protein 3. UCP3: thermogenesis: mammal; enhancer; drug;
Drotein catabolism: anti-obesity; inhibitor; muscle wasting; infection;
HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;
non-insulin dependent diabetes mellitus; diagnosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A preparation is described in the specification for the production of a tate2 fusion protein. The sequence given is the same length as the disclosed compound but it is not actually claimed as such. The fusion construct consisted of the first 62 amino acids of the tat protein from HIVI, a linker serine residue and the the last 249 amino acids of BPVI E2 protein. The fusion protein gained entry to cells via binding of the tat molecule with the cell surface and the nonspecific endocytosis. The E2 molecule acts as a repressor once
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "the encoding reading frame has internal stop codons which are not indicated in this protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2 trans-activation repressors of Papilloma-virus - dimerise with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                      .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1993 (first entry)
Putative tat-E2 fusion protein.
E2 protein; tat; HIV1; non-specific endocytosis; repressor.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length E2 polypeptide(s), for treating Papilloma-virus
                                                                                                                                                                                                                                  Length 302;
                                                                                                                                                                                                                                  Score 82; DB 36; Length 302
Pred. No. 1.60e+01;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 5; Length 312;
Pred. No. 1.93e+01;
15; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                               65 raypgtrdphdphgcpgsldphgnpaqpaglps-p-vpyapl 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 dgvwvasegpe-gdpagkeaepagpvssllgspacgpirpgl 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 DKIWPAGGEPDHGTPGSLDPN-TDPVPTLPAEP-CSPF-PQL 55
                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1992; U00652,
28-JAN-1991; US-646998.
(BIOJ ) BIOGEN INC.
(NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W81594 standard; Protein; 340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R26079 standard; Protein; 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections e.g. malignancies
                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 42.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Androphy EJ, Barsoum JG;
WPI; 92-284418/34.
N-PSDB; Q27279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..340
```

```
49 dgvwvasegpe-gdpagkeaepagpvssllgspacgpi 85
                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
          88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                     New isolated uncoupling protein, UCP-3 - used to develop products

Tor modulating thermogenesis in tissues, e.g. for treating obesity

or muscle wasting caused by infection or cancer

Disclosure; Fig 2A-B; 98pp; English.

Sequences W81592 to W81594 represent protein fragments encoded by the tree reading frames of the human uncoupling protein 3 short form

(UCP3sh) gene. The invention provides human and mouse UCP3 genes (V7/110 and V7/712) encoding UCP3 proteins (W81597 and W81595) respectively. A cost cell transformed with a construct comprising the UCP3 uncleic acid can be used for the recombinant production of the protein. The UCP3 is involved in the regulation of thermogenesis in mammals. The nucleic acids (V7/710 to V7/712) can be used for identifying compounds which alter UCP3 activity. Enhancers of UCP3 can be used for enhancing protein catabolism in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can be used for inhibiting protein catabolism in a mammal such as inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V71110.

New isolated uncoupling protein, UCP-3 - used to develop products
New isolated uncoupling protein, UCP-3 - used to develop products
for modulating thermogenesis in tissues, e.g. for treating obesity
or muscle wasting caused by infection or cancer
Disclosure; Fig 1A-C; 98pp; English.
Sequences W81588 to W81590 represent protein fragments encoded by the
three reading frames of the human uncoupling protein 3 (UCP3) gene. The
invention provides human and mouse UCP3 genes (V71710 and V77712)
encoding UCP3 proteins (W81587 and W81595) respectively. A host cell
transformed with a construct comprising the UCP3 nucleic acid can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscle wasting. They can be used for curtailing muscle wasting due to infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g. muscular dystrophy) or as a possible treatment for non-insulin dependent diabetes mallitus. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W81590;
09-FEB-1999 (first entry)
Protein encoded by human UCP3 gene reading frame 3.
Protein encoded by human UCP3; thermogenesis; mammal; enhancer; drug; Uncoupling protein 3 uUCP3; thermogenesis; muscle wasting; infection; protein catabolism; anti-obesity; inhibitor; muscle wasting; infection; HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy; non-insulin dependent diabetes mellitus; diagnosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stop codons which are not indicated in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "the encoding reading frame has internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 37; Length 340;
Pred. No. 1.93e+01;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-0CT-1998.

08-APR-1998.

15-UUL-1997; UG-892745.

09-APR-1997; US-043447.

12-MAY-1997; US-046254.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

FLIER JS, LOWELL BB;

WPI: 98-594483/50.
08-APR-1998; U06959.
15-JUL-1997; US-882745.
09-APR-1997; US-043447.
12-MAY-1997; US-046254.
18ETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Flier JS, Lowell BB;
WPI; 98-594483/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W81590 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.9%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 wraghhpdhgadgslqp 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.9%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 WPAGGEPDHGTPGSLDP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 AA;
                                                                                                                                                                                   N-PSDB; V71711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9845438-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
While year of the control of the control of cells biological actived transport fusion proteins - used to deliver

PT HV tat derived transport fusion proteins - used to deliver

PT biological active molecules e.g. peptide(s) or nucleic acids,

PT specifically into cytoplasm or nuclei of cells

Disclosure; Column 105-106; 83pp; English.

CC this specification describes a method for the delivery of biologically

CC crity cargo molecules into the cytoplasm and nuclei of cells, for

therapeutic, prophylactic or diagnostic purposes. This is accomplished

by the presence of a small, basic section of the human immunodeficiency

ctherapeutic, prophylactic or diagnostic purposes. This is used as it is this

CC therapeutic, prophylactic or diagnostic purposes. This is used to take up HIV.

CC transport molety usually in the form of a fusion protein. The cargo

CM the method involves the use of a cargo moiety in combination with a

CC transport molety usually in the form of a fusion protein. The cargo

CM of pubmide a pumman papillomavirus E2 repressor that retains its biological

CC (c) 38-72, (d) as 38-62. The protein fragments (a) as 47-52,

CC (g) as 47-62 or as 38-62. The proteins allow delivery of specific

CC (g) as 47-62 or as 38-62. The proteins allow delivery of specific

CC (g) as 47-62 or as 38-62. The proteins allow delivery of specific

CC (e) as A7-62 or as an additionally damage cells as they cause physical opening

CC (c) transporters. Previous methods of delivery include bombardment and

CC (c) infected and can additionally damage cells as they cause physical opening
for the recombinant production of the protein. The UCP3 is involved in the regulation of thermogenesis in mammals. The nucleic acids (V71710 to V71712) can be used for identifying compounds which alter UCP3 activity. Enhancers of UCP3 can be used for enhancing protein catabolism in a mammal and can be used for enhancing protein catabolism in a mammal and can be used for curtailing muscle wasting of UCP3 can be used for curtailing muscle wasting due to infection (e.g. HIV), cancer, tumour cachexia, muscle wasting due to muscular dystrophy) or as a possible treatment for non-insulin dependent diabetes mellitus. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the cell walls/membranes to allow entry.

Note: This sequence is not described in the specification but is listed in the Seq ID lising.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus E2 repressor; target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
ώ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOJ ) BIOGEN INC.
Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
WPI; 98-505702/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 35; Le
Pred. No. 2.82e+01;
15; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 37; I
Pred. No. 1.93e+01;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W76166 standard; protein; 249 AA.
W76166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.9%;
larity 64.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%;
llarity 31.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-1998 (first entry)
Seq ID 57 from US5804604
TAT protein; cargo molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 wraghhpdhgadgslqp 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 WPAGGEPDHGTPGSLDP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1993; WO-U07833.
24-NOV-1993; US-158015.
25-MAY-1995; US-450236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-636662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1995; 450236.
28-APR-1994; US-235403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1994;
21-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5804604-A.
                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis.
```

ò

```
Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
RWPI; 97-322943/36.

New DINA constructs for transporting molecules to cells - encode a fusion protein comprising a modified HIV tat protein and a carboxy-terminal cargo molety
This sequence comprises a protein provided in the specification of US5652122. The invention relates to novel DNA molecules that encode fusion proteins (see W26436-42) between a modified HIV tat protein is modified by deletion of the Cys-rich domain and the exon 2-encoded C-terminal region. It is used to deliver the convently attached cargo molecule to a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 18.4%;
Similarity 31.6%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                 (PEDL), PEPINSKY R B.
Barsoum JG, Fawell SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53 tumour repressor.
Bovine papillomavirus.
WO9832861-A1.
                                   (BARS/) BARSOUM J G.
                                                                FAWELL S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 12; Conser
                                                                                           FRANKEL A.
                                                             (FRANZ) FRANKEL
(PRANZ) FRANKEL
(PABOZ) PABO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W68493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT AND A MARKE WAS A LOOK A MARKE WAS A LOOK A MARKE WAS A LOOK A MARKE WAS A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK A LOOK
           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular delivery of viral repressor proteins
Disclosure; Column 103-104; 77pp; English.
This peptide is used to devise a novel method for delivery of biologically active cargo molecules into the cytoplasm and nuclei of eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-1, HIV-2, SIV) is readily taken up into cells when present extracellularly and can be modified to covalently link to cargo proteins e.g. E2 repressor proteins producing a fusion protein without the problems of spurious trans-activation and disulphide aggregation. These transport polypeptides also minimise interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophlactic or diagnostic intracellular delivery of small molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion proteins containing truncated HIV tat sequences - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1997 (first entry)
Protein of the invention.
HIV; human immunodeficiency virus; tat protein; transport protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macromolecules e.g. proteins, nucleic acids and polysaccharides. Sequence 249 AA;
                                                                                                                                                                                 20-Mar.1998 (first entry)
HIV-TAT protein transport moiety peptide 11.
Human Immunodeficiency Virus; HIV Type 1; Tat protein;
cargo molecule; intracellular delivery; fusion protein;
therapeutic; prophylactic; diagnostic; transport polypeptide;
E2 repressor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PABO/) PABO.
(PEDIVI) PEPINSKY R B.
BEEPUL, PEPINSKY R B.
WPI: 97-502388,46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 27; Le
Pred. No. 2.82e+01;
15; Mismatches 8;
49 dgvwvasegpe-gdpagkeaepagpvssllgspacgpi 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ.
                                                                                                                                             W31220 standard; Peptide; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 12
W26460 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1994; US-235403.
21-DEC-1989; US-44450.
02-JAN-1991; US-636662.
21-AUG-1992; US-94375.
19-AUG-1993; WO-U07833.
24-NOV-1993; US-158015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-1995; US-450098.
(BARS/) BARSOUM J G.
(FAWE/) FAWELL S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-235403.
US-454450.
US-636662.
US-934375.
WO-U07833.
US-158015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1989; 454450.
28-APR-1994; US-2354
21-DEC-1989; US-4544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANKEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cargo delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1993;
24-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5652122-A.
                                                                                                                                                                                                                                                                                                                                                                                                     US5674980-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FRAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W26460;
                                                                                                                RESULT
```

NEW WENT WANTED BY A PROPERTY OF THE PROPERTY

```
reating and preventing cancer of the cervix
Disclosure: Fig 10; 11pp: French.
The present sequence represents EZTR, a truncated Bovine papillomavirus
The present sequence represents EZTR, a truncated Bovine papillomavirus
The present sequence represents EZTR protein does not contain the
N'terminal transactivation domain. Compounds derived from EZ are able
to induce apoptosis in cells that have integrated part of the human
Papillomavirus (HPV) genome. The EZ protein and its derivatives, the
vectors (including those expressing wild-type EZ) and the corresponding
proteins or truncated EZ (EZTR) are all useful for treating or preventing
papillomavirus infection, particularly papillomavirus-associated cancers
(especially of the cervix uteri). The proteins, and sequences expressing
them, also induce apoptosis of virus-infected cells and increasing the
sequence 295 AA;
                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             A truncated papillomavirus E2 protein designated E2TR.
E2TR; papillomavirus; BVP-1; E2 protein; apoptosis; HPV; infection;
papillomavirus-associated cancer; cervix; virus-infected cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papilloma virus E2 protein or nucleic acid encoding it - useful for
                                                                               ..
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n.
Score 79; DB 24; Length 249;
Pred. No. 2.82e+01;
15; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.4%; Score 79; DB 37; Length 295; larity 31.6%; Pred. No. 2.82e+01; Conservative 15; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1998; F00169.
29-JAN-1997; FR-000964.
(INSP.) INST PASTEUR.
(UYME-) UNIV MEXICO NACIONAL AUTONOMA.
WPI: 98-427957/36.
N-PSDB; V60832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 dgvwvasegpe-gdpagkeaepagpvssllgspacgpi 114
                                                                                                                                          49 dgvwvasegpe-gdpagkeaepagpvssllgspacgpi 85
                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 13
W68493 standard; Protein; 295 AA
```

8 ö

```
Example 1; Pages 46-47; 83pp; English.

Example 1; Pages 46-47; 83pp; English.

This represents a Bacillus agaradherens endoglucanase enzyme. This is

This represents a Bacillus agaradherens endoglucanase enzyme. This is

CC used in the construction of enzyme hybrids for liquefaction of starch.

The enzyme hybrids contain amino acid sequences of alpha-amylase linked

CC to a cellulose binding domain (CBD)..The starch.is liquefied.by treating, in aqueous medium, with such an enzyme hybrid. A recombinant expression vector comprising a construct containing isolated DNA encoding enzyme

CC to transform host cells for the production of the recombinant enzyme hybrids. The enzyme hybrids are useful in industrial starch processing especially for the production of sweeteners. Hybrid enzymes have altered affinity for substrate and increased activity, resulting in at least 1 of reduced calcium ion dependence, reduced formation of Maillard reaction

C saccharification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleaning of cellulosic fabrics - using an enzyme hybrid comprising sequence of a non-cellulolytic enzyme linked to a cellulose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liquefaction of starch for, e.g. production of sweeteners -comprises use of enzyme hybrids including cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Der Osten C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 95-96; 124pp; English.
This protein comprises the alkaline cellulase (endoglucanase) of Bacillus agaradherens NCIMB 40482. It was expressed in Bacillus subtilis PL2306 transformants following PCR amplification (see T74288-89) of B. agaradherens genomic DNA and ligation of the PCR product into vector pDNI981. DNA encoding the cellulose binding domain (CBD) of the alkaline cellulase was subsequently amplified
                                                                                                                                Bacillus agaradherens endóglucanase enzyme.
Starch, liquefaction: sweetener; enzyme hybrid; endoglucanase; e
cellulose binding domain; CBD; starch processing; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     volumi agradherns alkaline cellulase Cel5A;
Desizing; cellulose; fabric; enzyme hybrid; alkaline cellulase;
endoglucanase; Bacillus agaradherens; cellulose binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 32; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bisgardfrantzen H, Bjornvad M, Pedersen S, Schulein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 tfvrekiresasippsdptpps-dpg-epdptppsdp-geyp 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS.
Bjornvad ME, Cherry JR, Rasmussen MD, Vind J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SFFWDKIWPAGG-EPDHGTPGSLDPNTDPVPTLPAEPCSPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cel5A.
'Bacillus agaradherens strain NCIMB 40482
                            W57431 standard; Protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 15
W23601 standard; Protein; 400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-1998 (first entry)
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 35.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                        23-APR-1998.
13-OCT-1997; DK0448.
11-OCT-1996; DK-001130.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V. -AUG-1997;
P9-JAN-1997; DK0042.
29-JAN-1996; DK-000094.
                                                                                                                                                                                                                                                                       Bacillus agaradherens.
WO9816633-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 98-251283/22.
N-PSDB; V29654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjornvad ME, Cher:
WPI; 97-402598/37.
                                                                                                                                                                                                                                           saccharification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T74270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9728243-A1.
07-AUG-1997.
                                                                                                01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W23601;
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                   NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

* * *	a
* *	(TM)
****	' <u>-</u>
* * * * *	' '

******	-2

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:33:58 1999; MasPar time 7.06 Seconds291:741-Million cell-updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (1-55) from US09099053.pep (2 of 6) 429 1 MEPFLRRLAFLSFFWDKIW......PNTDPVPTLPAEPCSPFPQL 55 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

116695 segs, 37453910 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 35.867; Variance 69.695; scale 0.515

Statistics:

SUMMARIES

Pred. No.	4.08e-26	4.08e-26	1.28e-01	3.38e-01	6.39e-01	1.20e+00	2.22e+00	3.02e+00	4.08e+00	4.08e+00	4.08e+00	5.52e+00	7.43e+00	7.43e+00	7.43e+00	7.43e+00	9.99e+00	9.99e+00	9.99e+00	1.34e+01	1.34e+01	1.34e+01	1.34e+01
Description	.srm - mouse	protein-tyrosine kina	beta-lactamase (EC 3.	probable nuoL protein	regulatory component	cellulase (EC 3.2.1.4	transcription factor	cobalamin biosynthesi	E2 protein - bovine p	hypothetical protein	glucose regulated pro	hypothetical protein		tellurium resistance	latency-related prote	glutamate receptor de	hypothetical protein	dopamine receptor D4	hypothetical protein	aldehyde reductase (E	collagen alpha 1(IX)	MAPK-activated protei	beta-galactosidase (E
a	I56322	A56040	S36188	B70946	S74644	A25156	A35658	G69167	WZWLEB	857089	868689	S74847	E64522	H69756	WMBEL1	S28858	D70675	DYHUD4	S77255	A59021	S02170	S78100	300767
DB	~	7	7	7	~	~	~	7	Н	7	~	~	~	~	Н	N	N	H	7	~	N	7	7
Length	496	496	302	633	282	488	514	1045	306	325	666	365	190	257	340	1008	375	387	517	316	325	385	489
% Query Match	53.8	53.8	•	20.3	19.8	19.3	18.9	18.6	18.4	18.4	18.4	18.2	17.9	17.9	17.9	17.9	17.7	17.7	•	•	17.5	•	17.5
Score	231	231	90	87	82	83	81	80	79	79	79	78	77	77	77	77	16	16	92	75	75	75	75
Result No.	П	7	m	4	'n	ø	7	ω	σ	10	11	12	13	14	12	16	17	18	19	50	21	22	23

#formal_name Mus musculus #common_name house mouse
01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
12-Jun-1998
A56040
A56040
Rohmura, N.; Yagi, T.; Tomooka, Y.; Oyanagi, M.; Kominami,
R.; Takeda, N.; Chiba, J.; Ikawa, Y.; Aizawa, S.
Mol. Cell. Biol. (1994) 14:6915-6925
A novel nonreceptor tyrosine kinase, Srm: cloning and

ACCESSIONS REFERENCE #authors

#journal #title

- mouse

ORGANISM DATE

34 6 e + 01 34 6 e + 01 34 6 e + 01 79 e + 01 70 e + 01	n nge ein	ips 3;	
huntingtin-associated huntingtin-associated 1.7-cell receptor alpha 1cell receptor alpha 1Autograf 1Autogr	ommon_name house mouse on 26-Jul-1996 #text_cha tsuka, F. 21:533-538 NA clone encoding protei from GB/EMBL/DDBJ 71; PID:9684972 Thr or Tyr-specific prot mology; SH3 homology	tein kinase homology #label KIN, tein kinase ATP-binding motif lecular-weight 55731 #checksum 859 Score 231; DB 2; Length 496; Pred. No. 4.08e-26; 7; Mismatches 12; Indels 4; Gaps FEEDIPRIGHDDNPVPEQAAVEPCS-FP 53 GEPDHGTPGSLDPNTDPVPTLPAEPCSPFP 53 Complete Kinase (EC 2.7.1.112) Srm, nonreceptor	
2 S67495 2 S67495 2 S67495 2 D24092 2 D24092 2 D24092 2 D24092 2 S55128 1 H40781 1 B4584 2 A28452 2 CC4943 2 CC6083 2 A35617 2 A35617 2 A3355 2 A564453 2 A564453 2 A564453 2 A564453 2 A564453 2 A564453 2 A564453 2 A564453	ALIGNMENTS type complete Mus musculus #sequence_rev's Nakauchi, H.; ermatol. (1999) on of a novel inase in murii nary; translat #label RES 49427; NIDI956 rotein kinase SH3 homology	#domain protein kinase homology #1 #region protein kinase ATP-binding #length 496 #molecular-weight 55731 # al Similarity 58.2%; Score 231; DB 2; Leng al Similarity 58.2%; Pred. No. 4.08e-26; BreprikkELFERRETIESFWDKIWPAD-ESEDIPRIGGHDDNPVPEQAA	
75 17.5 6299 75 17.5 843 74 17.2 131 74 17.2 131 74 17.2 543 74 17.2 543 74 17.2 543 74 17.2 223 74 17.2 243 74 17.2 2124 77 17.0 200 73 17.0 200 73 17.0 3399 73 17.0 3399 73 17.0 3399 73 17.0 3399 73 17.0 478 73 17.0 478	1 156 2 45 2 85 2 10 1 156 2 8	14 #8 #8 #8 #8 #8 #8 #8 #8 #8 #8 #8 #8 #8	esnow -
40000000000000000000000000000000000000		232-44 240-2 240-2 240-2 Query N Best L Matche Db Oy OY RESULT ENTRY TITLE	

17-Jul-1998

```
ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                 ##status
                                                                                                                                                                                                                                                                                                                #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #variety
                         ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
58-170
107
                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coque, J.J.R.; Liras, P.; Martin, J.F.
EMBO J. (1993) 12:631-639
Genes for a beta-lactamase, a penicillin-binding protein and a transmembrane protein are clustered with the cephamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain signal sequence #status predicted #label SIG\
#product beta-lactamase I #status predicted #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:213971; NID:944996; PID:9581412
the nucleotide sequence was submitted to the EMBL Data
Library, June 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B70946 #type complete
probable nuoL protein - Mycobacterium tuberculosis (strain
                                                                        ##residues 1-496 ##label KOH
##cross-references GB:D26186; NID:9529072; PID:d1005873; PID:9529073
                                                                                                                                              *superfamily unassigned Ser/Thr or Tyr-specific protein
kinases; protein kinase homology; SH3 homology
ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Streptomyces lactamdurans
13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *superfamily beta-lactamase I
antibiotic resistance; hydrolase; penicillin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #active_site Ser #status predicted
#length 302 #molecular-weight 32084 #checksum 8442
                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain protein Kinase homology #label KIN\
#equion protein kinase ATP-binding motif
rth 496 #molecular-weight 55593 #checksum 301
                                                                                                                                                                                                                                                                                                                                                                                                    1 MEPFLRKRLTFLSFFWDKIWPAD-ESEEDIPRIQGHDDNPVPEQAAAVEPCS-FP 53
                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a transmembrane protein are clustered with the biosynthetic genes in Nocardia lactamdurans.
                                                                                                                                                                                                                                                                                                            Score 231; DB 2; Length 496; Pred. No. 4.08e-26; 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S36188 #type complete
beta-lactamase (EC 3.5.2.6) I precursor
lactamdurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.28e-01;
9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 90; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 WARARPAAPEPAPPTPSAAAPSVAPGPAATPPDP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 WDKIWPAGGEPDHGIPGSLDPNTDPVPIL-PAEP 48
targeted disruption.
A56040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-302 ##label COQ
                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                            53.8%;
ilarity 58.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 21.0%;
Best Local Similarity 35.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S36188; S22750
S36188
                                                                                                                                                                                                                                                                           #length 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type.DNA
##residues 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H37RV)
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bla
GTG
                                                                                                                                #map_position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #Start_codon
CLASSIFICATION
KEYWORDS
FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
                         #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
#authors
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m
                                                                                                                                                                                                                                      232-491
240-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
                                                                                                                                                                                                                       62-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-302
                                                                                                               GENETICS
                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry II. C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felrwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Horrsby, T.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Murphy, L.; Oliver, S.; Gsborne, J.; Quall, M.A.; Sagares, R.; Sulston, J.E.; Skelton, S.; Squares, S.; Squares, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Taylor, K.; Whitehead, S.; Barrell, B.G. Deciphering the Diology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##INOJECULE_LYPE L....
##residues 1-633 ##label COL
##cross-references GB:AL021646; GB:AL123456; NID:g3242278; PID:e1300744;
##cross-references PID:g3242279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:D90900; GB:AB001339; NID:g1651768; PID:d1017529; PID:g1651869 ##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574644 #type complete
regulatory component slr1783 - Synechocystis sp. (strain PCC
6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimpo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
Ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; #journal DNA Res. (1996) 3:100-136
Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803: II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain response regulator homology #label RRH\
#binding_site phosphate (Asp) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 633 #molecular-weight 66167 #checksum 6554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87; DB 2; Length 633;
Pred. No. 3.38e-01;
11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library, June 1996
*superfamily response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein s1r1783 #formal_name Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AFYMTRVMLMTFFGEKRWTPGAHP-HEAPAVM 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | : :::|| : | | :|: | | :|: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
##molecule_type DNA
1-282 ##label KAN
1-282 ##label KAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.3%;
Best Local Similarity 31.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCC 6803
B70946
A70500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S74322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B70946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S74644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S74644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuol
```

```
##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
REFERENCE
#authors
#journal
                                                                                                       ω
                                                                                                                                                                                                                                                REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                                                ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title
                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE
                    g
                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                     #authors Fukumori, F.; Sashihara, N.; Kudo, T.; Horikoshi, K.
#journal J. Bacteriol. (1986) 168:479-485
#title Nucleotide sequences of two cellulase genes from alkalophilic
Bacillus sp. strain N-4 and their strong homology.
#cross-references MID:87056924
#accession A25156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydrolysis of 1,4-beta-D-glucosidic linkages in
beta-D-glucans such as cellulose and lichenin; can
hydrolyze such linkages in beta-D-glucans that also contain
                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr, C.S.; Sharp, P.A.
Mol. Cell. Biol. (1990) 10:4384-4388
A helix-loop-helix protein related to the immunoglobulin box-binding proteins.
                                                                                                                                                                                                                          A25156 #type complete cellulase (EC 3.2.1.4) 1 - Bacillus sp. endo-1.4-beta-glucanase #formal_name Bacillus sp. 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A35658 #type fragment transcription factor TFEB - human (fragment) transcription factor TFEB - human (fragment) #formal_name Homo sapiens #common_name man 28-5ep-1990 #sequence_revision 28-Sep-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-488 ##label FUK
##cross-references GB:M14781; GB:X53449; NID:g142659; PID:g142660
##experimental_source strain N-4, plasmid pNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulose degradation
glycosidase; hydrolase; polysaccharide degradation
#length 488 #molecular-weight 54264 #checksum 2043
              #length 282 #molecular-Weight 31395 #checksum 7299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                               19.8%; Score 85; DB 2; Length 282;
larity 37.5%; Pred. No. 6.39e-01;
Conservative 9; Mismatches 17; Indels
                                                                                                                                        FLIRRLAFLSFF-WDKIWPAGGEPDHGTPGSLDPNTDPVPTLPAEPC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 514;
                                                                                                                    4 SLLRPRLVFLEFIPRDRL-MGGGISQSGNLLR-SPPTKP-PYLPLHDC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues__1-514 ##label CAR
##cross-references GB.M33782
DS MDNA binding: transcription regulation
:X #length 514 #checksum 4667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 2; Le
Pred. No. 2.22e+00;
7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB 2; I Pred. No. 1.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSEPEPDPGEPDPGEPDPGEPDPTPPSDP-GEYP 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.3%;
Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.9%;
Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,3-linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A35658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A35658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #cross-references
                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #description
                                                                                                                                                                                                                                                             ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors
                                                                                                                                                                                                                                                                                                                                      ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARY
                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATE
                                                                                                                    a
                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, Lumm, W.; Pothier, B.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.; Safer, H.; Pathell, D.; Prabhakar, S.; McDougall, S.; Safer, G.; Goyal, A.; Pietrokovski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The primary structure and genetic organization of the bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:92621587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WZWLEB #type complete
E2 protein - bovine papillomavirus type 1
#formal_name bovine papillomavirus type 1
17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                          #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily papillomavirus E2 protein
#superfamily papillomavirus E2 protein
DNA binding; early protein; transcription regulation
#length 306 #molecular-weight 34307 #checksum 1656
                                                                                                                                      G69167 *type complete cobalamin biosynthesis protein N - Methanobacterium thermoautotrophicum (strain Delta H) *formal_mame Methanobacterium thermoautotrophicum 05-Dec-1997 *sequence_revision 05-Dec-1997 *sequence_revision 05-Dec-1997 *sequence_revision 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, Nature (1982) 299:529-534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 1045 #molecular-weight 116537 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GB:AE000835; GB:AE000666; NID:g2621586;
##experimental_source strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB 1; L6
Pred. No. 4.08e+00;
15; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.02e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Reeve, J.N.
J. Bacteriol. (1997) 179:7135-7155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 NPYLPPHHQYLAFYRWIDEVLGADAMVHLGTHGTLE 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
460 GAEVPDPEPLPALPPQA-PLP-LPTQPPSPFHHL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     papillomavirus type 1 genome.
#cross-references MUID:83012974
                               1-1045 ##label MTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references MUID:98037514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%;
.larity 30.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.4%;
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                               05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                          G69167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G69167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A93289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A03672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
CLASSIFICATION #
KEYWORDS D
SUMMARY #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
```

?

'n

```
939 EKVIPPAGQPEEAKP-ILEPDKEETTTEPTDS 969
                                                            :|: |::|::|::| | |:|::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E64522
A64520
                                                                                                                                                                                                                                                                                                                                                                                                                                             S74847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S74847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E64522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##note
                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal
                                                                                                                                                                                                                                                                                                                                                         #variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTRY
                                                                                                                                                                                                                                                                                                                                                                                       DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-325 ##label MAN
##cross-references EMBL:249570; NID:g1015750; PID:g1015751; MIPS:YJR070c
NCE S71676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucose regulated-protein, 470K---Chinese hamster....
#formal_name Cricetulus griseus #common_name Chinese hamster
15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:U34206; NID:g1000295; PID:g1000296
##note the nucleotide sequence was submitted to the EMBL Data
Library, August 1995
:X #length 999 #mo.lecular-weight 111270 #checksum 7243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frames and a gene cluster with a counterpart on chromosome XI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, X.; Baston, D.; Oh, H.J.; Lee-Yoon, D.S.; Liu, X.; Subjeck, J. FESS Lett. (1996) 380:68-72
The 170 kpa glucose regulated stress protein is a large HSP70-, HSP110-like protein of the endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manus, V.; Huang, M.E.; Galibert, F. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                      hypothetical protein J1814
#formal_name Saccharomyces cerevisiae
(8-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #checksum 3014
                                                                                                                                                                                        S57089 #type complete
hypothetical protein YJR070c - yeast (Saccharomyces
cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:L47993; NID:q1019675; PID:q1019692
##note the nucleotide sequence was submitted to the
Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F. Yeast (1996) 12:869-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.4%; Score 79; DB 2; Length 325; Best Local Similarity 36.6%; Pred. No. 4.08e+00; Matches 15; Conservative 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 2; Length 999;
Pred. No. 4.08e+00;
13; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 NRINWTHGGAKDKENLQQSLYSSIDPAPPLPLEKDATIPEL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #map_position 10R
#mapy = #length 325 #molecular-weight 36164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 DGVWVASEGPE-GDPAGKEAEPAQPVSSLLGSPACGPI.246
                                 #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-999 ##label CHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-325 ##label HUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%;
ilarity 28.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      S57089; S71692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        868689
                                                                                                                                                                                                                                                                                                                                                                                                                                                    S57085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    871692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          868689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues
                                                                                                                                                                                                                                                                                      ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal
                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
g
                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
##residues 1-365 ##label KAN
##cross-references EMBL:D90909; GB:AB001339; NID:g1652844; PID:d1018541;
PID:g1652890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Relley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
S74847 #type complete
hypothetical protein sll0843 - Synechocystis sp. (strain PCC
6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Sinmpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.; Yasuda, M.; Tabata, S.; Yasuda, M.; Tabata, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Yasuda, M.; Tabata, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, Tabata, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Takeuchi, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, S.; Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimpo, Shimp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E64522 #type complete
hypothetical protein HP0021 - Helicobacter pylori (strain
26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
                                                                                                                                                                                                                                                                                                                          25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the nucleotide sequence was submitted to the EMBL
Library, June 1996
#length 365 #molecular-weight 41493 #checksum 9379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the gastric pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.2%; Score 78; DB 2; Length 365; Best Local Similarity 40.0%; Pred. No. 5.52e+00; Matches 8; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title The complete genome sequence of
    Helicobacter pylori.
#cross-references MUID:97394467
                                                                                                                                                                                                                 #formai_name Synechocystis sp
PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.M.; Venter, J.C.
Nature (1997) 388:539-547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PFLRRRLAFLSFFWDKIWPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AFFOKCLSFLGFIWLLSWEA 23
```

```
#superfamily hypothetical protein s111022
#length 257 #molecular-weight 29167 #checksum 3438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: Th
Job time : 112 secs.
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-43,59-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aubost, E.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Boltolin, A.; Brachert, S.; Borisser, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.T.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Demison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Edyita, Y.; Femarson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Edyita, Y.; Femarson, P.T.; Entian, K.D.; Errington, J.; Guisepi, G.; Guy, B.J.; Haga, K.; Hatech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kurita, K.; Lapidus, M.; Jones, L.; Joris, B.; Karamata, D.; Kurita, K.; Lapidus, C.; Medine, N.; Luwber, J.; Masuda, S.; Maueel, C.; Medigue, C.; Medine, N.; Lauber, J.; Parro, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Median, N.; Mosetl, D.; Nedigue, C.; Median, N.; Mone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Doudega, B.; Razpoport, G.; Rey, M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Takemaru, K.; Vasaarotti, A.; Wanamoto, H.; Vanamoto, H.; Vanamoto, H.; Vanamoto, H.; Vanamoto, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H69756  #type complete
tellurium resistance protein homolog yceF - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997  #text_change
24-Sep-1998
                                                                                ##cross-references GB:AE000524; GB:AE000511; NID:g2313090; PID:g2313099;
TIGR:HP0021
                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residues 1-257 ##label KUN
##cross-references GB:299105, GB:AL009126; NID:g2632457; PID:e1182244;
##cross-references PID:g2632578
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                         #molecular-weight 21183 #checksum 5365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                               Score 77; DB 2; Length 190;
Pred. No. 7.43e+00;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation not shown
translation not shown
                                                     1-190 ##label TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #cross-references MUID:98044033
                                                                                                                                                                                                     17.9%;
50.0%;
                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                            #length 190
                                                                                                                                                                                                                                                                                                                    134 AFLMRRYSFKKYFW 147
                                                                                                                                                                                                                                                                                                                                                        3 PFLRRRLAFLSFFW 16
                             ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE
                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Wechsler, S.L.; Nesburn, A.B.; Zwaagstra, J.; Ghiasi, H.
Virology (1989) 168:168-172
Sequence of the latency-related gene of herpes simplex virus
                                                                    4
                                                                                                                                                                                                                          WMBEL1 #type complete
latency-related protein 1 - human herpesvirus 1 (strain F)
#formal_name human herpesvirus 1
host Homo sapiens (man)
31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #region tandem repeats
#length 340 #molecular-weight 35604 #checksum 44:07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily herpesvirus latency-related protein 1 tandem repeat
Score 77; DB 2; Length 22/;
Pred. No. 7.43e+00;
"...matches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 77; DB 1; Length 340;
Pred. No. 7.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-340 ##label WEC
##cross-references GB:J04323; NID:g330133; PID:g330134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LWLTPEPAQHGTPTHPHSHA-PPLPRTPTPSHPH 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation not shown
                                                                                                              1 MD-FLHHILSTYASFFDW-KMW 20
                                                                                                                                        |: ||:: |: : ||| |:|
1 MEPFLRRRLA-FLSFF-WDKIW 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #cross-references MUID:89085598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
Local Similarity 30.6%;
hes 11; Conservative
                Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type
                                                                                                                                                                                                                                                                                                                                                                                                                 A94388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A33337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249/2
```

completed: Thu May 20 12:35:50 1999

*****	(TM)

******	''

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:36:09 1999; MasPar time 4.00 Seconds 388.629 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (1-55) from US09099053.pep (2 of 6) 429

1 MEPFLRRLAFLSFFWDKIW......PNTDPVPTLPAEPCSPFPQL 55 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 36.911; Variance 63.964; scale 0.577

SUMMARIES

		æ			CHTANTION			
Result No.	Score	Query Match	Length	DB	QI	Description	Pred. No.	
-	231	53.8	496	-	SRM_MOUSE	TYROSINE-PROTEIN KINAS	2.66e-29	
7	06	21.0	302	Н	BLAC_NOCLA	BETA-LACTAMASE PRECURS	3.87e-02	
m	83	19.3	488	Н	GUN1_BACS4	ENDOGLUCANASE A (EC 3.	4.46e-01	
4	81	18.9	514	Н	TFEB HUMAN	TFEB PROTEIN (FRAGMENT	8.77e-01	
S	79	18.4	325	Н	YJ40_YEAST		1.70e+00	
9	79	18.4	410	Н	VE2_BPV1	REGULATORY PROTEIN E2.	1.70e+00	
7	78	18.2	324	Н	FKH5_MOUSE	TRANSCRIPTION FACTOR F	2.36e+00	
ω	77	17.9	340	Н	LRP1_HSV1F	LATENCY-RELATED PROTEI	3.27e+00	
σ	16	17.7	467	Н	D4DR_HUMAN	D(4) DOPAMINE RECEPTOR	4.51e+00	
10	16		1197	Н	Y4CA_RHISN	HYPOTHETICAL 133.7 KD	4.51e+00	
11	75	•	283	Н	TONB_NEIGO	TONB PROTEIN.	6.20e+00	
12	75	17.5	325	Н	CA19_RAT	COLLAGEN ALPHA 1(IX) C	6.20e+00	
13	75	17.5	385	Н	MKK2_MOUSE	MAP KINASE-ACTIVATED P	6.20e+00	
14	75	17.5	489	-	BGAL_SULSO	BETA-GALACTOSIDASE (EC	6.20e+00	
15	7.5	17.5	489	П	BGAL_SULSH	BETA-GALACTOSIDASE (EC	6.20e+00	
16	75	17.5	629	Н	HAP1_RAT	HUNTINGTIN ASSOCIATED	6.20e+00	
17	75	•	986	Н	GNF1_DROME	GERMLINE TRANSCRIPTION	6.20e+00	
18	74	17.2	278	-	TONB_NEIME	TONB PROTEIN.	8.50e+00	
19	74	17.2	543	Н	VP61_NPVAC	61 KD PROTEIN.	8.50e+00	
20	74	17.2	700	Н	NUOL_RHOCA	NADH DEHYDROGENASE I C	8.50e+00	
21	74		718	Н	ATI2_HSV11	ALPHA TRANS-INDUCING F	8.50e+00	
22	74	-	1733	-	VNUA_PRVKA	PROBABLE NUCLEAR ANTIG	8.50e+00	
23	74	17.2	2124	Н	PGCA_RAT	AGGRECAN CORE PROTEIN	8.50e+00	

1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	2.14e+01	2.14e+01	2.14e+01	2.14e+01	2.14e÷01	2.14e+01	2.14e+01	2.14e+01	2.14e+01
ER LUMEN PROTEIN RETAI	HOMEOBOX PROTEIN LIM-2	CALCIUM/CALMODULIN-DEP	CALCIUM/CALMODULIN-DEP	X-LINKED PEST-CONTAINI	HYPOTHETICAL PROTEIN K	ALDOSE REDUCTASE (EC 1	CUTICLE COLLAGEN 14.	3-KETOACYL-COA THIOLAS	ER81 PROTEIN (ETS TRAN	BETA-GALACTOSIDASE (EC	SON OF SEVENLESS PROTE	AGGRECAN CORE PROTEIN	HYPOTHETICAL 26.9 KD P	TRANSCRIPTIONAL ENHANC	CELL DIVISION PROTEIN	PUTATIVE THIOSULFATE S	CAMP-DEPENDENT PROTEIN	POLY (3-HYDROXYALKANOAT	HYPHAL WALL PROTEIN 1	CHROMOSOMAL REPLICATIO	FIBRIL-FORMING COLLAGE
ERD2_YEAST	LIM2_MOUSE	KCCA_RAT	KCCA_MOUSE	XPCT_HUMAN	Y250_HUMAN	ALDR_PIG	CC14_CAEEL	THIK_RAT	ETV1_MOUSE	BGAL_SULAC	SOS_DROME	PGCA_MOUSE	YXP2_XANCP	TEF4_HUMAN	FTSZ_STRCO	YNJE_ECOLI	KAPR_USTMA	PHAC_METEX	HWP1_CANAL	DNAA_STRCO	CAFF_RIFPA
Ц	Н	Н	٦	-	-	Н	н	Н	Н	Н	Н	Н	Н	ч	Н	Н	-	Н	ч	Ч	П
219	402	478	478	613	802	315	326	424	477	491	1595	2132	257	336	399	435	522	605	634	929	1027
17.0	17.0	17.0	17.0	17.0	17.0	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6
73	73	73	73	73	73	72	72	72	72	72	72	72	71	71	71	7.1	71	7.1	71	71	71
24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
TFEB_HUMAN
P19484;
                                                                                                                                                                                                                                                                                                                              RESULT 3
ID GUN1_BACS4
AC P06566;
  BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS.
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
ID TE
AC P1
DT 01
DT 15
DD TE
OC EU
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
CO ER
                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93178438.
COQUE J.R., LIRAS P., MARTIN J.F.;
Genes for a beta-lactamase, a penicillin-binding protein and a transmembrane protein are clustered with the cephamycin biosynthetic genes in Nocardia lactamdurans.";
EMBO J. 12:631-639(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEPFLRKRLTFLSFFWDKIWPAD-ESEEDIPRIQGHDDNPVPEQAAAVEPCS-FP 53
                                                                                                                                                                                                                      TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: ACTIVE ON PENICILLINS BUT NOT ON CEPHALOSPORINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA-AMINO ACID.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).

BY SIMILARITY

BY SIMILARITY

PHOSPHOYZATION (AUTO-) (BY SI

R -> G (IN REF. 2).

LRK -> FGR (IN REF. 2).

N -> I (IN REF. 2).

N -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 231; DB 1; Length 496
Pred. No. 2.66e-29;
7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-CT-1994 (REL. 30, LAST ANNOTATION UPDATE)
BETA-LACTAMASE PRECURSOR (EC 3.5.2.6) (PENICILLINASE).
                                                                                                                                                                                                                                                                                            SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA-LACTAMASE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE; ANTIBIOTIC RESISTANCE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00146; BETA_LACTAMASE_A; 1. PFAM; PF00144; beta-lactamase; 1. HSSP; P00808; 1MBL.
  PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MM;
                      PROSITE; PS50011; PROTEIN_KI
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000618; SH3; 1.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                  PHOSPHORYLATION
                                                                                                                                                                                                                                                                      116
495
495
248
262
384
384
78
278
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.8%;
Best Local Similarity 58.2%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 213971; G581412; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOCARDIA LACTAMDURANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
236
278
496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=LC411
                                                                                                                                                                                                                                               SH3 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLAC_NOCLA
                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
MOD_RES
CONFLICT
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                        DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DONA REFERENCE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ñ
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKAGES IN CELLULOSE.
                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
ENDOGLUCANASE A (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 87056924.
FUKUWORI F., SASHIHARA N., KUDO T., HORIKOSHI K.;
FUKUWORI F., SASHIHARA N., KUDO T., HORIKOSHI K.;
Nucleotide sequences of two cellulases genes from alkalophilic
Bacillus sp. strain N-4 and their strong homology.";
J. BACTERIOL. 168:479-485(1986).
-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACILLUS SP. (STRAIN N-4).
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTON DONOR (BY SIMILARITY). NUCLEOPHILE (BY SIMILARITY).
                                                                   Length 302;
                                                                                                                9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
SUBSTRATE (BY SIMILARITY). 3AF376AC CRC32;
                                                                   90; DB 1; I
No. 3.87e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1C14BCFB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (REL. 17, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83; DB 1;
Pred. No. 4.46e-
9; Mismatches
                                                                                                                                                                                                                                                                                             488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 PSEPEPDPGEPDPGEPDPGEPDPTPPSDP-GEYP 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 AA
                                                                                                                                                          10 WARARPAAPEPAPPTPSAAAPSVAPGPAATPPDP 43
                                                                                                                                                                                         | : :||: || ||::|
16 WDKIWPAGGEPDHGTPGSLDPNTDPVPTL-PAEP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54264 MW;
249 S
32084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 19.3%;
Local Similarity 38.2%;
es 13; Conservative
                                                                   21.0%;
                                                                                                                12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M14781; G142660; -.
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFEB PROTEIN (FRAGMENT).
HOMO SAPIENS (HUMAN).
247 3
302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 AA;
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLONE PNK1).
```

```
CT 6
VE2_BPV1
P03122;
                                                                                               SEQUENCE
                                                                                                                     Query Match
                                                                                                                                          Matches
                                                                                                                                                                                                                    RESULT
  g
                                                                                                                                                                                    ò
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                        box-binding proteins.";
MOL. CELL, BIOL. 10:4344-4388(1990).
-!- CELL, BIOL. 10:4344-4388(1990).
-!- SIMILARITY: THIS PUTATIVE TRANSCRIPTION FACTOR BINDS TO THE USF/MLTF SITE AND PROBABLY RECOGNIZES E-BOX SEQUENCES IN THE HEAVY-CHAIN IMMUNOGLOBULIN ENHANCER.
-!- SUBJUBLIARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
LEUCINE-ZIPPER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                             STRONG TRANSCRIPTION ACTIVATION DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUANG M.E., MANUS V., CHUAT J.-C., GALIBERT F.; "Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frames and a gene cluster with a counterpart on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 36.2 KD PROTEIN IN HAMI-PEM2 INTERGENIC REGION.
                                ы
                     CARR C.S., SHARP P.A.; "A helix loop-helix protein related to the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB 1; Length 514; Pred. No. 8.77e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                              DNA-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                   GLY/ALA-RICH.
GLN-RICH.
POLY-GLN.
TO TFE3 (AA 40-127).
                                                                                                                                                                                                                                                                                                                                                                                                                             56687 MW; D3003AE1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAEVPDPEPLPALPPQA-PLP-LPTQPPSPFHHL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A35658; A35658.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33, CREATED)
33, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.9%;
Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                   IRANSFAC; T00812; -.
IRANSCRIPTION REGULATION;
                                                                                                                                                                                                                             EMBL; M33782; G553790; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEAST 12:869-875(1996).
                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                   320
262
                                                                                                                                                                                                                                                            PFAM; PF00010; HLH; 1.
HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                                                                                                                                                                 514
514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A. MEDLINE; 90318407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288C;
MEDLINE; 96437976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KJR070C OR J1814
                                                                                                                                                                                                                                                                                                                             106
131
240
253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YJ40_YEAST
P47120;
                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
                                                                                                                                                                                                                                                                                                                                        DOMAIN
SIMILAR
                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCBRIDE A.A., BOLEN J.B., HOWLEY P.M.;
"Phosphorylation sites of the E2 transcriptional regulatory proteins of bovine papillomavirus type 1.";
J. VIROL. 63:5076-5085(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVINE PAPILLOMAVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES; NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 93024918.

HEGDE R.S., GROSSMAN S.R., LAIMINS L.A., SIGLER P.B.;

"Crystal structure at 1.7 A of the bovine papillomavirus-1 E2 DNA-binding domain bound to its DNA target.";

NATURE 359:505-512(1992).

-I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USTAV M., STENLUNG A.; "Translent replication of BPV-1 requires two viral polypeptides encoded by the E1 and E2 open reading frames."; EMBO J. 10:449-457(1991).
                                                                                                                                                                                                                                                                                                                                                                                                               5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEN E.Y., HOWLEY P.M., LEVINSON A.D., SEEBURG P.H.;
"The primary structure and genetic organization of the bovine papillomavirus type 1 genome.";
NATURE 299:529-534(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR.
SUBUNIT: BINDS DNA AS A DIMER.
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 280.
                                                                                                                                                                                                                                                                                                                                               Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 NRINWTHGGAKDKENLQQSLYSSIDPAPPLPLEKDATIPEL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 DKI-WPAGGEPDHGT-PGSLDPNTDPVPTLPAEPCSPFPQL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 326-410.
                                                                                                                                                                                                                                                                                                                                               Score 79; DB 1; L
Pred. No. 1.70e+00;
                                                                                                                                                                                                                                                                                      325 AA; 36164 MW; 3AB9A9A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 36, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                                                                                                                                                               18.4%;
larity 36.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REQUIREMENT FOR REPLICATION. MEDLINE; 91122053.
                                                                                                                                                                                   EMBL; 249570; G1015751; -. EMBL; L47993; G1019692; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATORY PROTEIN E2.
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION. MEDLINE; 90064770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 83012974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPLICATION.
```

```
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                             RESULT
   셤
                                                                                                                                                                                        δy
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93361500.
KAESTNER K.H., LEE K.H., SCHLOENDORFF J., HIEMISCH H., MONAGHAN A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZARET K.S.;
"The formation and maintenance of the definitive endoderm lineage in the mouse: involvement of HNF3/forkhead proteins.";
-i. SUBCELLUIAN LOCATION: NUCLEAR.
-i. SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94139570.

ANG S.-L., WIERDA A., WONG D., STEVENS K.A., CASCIO S., ROSSANT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Six members of the mouse forkhead gene family are developmentally regulated.";
                                                                                                                                                   TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN
                                                                                                                                      EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                  Score 79; DB 1; Length 410;
Pred. No. 1.70e+00;
15; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. KAESTNER K.H., SCHUETZ G., MONAGHAN A.P.; SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROC. NATL. ACAD. SCI. U.S.A. 90:7628-7631(1993)
                                                                                                                                                                                                                                                    DGVWVASEGPE-GDPAGKEAEPAQPVSSLLGSPACGPI 246
                                                                                                                                                                                                                                                                 45449 MW; F1D75660 CRC32;
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR FKH-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-68 FROM N.A.
                                                                                                                                                                                                                                                                                                                           324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                          EMBL; X02346; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:103153; MF3.
ITE; PS00657; FORK_HEAD_1; 1.
                                                                                                                                                               PHOSPHORYLATION; 3D-STRUCTURE.
                                                                                                                                                                                                 Query Match
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 4-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X92592; E208624; -. EMBL; X71943; G311745; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G433397; -.
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                     PIR; A03672; W2WLEB.
PDB; 2BOP; 31-JAN-94.
PFAM; PF00508; E2_N; 1.
TRANSFAC; T00205; -.
                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE)
                                                                                                                                                                           410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             004198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHUETZ G.;
                                                                                                                                                                                                                                                                                                                                                                                                    FKH5 OR MF3
                                                                                                                                                                                                                                                                                                                          FKH5_MOUSE
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                             RESULT
 엄
                                                                                                                                                                                                                                                                           ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WECHSLER S.L., NESBURN A.B., ZWAAGSTRA J., GHIASI H.; "Sequence of the latency-related gene of herpes simplex virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOIA; METAZOA; CHORDAIA; VERTEBRAIA; MAMMALIA; EUTHERIA;
FILMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                    HNLSFN -> PLTVRH (IN REF. 3)
30FACE24 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 17.9%; Score 77; DB 1; Length 340; Local Similarity 30.6%; Pred. No. 3.27e+00; les 11; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                     DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LATENOY-RELATED PROTEIN 1.
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; SIMPLEXVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 1; L
Pred. No. 2.36e+00;
9; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 X 17 AA REPEATS.
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7BB73CB3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LWLTPEPAQHGTPTPTHPHSHA-PPLPRTPTPSHPH 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | | | | : | | | | 11 | | 12 | | 13 | | 14 | | 15 | | 14 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | | 15 | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 AAGQTLPAIPVPIKPTPAAVPALPALP-APIPTL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AGGEPDHGTPGSLDPNTDPVPTLPAEPCSPFPQL 55
                                                                                                                                                                                                                                                   FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
PROSITE; PS00658; FORK_HEAD_2; 1. PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 75 2 2 3 43 1. 59 75 59 340 AA; 35604 MW;
                                                                                                                                                                                                                                                                                    68 H
34937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (REL. 18, CREATED)
01-FEB-1996 (REL. 33, LAST SEQI
15-JUL-1998 (REL. 36, LAST ANN
                                                                                               PFAM; PF00250; Fork_head; 1.
TRANSFAC; T02443; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIROLOGY 168:168-172(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04323; G330134; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A33337; WMBEL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 89085598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D4DR_HUMAN
P21917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRP1_HSV1F
P17588;
                                                                                                                                                                                                                                         DNA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

```
LT 11
TONB_NEIGO
006432;
                                                                                                                                                                                     VARIANT
VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                               REPEAT
CARBOHYD
                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ID TO
AC 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
a
   g
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ţ
                                                                                                                                                                                                                                                                                                                                                                                                                 WARIANT GLY-194.
MEDLINE; 95243275.
SEEMAN P., ULPIAN C., CHOUINARD G., VAN TOL H.H.M., DWOSH H.,
LEBBERMAN P., ULPIAN C., CHOUINARD G., VAN TOL H.H.M., DWOSH H.,
HUDSON C., SERJEANT G.R., MASIBAY A.S., SEEMAN M.V.;
"Dopamine D4 receptor variant, D4-glycine-194, in Africans, but not caucasians: no association with schizophrenia.";
AM. J. MED. GENET. 54.384.390(1994).
--i- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS NOT MEDIATED BY G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLELE D4.7.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                     VAN TOL H.H., WU C.M., GUAN H.C., OHARA K., BUNZOW J.R., CYDELLI O., KENNEDY J., SEEMAN P., NIZNIK H.B., JOVANOVIC V.; "Multiple dopamine D4 receptor variants in the human population."; NATURE 358:149-152(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 X 16 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROFEINS WHICH INTERACT WITH ADENYLYL CYCLASE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES. THE SEQUENCE SHOWN IS THAT OF
                                                                                                                                                                 MEDLINE; 91204054.

VAN TOL H.H.M., BUNZOW J.R., GUAN H.-C., SUNAHARA R.K., SEEMAN F. NIZNIK H.B., CIVELLI O.;

"Cloning of the gene for a human dopamine D4 receptor with high affinity for the antipsychotic clozapine.";

NATURE 350:610-614(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L12397; -; NOT_ANNOTATED_CDS.

PIR; S15079; DYHUD4.

GCRDB; GCR_0064; -.

GCRDB; GCR_011; -.

MIM; 126452; -.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1..

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLXCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULTIGENE FAMILY; POLYMORPHISM; REPEAT.

DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       LIVINGSTONE C.D., STRANGE P.G., NAYLOR L.H.; "Molecular modelling of D2-like dopamine receptors."; BIOCHEM. J. 287:277-282(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEQUENCE FROM N.A. (ALLELE D4.7). MEDLINE; 92310588.
                                                                                                                                  SEQUENCE FROM N.A. (ALLELE D4.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L12398; G291946; -.
                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93038566.
                                                                                                                                                    TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
   RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR RARAR
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAX R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHIZOBIUM SP. (STRAIN NGR234).
PLASMID SYM PNOR8234A.
BACTERIA, PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERRET X.; "Molecular basis of symbiosis between Rhizobium and legumes."; MATURE 387:394-401(1997). -- SIMILARITY: NONE OBVIOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                          POTENTIAL.

V -> G (IN AFRO-CARRIBEANS).
MISSING (IN ALLELE D4.2).
MISSING (IN ALLELE D4.4).
P -> A (IN ALLELE D4.4).
G -> S (IN ALLELE D4.4).
G -> S (IN ALLELE D4.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 1; Length 1197;
Pred. No. 4.51e+00;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                     Score 76; DB 1; Length 467;
Pred. No. 4.51e+00;
                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA.
IW; 2428461F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
10-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 133.7 KD PROTEIN Y4CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 POLY
425 POLY
4133714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 QLALPANWWDRLWQAAEGEPD 873
                                                                                                                                                                                                                                                                                                                                                                                  241 PGPPSP-TPPAPRLPQDPCGP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000067; G2182325; -. HYPOTHETICAL PROTEIN; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      31 PGSLDPNTDPVPTLPAEPCSP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                       17.78;
                                                                                                                                                                                                                                                                                                                         Local Similarity 52.4%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 25
419 42
1197 AA;
                                                                                                                              108
194
194
265
281
329
332
467 AA;
249
281
281
329
345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
Y4CA_RHISN
P55383;
```

```
Query Match
                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                       RESULT
         g
                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLISEN B.R.;
"Molecular cloning of rat and human type IX collagen cDNA and localization of the alpha 1(IX) gene on the human chromosome 6.";
EUR. J. BIOCHEM. 179:71-78(1989).
-! FUNCTION: COLLAGEN TYPE IX IS A MINOR CARTILAGE NONFIBRILLAR
COLLAGEN IT IS ASSOCIATED WITH TYPE II COLLAGEN FIBRILS.
-! SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(IX),
ALPHA 2(IX), AND ALPHA 3(IX).
                                                                           PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                 BISWAS G.D., ANDERSON J.E., SPARLING P.F.;
"Cloning and functional characterization of Neisseria gonorrhoeae tonb exba and exbD genes."
MACL. MICROBIOL. 24:169-179(1997).
-!- FUNCTION: PATHWAYS OF UTILIZATION OF IRON BOUND TO TRANSFERRIN, LACTOFERRIN AND HEWGLOBEN BUT NOT TO HAEMIN OR CITRATE WHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       DEPENDENT ON THE TONB SYSTEM.
SUBUNIT: THE ACCESSORY PROTEINS EXBB AND EXBD SEEM TO FORM A COMPLEX WITH TONB (BY SIMILARITY).
SUBCELLULAR LOCATION. PRIPASMIC. ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89137096.
KIMURA I., MATTEI M.-G., STEVENS J.W., GOLDRING M.B., NINOMIYA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U79563; G2098621; -.
TRANSPORT; PROTEIN TRANSPORT; INNER MEMBRANE; PERIPLASMIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              ANCHOR (POTENTIAL).
PERIPLASMIC (POTENTIAL).
964F0942 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 1; L. Pred. No. 6.20e+00;
                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AA
                                                                                                                                                                                                                                                                  PERIPLASM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAPEGAGAPAPEPQPAPDPPKPVEPPKP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AGGEPD-HGTPGSLDPNTDPVPTLPAEPCSP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
       CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28749 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%;
larity 38.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT)
       37,
37,
                                                              NEISSERIA GONORRHOEAE
15-DEC-1998 (REL. 37, 15-DEC-1998 (REL. 37, TONB PROTEIN, TONB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89137096.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                          MEDLINE; 97285757
                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                               STRAIN-FA19
                                                                           BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA19_RAT P20850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGEL K., PLANE K., GAESTEL M.;
The MAP kinase-activated protein kinase 2 contains a proline-rich
The MAP kinase-activated protein kinase 2 contains a proline-rich
SH3-binding domain.";

EEBS LETT. 336:143-147(1993).

-!- FUNCTION: ITS PHYSIOLOGICAL SUBSTRATE SEEMS TO BE THE SMALL HEAT
SHOCK PROTEIN (HSPZT/H8225). IN VITRO CAN PHOSPHORYLARES GLYCOGEN
SYNTHASE AT SER-7 AND TYROSINE HEDROXYLASE (ON SER-19 AND SER-40).

THIS KINASE PHOSPHORYLATES SER IN THE PEPTIDE SEQUENCE, HYD-X-R-
X(2)-S., WHERE HYD IS A LARGE HYDROPHOBE RESIDUE (BY SIMILARITY).

THE FIRST INVOLVES THE STIMULATION OF P42/P44 MAPK BY GROWTH
CHARLY SHALLAND OF MRY2 AND UPSTREAM MAPKK/MAPKKK.

ON THE ACTIVATION OF MRY2 AND UPSTREAM MAPKK/MAPKKK.

-!- PTW: PHOSPHORYLATED BY MAP KIRASE.

-!- PTW: PHOSPHORYLATED BY MAP KIRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
-!- DOMAIN: EACH SUBUNIT IS COMPOSED OF THREE TRIPLE-HELICAL DOMAINS INTERSPERSED WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE N-TERMINUS OF TYPE IX COLLAGEN MOLECULES REPRESENTS THE NC4 DOMAIN WHICH MAY PARTICIPATE IN ELECTROSTRIC INTERACTIONS WITH POLYANIONIC GLYCOSAMINOGLYCANS IN CARTILAGE.
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL.OF THE CHAINS.
-!- SIMILARITY: THE COLLAGEN ALPHA 1(IX) CHAIN STRUCTURE DIFFERS FROM THAT OF THE POLYAPEPTIDE CHAINS OF FIBRILLAR COLLAGENS I - III; IT PIR, S02170; S02170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MAP KINASE-ACTIVATED PROTEIN KINASE 2 (EC 2.71.-) (MAPK-ACTIVATED PROTEIN KINASE 2) (MAPKAPK-2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR MATRIX; CONNECTIVE TISSUE; REPEAT; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN; CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAMMALIA; EUTHERIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.20e+00;
2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 AA; 31256 MW; 589B277D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 PVGPEGSPGIPGKLGPLGSPGLPGLPGPP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 33, CREATED)
(REL. 33, LAST SEQ
(REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 17.5%;
Local Similarity 44.8%;
les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X76850; E211679; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:109298; RPS6KC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00069; pkir
HSSP; 063450; 1A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94085571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKK2_MOUSE
P49138;
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
```

```
489 AA; 56757 MW; 6B8E9647 CRC32;
                                                                                                                                                                                                                                                LT 15
BGAL_SULSH
P50388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
SEQUENCE
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                    g
                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              .
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGUILAR C.F., SANDERSON I., MORACCI M., CIARAMELLA M., NUCCI R.,
ROSSI M., PBARL L.H.;
"Crystal structure of the beta-glycosidase from the hyperthermophilic
archeon Sulfolobus solfataricus: resilience as a key factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermostability.";
J. MOL. BIOL. 271:789-802(1997).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-33.
STRAIN-ATCC 49255 / MT4;
MEDLINE, 91033070.
CUBELLIS M.V., ROZZO C., MONTECUCCHI P., ROSSI M.;
"Isolation and sequencing of a new beta-galactosidase-encoding archaebacterial gene.";
GENE 94:89-94(1990).
                                                                                                                                                                                                                                                                                                                                                              ٠,
ش
                                                                                                                                                                                                  BY SIMILARITY.
PHOSPHORYLATION (BY MAPK) (BY
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                Score 75; DB 1; Length 385;
Pred. No. 6.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTON DONOR (POTENTIAL). NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                    POLY-PRO.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULFOLOBUS SOLFATARICUS.
ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
                                                                                                                                                                                                                                                SIMILARITY).
E3629FEA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0572; GLYCOSYL_HYDROL_F1_1; 1. PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1. PFAM; PF00232; glycosyl_hydrol; 1. PYDROLASE; GLYCOSIDASE; 3D-SIRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                              3 GSPGQTPPAPF-PSPPP-PA-PAQPPPFPQF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
STRAIN-ATCC 49255 / MT4;
MEDLINE; 97446327.
                                                                                                                                                                                                                                                                     385 AA; 43952 MW;
                                                                                                                                                                                                                                                                                                                17.5%;
40.6%;
                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M34696; G152929; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JQ0767; JQ0767.
PDB; JGOW; 20-AUG-97
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                      PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BGAL_SULSO
P22498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
                                                                                                                                                                                                     ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                    DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
                                           NON_TER
                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
  KKK
FILLETTER
FILLETTER
SO
                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNARIS H., CHARALAMBOUS B.M.;
SUBMITTED (XXX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVIT: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOGE RESIDUES IN BETA-D-GALACTOSIDES.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
06E7FBF5 CRC32;
                     Score 75; DB 1; Length 489;
Pred. No. 6.20e+00;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; DB 1; Lv
Pred. No. 6.20e+00;
                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                          489 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L47841; G1009227; -.
PROSITE: PS00572; GLYCOSYL_HYDROL_F1_1; 1.
SPOSITE: PS00653; GLYCOSYL_HYDROL_F1_2; 1.
PFAM: PF00232; 91ycosyl_hydrol; 1.
HSSP; P22498; 1GOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Thu May 20 12:36:22 1999 Job time : 13 secs.
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                          20 WPAGG-EPDHGTPGSLDPNTD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 AA; 56564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: :| ::: ||||| |||||| 20 WPAGG-EPDHGTPGSLDPNTD 39
                                                                                                                                12 WSQAGFQSEMGTPGSEDPNTD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 WSQAGFQSEMGTPGSEDPNTD 32
                          17.5%;
1larity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROLASE; GLYCOSIDASE.
Query Match
Best Local Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SULFOLOBUS SHIBATAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DSM 5389;
```

* * * * * *	(MT)	****
***************************************	. '	************************
****		*****
*****		*******
*******		*******
******		*****
******		*******
*****		******

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:36:41 1999; MasPar time 11.97 Seconds 250.805 Million cell updates/sec Tabular output not generated. Run on:

>US-09-099-053-2 (1-55) from US09099053.pep (2 of 6) 429 1 MEPELRRELAFLSFFWDKIW......PNTDPVPTLPAEPCSPFPQL 55 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

179066 seqs, 54579741 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl9
1.sp_archea 2.sp_bacteria 3.sp_fungi 4.sp_human
5.sp_invertebrate 6.sp_mammal 7.sp_mhc 8.sp_organelle
5.sp_phage 10.sp_blant 11.sp_rodent 12.sp_unclassified
13.sp_vertebrate 14.sp_virus

Mean 36.074; Variance 71.903; scale 0.502 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																_					
	Pred. No.	2.10e-01	3.96e-01	5.43e-01	5.43e-01	5.43e - 01	7.42e-01	1.01e+00	1.38e+00	1.38e+00	2.54e+00	3.44e+00	3.44e+00	3.44e+00	4.64e+00	6.24e+00	6.24e+00	6.24e+00	6.24e+00	6.24e+00	6.24e+00
	д	:	PR			Д		Ę		Д								н	H	Д	S
	Description	EYELID.	WUGSC:H_DJ0751H13.1 F		PGA67 PRECURSOR.	CELL SURFACE PROTEIN P	NUOL.	SIMILAR TO S. PURPURAT	REGULATORY COMPONENTS	CELL SURFACE PROTEIN	GAG POLYPROTEIN.	VIRION PROTEIN.	F33D11.2 PROTEIN:	V-SERA 1.	PBP2 PROTEIN.	ORF 3-1 GENE.	F15E6.2 PROTEIN.	PROLINE AND GLYCINE-R.	E6-AP UBIQUITIN-PROTE:	HYPOTHETICAL 77.1 KD	COBALAMIN BIOSYNTHESIS
	e e	061603	075851	083017	024773	Q51819	086350	020942	P72781	051820	P88150	P89478	044776	026155	054201	084959	044497	018756	015979	085969	026614
	DB	Ŋ	4	7	7	~	~	S	7	7	14	14	ហ	Ŋ	~	14	വ	'n	വ	~	Н
	Match Length DB	2715	4123	563	563	563	633	770	282	563	498	302	408	1089	969	205	429	589	655	705	1045
& Ouerv	Match	21.2	20.7	20.5	20.5	20.5	20.3	20.0	19.8	19.8	19.3	19.1	19.1	19.1	18.9	18.6	18.6	18.6	18.6	18.6	18.6
	Score	91	68	88	88	88	87	98	82	82	83	82	82	82	81	80	80	80	80	80	80
Result	NO.	1	7	m	4	S	φ	7	ω	σ	10	11	12	13	14	15	16	17	18	19	50

8.39e+00 8.39e+00 8.39e+00 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.15e+01 1.15e+01 1.20e+01 1.50e+01 2.00e+01 2.00e+01 2.00e+01	
HYPOTHETICAL 19.9 KD PALKALINE CELLULASE CEL. 170 KDA GLUCOSE REGULA WINGED-HELIX TRANSCRIP FORKHEAD/WINGED HELIX WINGED-HELIX PROTEIN. HYPOTHETICAL 11.5 KD P HYPOTHETICAL 21.2 KD P YCEF. GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR DEL GLUTAMATE RECEPTOR SUB COSMID CASCUL I ATENTI O' TOREL I ATENTI TYPE I . SIMILAR TO C18F10.5. GAG POLYPROTEIN PRECUR	· L H · H
086545 00606432 00606432 0075917 0075917 0075917 0076017 0076013 0076013	P73549 054875 061799 089242 050510 Q39086
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	110 14 11 11 11 11 11 11 11 11 11 11 11 11
186 9400 9400 3329 3329 1100 1100 1100 1100 1100 1100 1100 11	517 1702 135 478 818 843 1932
4.4.4.2.9.9.1.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	17.7 17.7 17.5 17.5 17.5 17.5
7 7 7 7 8 8 8 8 7 7 7 7 7 7 7 8 8 8 8 7 7 7 7 7 7 7 8 9 7 7 9 7 9	77 75 75 75 75
4264456486888888888888888888888888888888	W 4 4 4 4 4 0 0 11 0 12 4 12

ALIGNMENTS

<u>ښ</u>

N

```
EMBL; AB006481; D1023712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis
                                                          CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ose350
086350
086350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                               JLT 5
051819
051819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGAWA T
                     SIGNAL
                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
ON ACCOMENT
     S FT S
                                                                                                                                                                                         g
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HONGYO H., KOKEGUCHI S., MAEDA H., MIYAMOTO M., TAKASHIBA S.,
KURIHARA H., MURAYAMA Y.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                               Length 4123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).
BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).
BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 33277;
HAMADA N., UMEMOTO T.;
"POPPHYZOMONAS GINGIVALIS 67kDa fimbrillin gene.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; ABO16284; D1032915; -.
SEQUENCE 563 AA; 60786 MW; 524635A6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 LGFNWNPLVPDPDPSNPENPNNPDPNPDEPGTPVPTDPENPLPD 540
                                      SEQUENCE FROM N.A.
LEDNARD S., GRAVES T., STROWMATT C.;
ATHE SEQUENCE OF HOMO SAPIENS PAC CLONE DJ0751H13.";
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                            SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC004877; G3638957; -.
PROSITE; PS01209; LDLRA_1; 9.
                                                                                                                                                       WATERSTON R.H.;
SUBMITIED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 4; Leng
Pred. No. 3.96e-01;
                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 SEQUENCE 4123 AA; 434981 MW; 0D93C3B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.5%; Score 88; DB 2; L
larity 31.8%; Pred. No. 5.43e-01;
Conservative 12; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT :- .. 563 AA-- ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1333 PASTLPGP-SPGSLDTASSPLASASPAPPCGPF 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 PAGGEPDHGTPGSLDPNTDPVPIL-PAEPCSPF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
08,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
05,
   CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.7%;
Best Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
PGA67 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. 67KDA FIMBRILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC33277;
                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN
                                                                                                                                                                                                                            WATERSTON R.
SUBMITTED (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 4
024773
024773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   083017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1T 3
083017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGA67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., BIGIAMEIER K., GAS S., BARRY III C.E., TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY E., OLLVER S., SEEGER K., SKELTON S., SQUARES S., SQARES J., RATION S., SQUARES S., SQARES R., SULSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGAWA T., MORI H., YASUDA K., HASEGAWA M.; *Molecular cloning and characterization of the genes encoding the
                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoreactive major cell-surface proteins of Porphyromonas
                                                                                       Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 563;
                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
CELL SURFACE PROTEIN PRECURSOR.
PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).
BACTERIA; CYIOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS.
                                                                                                                                                                          540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 LGFNWNPLVPDPDPSNPENPNNPDPNPDEPGTPVPTDPENPLPD 540
                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                     POTENTIAL.
CELL SURFACE PROTEIN.
45D4ECB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 LGFNWNPLVPDPDPSNPENPNNPDPNPDEPGTPVPTDPENPLPD
                                                                                       Score 88; DB 2; L
Pred. No. 5.43e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 5.43e-01;
                        POTENTIAL.
204E6E96 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 AA
  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%; Score 88; 31.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEMS MICROBIOL, LETT, 120:23-30(1994).
EMBL, D28770; D1006510; -.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 PO
563 CE
60785 MW;
49 PC
563 PC
60811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           086
086
                                                                                     Query Match 20.5%;
Best Local Similarity 31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
  1
50
563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-381;
MEDLINE; 94333763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
```

ന

Matches

g

ò

RESULT

```
STRAIN=PCC6803;
MEDLINE: 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMI N., HIROSAWA M., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGAWA T., MORI H., YASUDA K., HASEGAWA M.; "Molecular cloning and characterization of the genes encoding the immunoreactive major cell-surface proteins of Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|| || || || |: :|:: :|| :: |
3 PFLRRLAFLSFF-WDKIWPAGGEPDHGTPGSLDPNTDPVPTLPAEPC 49
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEM. SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SLLRPRLVFLEFIPRDRL-MGGGISQSGNLLR-SPPTKP-PYLPLHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS
                                                                                                                                                                                             SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
CELL SURFACE PROTEIN PRECURSOR.
PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CELL SURFACE PROTEIN.
0036195A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 LGFNWNPLVPDPDPSNPENPNNPDPNPDEPGTPVPTDPEQPLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LSFFWDKIWPAGGEPDHGTPGSLDPNTD-PVPTLPAEPCSPFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 2; Leno
Pred. No. 1.38e+00;
11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85; DB 2; L
Pred. No. 1.38e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00072; response_reg; 1.
PFAM; PF00196; GerE; 1.
SEQUENCE 282 AA; 31395 MW; BB8E81A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gingivalis.";
FEMS MICROBIOL. LETT. 120:23-30(1994).
EMBL; D28771; D1006511; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 PC
563 CE
60786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.8%;
llarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 31.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
50
563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94333763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                         STRAIN=PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-409
                                                                                                                                                                      TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    051820
051820
051820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 10
P88150
P88150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAND DE PACE ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 2 5 E
                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J. BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FUTON L.,
GARDNER M., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAGGHAN K., WAITERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                        20.3%; Score 87; DB 2; Length 633; larity 31.3%; Pred. No. 7.42e-01; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 5; Length 770;
Pred. No. 1.01e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U41554; G1118070; --
PFAM: PF00099; zn-procease; 1.
PFAM: PF00431; CUB: 1.
SEQUENCE 770 AA; 86098 MW; 341BA274 CRC32;
                                                                                                       PARKHILL J.;
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL021646; E1300744; -.
SEQUENCE 633 AA; 66167 MW; 905899AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAVELLO T.;
SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO S. PURPURATUS SPAN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282
                                                                                                                                                                                                                                                                                                                                                                    434 AFYMTRVMLMTFFGEKRWTPGAHP-HEAPAVM 464
                                                                                                                                                                                                                                                                                                                                                                                                 :| |: ::|| :| :::| 34 PFLRRLAFLSFFWDKIWPAGGEPDHGTPGSL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 FKAKFWSNLGEPE-GVSTPLPPTTAPLPEIS 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05,
06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match
Local Similarity 38.7%;
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL.
  NATURE 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 8
P72781
P72781;
01-FEB-1997 (
                                                                                         STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O20942
Q20942;
```

DDT THE READ OF SERVING SOLUTION OF SERVING SO

Gaps

4

17; Indels

48

Length 282;

ï

Gaps

Ĥ

Indels 540

54

Length 563;

Matches

g

15

ò

RESULT

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
ID 02
AC 02
DT 01
DT 01
    g
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVERTY R., FENWICK M.;

"Comparative DNA sequence analysis of the host shutoff genes of

different strains of herpes simplex virus: type 2 strain HG52 encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 87111457.
MCGEOCH D.J., MOSS H.W., MCNAB D., FRAME M.C.;
"DNA sequence and genetic content of the HindIII 1 region in the short unique component of the harpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary
                                                                                                                    GAO F., ROBERTSON N.A.
GAO F., ROBERTSON D.L., MORRISON S.G., HUI H., CRAIG S., FULTZ P.N.,
DECKER J., GIRARD M., SHAW G.M., HAHN B.H., SHARP P.M.;
J. VIPOL. 0:0-0(0),
BEMBE, US1188; G1732475; -.
PFAM; PF00098; zf-CCHC; 2.
PFAM; PF00540; gag_p17; 1.
PFAM; PF005607; gag_p24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE, 92113549.
MCGEOCH D.J., CUNNINGHAM C., MCLNTYRE G., DOLAN A.;
"Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2.";
J. GEN. VIROL, 72:3057-3075(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92356101.

BARNETT B.C., DOLAN A., TELFORD E.A.R., DAVISON A.J., MCGEOCH D.J.;
"A novel herpes simplex virus gene (UL49A) encodes a putative
membrane protein with counterparts in other herpesviruses.";
J. GEN. VIROL. 73:2167-2171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                             Score 83; DB 14; Length 498; Pred. No. 2.54e+00;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN HERPESVIRUS 2.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; SIMPLEXVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                           HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 FLGKIWPSSKGRPGNFPQSRPEPTAPPMESLGMGEEITSFP 471
                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 AA; 55367 MW; F2C5C86B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runcated UL41 product.";
GEN. VIROL. 71:1387-1390(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comparisons.";
J. GEN. VIROL. 68:19-38(1987)
                                                                                                                                                                                                                                                                                                                                                             19.3%;
31.7%;
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 31.7%;
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90278430
                      GAG POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRION PROTEIN
                                                                                                                                                                                                                                                                                                  POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HG52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-HG52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HG52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=HG52
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 11
P89478
P89478;
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESCLT
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPERTY
PROPE
ò
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN-BRISTOL N2;

MEDLINE; 9415071B

AND VILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,

CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., SONNHAMER E., STADEN R., SHOWNKEEN R.,

AMALDON N., SMITH A., SONNHAMER E., STADEN R., SULSTON J.,

ANTERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

ANTENNA A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

elegans.";
                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
?i
                                                                                                                                                                           Length 302;
                                                                                                                                                                         Score 82; DB 14; Length 302
Pred. No. 3.44e+00;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 RRLAFLSFFWDKIWPAGGEPDHGTPGSLDPNTDPVPTLPAEPCSP 51
                                                              DOLAN A.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAMMONS I., WOHLDMANN P., MULLEN G.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATERSTON R.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF039720; G2773176; -
SEQUENCE 408 AA; 45741 MW; B022DEF4 CRC32;
                                                                                                                                                                                                                                                                   65 RAYPGTRDPHDPHGCPGSLDPHGNPAQPAGLPS-P-VPYAPL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                        40 KKFTYGAF-WFTIWEHGGNKSPDSRTEPETAITPLPPSPA-PVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 5; L
Pred. No. 3.44e+00;
                                                                                                        EMBL; Z86099; E304201; -.
SEQUENCE 302 AA; 33150 MW; 072E6A65 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                       408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06,
06,
08,
                                                                                                                                                                                19.1%;
                                                                                                                                                                                                Best Local Similarity 42.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.18;
Best Local Similarity 26.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL. (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
[5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F33D11.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 13
Q26155
Q26155;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
                                         STRAIN-HG52;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                LT 12
044776
044776;
```

US-09-099-053-2-02.rspt

. . .

```
Query Match
                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                   Search co
  SOR
                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                               STRAIN-SALVADOR I:
MEDLINE; 940408670.
MEDLINE; 940408670.
MELLINE; 940408670.
KASLOW D.C., CRAMFORD K.A., BOLEY L.J., LANDSBERG K.E., GIBSON H.L.,
KASLOW D.C., BARR P.J.;
"Identification and cloning of a locus of serine repeat antigen
Mol. BIOCHEM. PARASITOL. 78:55-65(1996).
EMBL, U51725, G1381091; -.
EMBL, 1051725, G1381091; -.
EMBL, PRO0112; Cys-protease; 1.
SEQUENCE 1089 AA: 117498 MW; 370C08BD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PORCINE RESPIRATORY CORONAVIRUS (PRCV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; NIDOVIRALES;
CORONAVIRIDAE; CORONAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence comparison of porcine respiratory coronavirus isolates reveals heterogeneity in the S, 3, and 3-1 genes."; J. VIROL. 69:3176-3184(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                      PLASMODIUM VIVAX.
EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.9%; Score 81; DB 2; Length 696;
Best Local Similarity 38.7%; Pred. No. 4.64e+00;
Matches 12; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 27064;
PEREZ-LLARENA F.J., DE LA FUENTE J.L., RODRIGUEZ-GARCIA, MARIN J.F., LIRAS P.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ001743; E1228157; -.
SEQUENCE 696 AA; 74088 MW; SA3DE77E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82; DB 5; I
Pred. No. 3.44e+00;
4; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                696 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 GPPEQGSPGSPGPQETPGPQGPPVQQGSPGPQL 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GEPDHGTPGSLDPNTDPVP-TLPAEPCSPFPQL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 PADEKPESAVPGPKEPKPEPEPEATAEPAKP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PAGGEPDHGTPGSLDPNTDPVPTLPAEPCSP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PRCV ISU-1;
MEDLINE; 95222773.
VAUGHN E.M., HALBUR P.G., PAUL P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ULT 15
084959;
084959;
01-NOV-1996 (TREMBLREL. 01, CF
01-NOV-1996 (TREMBLREL. 01, LF
01-NOV-1998 (TREMBLREL. 08, LF
08. 3-1 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL. 06,
01-JUN-1998 (TREMBLREL. 06,
01-AUG-1998 (TREMBLREL. 07,
PBP2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.5%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREPIOMYCES CLAVULIGERUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
V-SERA 1.
V-SERA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 14
054201
054201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL ON THE COLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
DR EMBL; U26213; G847842; -.
SQ SEQUENCE 205 AA; 23234 MW; 1F0F0A42 CRC32;
Query Match 18.6%; Score 80; DB 14; Length 205;
Best Local Similarity 53.8%; Pred. No. 6.24e+00;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps
```

ô

69 FLSLRFAYLAYFW 81

4 FLRRRLAFLSFFW 16

arch completed: Thu May 20 12:39:45 1999 b time: 184 secs.

*		*
******	(TM)	******
*****	' 	******
******		*****
****		*******
*******		******
***************************************		***************************************
******		******
******		*****
*		*

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Thu May 20 12:41:20 1999; MasPar time 9.94 Seconds 115.582 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

Description:

>US-09-099-053-2 (56-109) from US09099053.pep (3 of 6) 399 1 FLALYDFTARCGGELSVRG.....ARRLSGQPSAGLVPITHVAK 54 Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part16 15:part15 16:part16 17:part16 17:part18 20:part20 21:part20 12:part20 22:part20 23:part20 23:part20 23:part20 23:part20 23:part20 30:part20 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 25.973; Variance 96.013; scale 0.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARTES

					SUMMAKIES		
Result No.	Score	% Query Match	% Query Match Length DB	DB	ជ	Description	Pred. No.
П	399	100.0	488	39.	W89248	Human SAD.	5.69e-33
~	114	28.6	5 298	15	R84183	Megakaryocyte kinase	1.06e-02
m	114	28.6	5 505	14	R85929	Protein tyrosine-kina	1.06e-02
4	114	28.6	5 505	æ	R41941	pTK gene LpTK-2 prod.	1.06e-02
ស	113	28.3	3 536	æ	R39706	Human pp60 c-src prot	1.32e-02
Q	111	27.8	9 60	22	W07876	Residues 81-140 of ch	2.04e-02
7	111	27.8	3 533	œ	R39705	Chicken pp60 c-src pr	2.04e-02
ထ	109	27.3		22	W13506	Human signal mediator	3.16e-02
6	94	23.6	5 1146		R15156	Abelson Related Gene,	7.77e-01
10	94	23.6		ო	R15157	Abelson Related Gene,	7.77e-01
11	93	23.3		25	W34228	SH3 domain B of mouse	9.57e-01
12	93	23.3	3 182	25	W05402	Human clone 53 protei	9.57e-01
13	93	23.3			W05393	Mouse SH3P12 protein.	9.57e-01
14	91	22.8	3 126	39	W73554	Lymphoid cell protein	1.45e+00
15	90	22.6	5 48	σ	R47126	Vector pHF2prNeoDT ju	1.79e+00
16	06	22.6	5 635	33	W48898	Candida albicans Cabe	1.79e+00

3.3.31e+00 6.10e+00 6.10e+00 6.10e+00 6.10e+00 7.46e+00 1.12e+00 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.12e+01 1.13e+01 1.36e+01 1
Human secreted protein wouse CRKL protein. Beta-1-4-galactosyltr Mouse eps8. Murine tyrosine phosp ITK tyrosine kinase. Human GRB-2. Growth factor recepto Human GRB-2. Growth factor recepto Amino acid sequence o EPH-11ke receptor promoved for the complexity of
M69429 M742071 M742071 M742071 M742071 M74595 M74595 M742070 M742070 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691 M759691
107 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
318 303 303 303 420 415 620 217 217 217 217 621 621 621 621 621 621 621 621 621 621
333328811111111111111111111111111111111
88 88 88 88 88 88 88 88 88 88 88 88 88
11112222222222222222222222222222222222

ALIGNMENTS

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzhelmer's disease; parkinson's disease; particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the 05-NOV-1998.
27-APR-1998; U08439.
28-APR-1997; US-044428.
20-MAY-1997; US-044428.
20-MAY-1997; US-049477.
31-JUN-1997; US-049477.
31-JUN-1997; US-049976.
31-JUN-1997; US-049976.
31-JUN-1997; US-049974.
31-JUN-1997; US-049974.
31-JUN-1997; US-049974.
31-JUN-1997; US-049974.
31-JUN-1997; US-049974.
31-JUN-1997; US-049974.
31-JUN-1998; US-049974.
31-JUN-1998; US-049974.
31-JUN-1998; US-049974.
31-JUN-1998; US-049974. W89248 standard; Protein; 488 AA. 10-MAR-1999 (first entry) Homo sapiens. W09849317-A2. Human SAD RESULT

```
Homo sapiens.
WO9315201-A.
      04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R41941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R39706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAME SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE SULT TO THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                   ö
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New poly: nucleotide(s) encoding megakaryocyte tyrosine kinase(s) used to develop prods. for the treatment and diagnosis of kinase related signal transduction abnormalities.

Claim 19; Fig 3A; 82pp; English.

Human megakaryocyte kinase MKK3 (R84183) is a 58 kDa cytosolic tyrosine kinase showing 478 homology with fyn. Recombinant MKK3 cabe produced in host cells by expression of encoding cDNA (T00618), and used in the treatment-and-diagness-of-e-g:-leukaemia-and---
                                                                                                                                                                                                                                                                                                                                             56 flalydftarcggelsvrrgdrlcaleegggyifarrlsggpsaglvpithvak 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                            Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 298;
                                                                                                                                                                                       Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jr. 3
R85929 standard; Protein; 505 AA.
R85929:
14-FEB-1996 (first entry)
Protein tyrosine-Kinase LpTK2.
Protein tyrosine-Kinase; pTK; LpTK2; agonist; cell growth;
differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1996 (first entry)
Megakaryocyte kinase MKK3.
Megakaryocyte kinase-3; MKK3; cytoplasmic tyrosine kinase; cellular signal transduction; leukaemia; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123..202
//label= SH2_domain
247..305
/label= Catalytic_domain
/note= "N.B. the sequence is incomplete;
Fig 3B is missing"
                                                                                                                                                                  Score 399; DB 39; Le
Pred. No. 5.69e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114; DB 15; L
Pred. No. 1.06e-02;
8; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 fvalfdygartaedlsfragdklgvldtlhegwwfarhl 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:||:|: || : :|| | ||:| |:
56 FLALYDFTARCGGELSVRRGDRLCALEE-GGGYIFARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56..113
/label= SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ullrich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             r 2
R84183 standard; Protein; 298
                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.6%;
Best Local Similarity 46.2%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-1994; US-232545.
21-APR-1995; US-426509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gishizky M, Sures I,
WPI; 95-382959/49.
N-PSDB; T00618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-0CT-1995.
04-APR-1995; U04228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1995; U05008
                                                                                                                         488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9527061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9529185-A1
                                                                                                proteins.
                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     888888
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
New protein tyrosine kinase genes and proteins encoded by genes -
are of human mega-karyocytic origin
Claim 3; Fig 5; 60pp; English.
PTR genes were identified using two sets of degenerative
Cligonucleotide primers: a first set which amplifies all pTK DNA
segments (049743-44), and a second set which amplifies highly
conserved sequences present in the catalytic domain of the c-kit
conserved sequences present in the pTK genes identified are described
in 049747-57 and R41897-02.
The LpTKs are expressed in lymphocytic cells, as well as
megakaryocytic cells. The partial and full-length LpTK2 gene
sequences are given in 049749 and 049754 respectively. The
protein sequence corresp. to 049749 is claimed (claim 7) and
stated as given in the specification, however is missing from
                                                                                                                        N-PSDB: T03097.

Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation
Disclosure; Pages 56-58; 125pp, English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. A LpTK2 gene (T03097) was isolated from lymphocytic and megakaryocytic cell libraries. The encoded novel pTK, LpTK2 (R85929), shows homology to known pTKs, and can be used to design drugs that modulate pTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pTK gene LpTK.2 prod. prod. pTK; protein tyrosine kinase; catalytic domain; c-kit; megakaryocyte; lymphocyte; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                     SP;
                                         Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 28.6%; Score 114; DB 14; I Local Similarity 46.2%; Pred. No. 1.06e-02; les 18; Conservative 8; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 28.6%; Score 114; DB 8; Le
Best Local Similarity 46.2%; Pred. No. 1.06e-02;
Matches 18; Conservative 8; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 fvalfdygartaedlsfragdklqvldtlhegwwfarhl 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-1993.
22-JAN-1993: U00586.
22-JAN-1992; US-826935.
AURE-) NEW ENGLAND DEACONESS HOSPITAL.
AVRAHAM H. COWLEY S, Groopman J, Scadden D;
                                     Matthews W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||:|: || : :|| | ||:| |: |
56 FLALYDFTARCGGELSVRRGDRLCALEE-GGGYIFARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 fvalfdygartaedlsfragdklgvldtlhegwwfarhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:||:|: || : :|| | ||:| |:
56 FLALYDFTARCGGELSVRRGDRLCALEE-GGGYIFARRL
                                  Lee JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 5
R39706 standard; Protein; 536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R41941 standard; Protein;
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-320330/40.
N-PSDB; Q49754.
                                                                                                   WPI; 95-366160/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the publication
```

ä

.. H

```
Gallus gallus.
WO9314193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lmplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues 81-140 of chicken c-SRC.
Residues 81-140 of chicken c-SRC.
Vasopressin, L-oligonucleotide; macromolecule; D-amino acid peptide; sugar production; carbohydrate production; phospholipid; immune response; RNA-protein complex; protein-lipid complex; ligand; hormone; antibody; protease; nuclease; c-SRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1: Page 25; 70pp; English.

This sequence represents a D-form amino acid SH3 domain, synthesised as residues 81.140 of chicken c-SRC. This sequence was produced using the method of the invention. The method of the invention is for the production of a macromolecule (WM) of non-natural handedness (NNH), which binds to a target MM of natural handedness (NH). The method involves providing an enantiomer of the target MM (or its characteristic domain), and a library of MM's of NH. The library is contacted with the enantiomer under suitable conditions for the enantiomer to bind a member of the
                                                                                                                                                                                                                                                                     Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced monounclear cell adhesion and fibronectin prodn Disclosure; Page 75-77; 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46688) is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced monounclear cell adhesion. They can coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Mismatches 19; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Specific binding non-natural configuration macromolecule prodn. by identifying natural analogue using library and producing enantiomer, used e.g. to form D-peptide or L-nucleic acid enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 fvalydyesrtetdlsfkkgerlqivnntegdwwlahslstgqt-gyipsnyva 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113; DB 8; Length 536; Pred. No. 1.32e-02;
                     -src protein.
tyrosine kinase protein; pp60 c-src; ss.
                                                                                                                                                                                                          Bell L, Luthringer DJ, Madri JA, Warren SL;
WPI; 93-243209/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995; US-482309.
11-JUL-1995; US-001067.
28-MAR-1996; US-627497.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 6
W07876 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.3%;
Similarity 35.2%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim PS, Schumacher ANM; WPI; 96-506096/50.
                                                                                                                                      05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-1995; US-433572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference 1..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1996; U06155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus domesticus
                        C-Src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistant drugs
                                                                                                                                                                                                                                                        P-PSDB; R39705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9634879-A1.
                     Human pp60 c-
Endothelial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1996
                                                                      Homo sapien
                                                                                            WO9314193-A
                                                                                                                     22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W07876:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DADDO MAKKE E DADDO MAKE E DADD
ò
```

```
~
library, and the bound enantiomer is then produced. The method can also be used to produce L-Oligonucleotides (such as T44064) and D-amino acid peptide which binds to target L-MM's and for identifying an L-amino acid peptide which binds a D-amino acid peptide of interest. The method is used for identifying an L-amino acid peptide which binds a D-amino acid peptides, proteins.

Used for identifying MB's of NNH (such as peptides, proteins, protein-lipid complexes) which are ligands for other target MM's, e.g. DNA, hormones, and antibodies. The method is especially useful for identifying D-peptides and L-nucleic acids (from naturally occurring L-peptides and D-nucleic acids) for use as drugs. These compounds maybe superior drugs to the corresponding compounds of NH since they are not good substrates for naturally occurring proteases and nucleases and do not elicit an efficient immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell migration, unckinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin produ pisclosure; page 64-66; 91pp; Bnglish.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46687) is used to transform endothelial ransformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1997 (first entry)
Human signal mediator protein encoded by HEF1 cDNA.
Signal mediator protein; SNP; human enhancer of filamentation;
HEF1; cell morphology; neoplasia; SH3; SH2; pseudohyphal budding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetically engineered endothelial cells - which exhibit enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 fvalydyesrtetdlsfkkgerlqivnntegdwwlahslttgqt-gyipsnyva 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 fvalydyesrtetdlsfkkgerlqivnntegdwwlahslttgqt-gyipsnyva 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches 19; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%; Score 111; DB 8; Length 533; 33.3%; Pred. No. 2.04e-02; ative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1993 (first entry)
Chicken pp60 c-src protein.
Endothelial; tyrosine kinase protein; pp60 c-src; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 111; DB 22;
Pred. No. 2.04e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madri JA, Warren SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W13506 standard; Protein; 834 AA. W13506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R39705 standard; Protein; 533 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.8%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1993.
05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYA.) UNIV YALE.
Bell L. Luthringer DJ, M. WPI; 93-243209/30.
P-PSDB; R39708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 AA;
```

```
Tidentifying polypeptide(s) having specific functional domain (esp. 1813 domain) - comprises detecting selective binding to recognition but, regardless of sequence homology

For unit, regardless of sequence homology

For Claim 55, Fig 10a; 174pp; English.

W3420-W34253 represent Src-homology region 3 (SH3) domains from human can mouse proteins, that can be used in the method of the invention. This sequence represents as H3 domain of the mouse SH312 protein (see W65393) corp.

For full length protein). SH3 domain of the method of the invention signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a multivalent recomplex. The recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins containing an SH3 domain due to the minimal sequence homology among known SH3 proteins. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that care similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common
                                                                                                                                                                                                                                                                                                                                                                                                        The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes. Arg is expressed as two transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A (Q14936) and B and it is assumed that they are joined to the arg second exon.

The amino acid sequence is represented as found in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1998 (first entry)
SH3 domain B of mouse SH3P12 protein.
SH3 domain B of mouse SH3P12 protein.
Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening;
                                                                                                                                                                                                                                                                                                        Novel human gene related to abl proto-oncogene - designated "Abelson Related Gene", arg, useful for tumour diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abelson Related Gene, B transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CYDC.) CYTOGEN CORP.
(UYNC.) UNIV NORTH CAROLINA.
FOWLKES DM, HOffman N, Kay BK, Mcconnell SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular signal transduction process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 fvalydfvasgdntlsitkgeklrvl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 FLALYDFTARCGGELSVRRGDRLCAL 81
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5D; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .T 11
W34228 standard; Protein; 59 AA.
W34228;
                                                                                                                       22-OCT-1991, 559029.
22-OCT-1991, 559029.
30-JUL-1990, US-559029.
(USSH ) NAT INST OF HEALTH.
Kruh G, Arronson SA, King CR;
WPI; 91-353425/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match 23.6%; Local Similarity 46.2%; nes 12; Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-1996.
04-APR-1996; U04454.
03-APR-1996; US-630915.
07-APR-1995; US-417872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 96-465045/46.
                                                                                                                                                                                                                                                                                N-PSDB; Q14937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9631625-A1.
                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                       US7559029-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                            therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes. Arg is expressed as two transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A and B (Q14937) and it is assumed that they are joined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the arg second exon.
The amino acid sequence is represented as found in the specification.
Sequence 1146 AA:
                                                                                                                                                                                                New nucleic acid encoding mammalian signal mediator protein that changes cell morphology - and related oligo:nucleotide(s), protein and antibodies, useful e.g. in diagnosis and treatment of neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 109; DB 22; Length 834;
Pred. No. 3.16e-02;
14; Mismatches 18; Indels 1; "Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                           Claim 20: Page 36-38; 54pp; English.

The mammalian signal mediator protein is involved in regulation of cellular morphological alterations. The encoded protein comprises an amino-terminal SH3 domain, an internal domain contg. several SH2 binding motifs, and a carboxy-terminal effector domain that can induce pseudohyphal budding in yeast. The DNA and related prods, are useful as research tools and as diagnostic and therapeutic agents for the identification, detection and regulation of complex signaling events leading to morphological, Sequence 834 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human gene related to abl proto-oncogene - designated "Abelson Related Gene", arg, useful for tumour diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 alydnvpecaeelafrkgdiltvieqntgglegwwlcslhgrqgivpgnrv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94; DB 3; Lengturered. No. 7.77e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abelson Related Gene, A transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 fvalydfvasgdntlsitkgeklrvl 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 9
R15156 standard; Protein; 1146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 FLALYDFTARCGGELSVRRGDRLCAL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5B; 40pp; English.
                                                                                                                          Law SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1991.
22-OCT-1991.
30-JUL-1990. US-559029.
(USSH ) NAT INST OF HEALTH.
KIUH G, ALTONSON SA, KING CR;
WPI: 91-353425/48.
N-PSDB; Q14936.
                                                                   30-JUN-1995; US-491357.
(FOXC-) FOX CHASE CANCER CENT.
ESECJAR J, GOLEMIS EA, LAW S
WPI; 97-108975/10.
N-PSDB; T51556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.6%;
Best Local Similarity 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 35.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                 25-JUN-1996; U10823
WO9702362-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US7559029-A.
```

Query Match

g ò

disease

ö

Gaps

ö

Length 1182;

Sparks AB;

LT 10
R15157 standard; Protein; 1182 AA.
R15157;

RESULT ID RI AC RI

Matches

g

ö

ö

22; Indels

14; Mismatches

Conservative

15;

Matches

```
Notice to the monomer Russ detective binding to recognition unit, regardless of sequence homology

Claim 54: Fig 65: 174pp; English.

Claim 54: Fig 65: 174pp; English.

Claim 54: Fig 65: 174pp; English.

Commain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for comparing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins which contain an SH3 domain due to the minimal sequence homology compared to monomer RUs. Multivalent RU complexes are particularly suited compared to monomer RUs. Multivalent RU complexes are particularly suited compared to monomer RUs. Multivalent RU complexes are particularly suited functional domain. The new method enables proteins having a common functional domain. The new method enables proteins having a common compared to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal cransduction processes, etc. New caldidate drugs can be assessed the neithod of the invention.
                                                                                                                                                                                                    ô
function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                  6 iakfnfngdtgvemsfrkgeritllrgvdenwyegripgtsrggifpityv 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay BK, Mcconnell SJ, Sparks AB;
                                                                                                                                                        Score 93; DB 25; Length 59;
Pred. No. 9.57e-01;
14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Src-homology region 3 domain"
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "encoded by GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by CCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellular signal transduction process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     WO5402 standard; Protein; 182 AA.
WO5402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Hoffman N, Kay
                                                                                                                                                   Query Match
Best Local Similarity 29.4%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130..176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1996, US-630915.
07-APR-1995, US-417872.
(CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human clone 53 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-1996; U04454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96-465045/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 96-46504:
N-PSDB; T3980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9631625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                         8888888
                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                   ô
```

Length 182;

Score 93; DB 25; | Pred. No. 9.57e-01;

23.3%; 29.4%;

Query Match Best Local Similarity

```
The standard of sequence homology and the standard of secondition unit, regardless of sequence homology with the sequence homology with the sequence homology selective binding to recognition with the sequence homology region 3 (5H3) and 54; Fig 43; 174pp; English.

Claim 54; Fig 43; 174pp; English.

Claim 54; Fig 43; 174pp; English.

Compared to the inchement of the incention is the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for interest containing polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent component (CC recognition unit (RN) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RV complex. The method is based on functional similarities and does not rely on sequence compared is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins which contain an SH3 domain due to the minimal sequence homology among known SH3 proteins. It has been found that small peptide RUS in multivalent form have reduced specificity for a given functional domains that are common compared to monomer RUS. Multivalent RUS (morplexes are particularly suited to screening for polypeptides containing functional domains that are common contained for a better understanding of cell growth, malignancy, signal contains the method of the invention.

CLOSSING COMPART SPECIFICIALS (e.g. pharmacological activities) can be assessed that specificities (e.g. pharmacological activities) can be assessed that specific interpretains with the compared contains the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                               Mouse SH3P12 protein.
Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymphoid cell protein-tyrosine kinase SH3 domain.
Lymphoid cell protein-tyrosine kinase; Lck; SH3 domain; inhibitor;
immune suppressant; autoimmune disease.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 lakfnfngdtqvemsfrkgeritllrqvdenwyegripgtsrqgifpityv 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 lakfnfngdtqvemsfrkgeritllrqvdenwyegripgtsrqgifpityv 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcconnell SJ, Sparks AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 25; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 9.57e-01;
                                                                                                                                                                                                                                                                                                                      cellular signal transduction process. Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Кау ВК,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                        Ä.
                                                                                                                                                                                                                                                                                                                                                                                 10 OCT 1996.
04 APR-1996; U04454.
07 APR-1995; US-630915.
07 APR-1995; US-417872.
(CYTO-) CYTOGEN CORP.
(UNC-) UNIV NORTH CAROLINA.
FOWIKES DM, HOLFMAN KAY B
WPI; 96-465045/46.
                                                                                                                                               JT 13
W05393 standard; Protein; 788
W05393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W73554 standard; Protein; 126
W73554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     788 AA;
                                                                                                                                                                                                                                                                                                                                                                WO9631625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-1999
                                                                                                                                                                                                             19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J10327864-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
ID W7
AC W7
DT 08
DE LY
KW LY
KW 1m
OS UE
                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                 δ
```

```
1;
                                                                                                                                                                                                                                                                                        protein-tyrosine kinase analogues
Claim 1: Page 4-5: 6pp: Japanese.
This sequence is the Lymphoid cell protein-tyrosine kinase (Lck) SH3
domain of the invention. The DNA and protein are useful as immune
suppressants, and are useful for inhibition and treatment of autoimmune
diseases caused by Lck analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure: Fig 4: 7pp; Japanese.

This sequence is encoded by a fragment of the vector pHFZprNeoDT. This sequence is encoded by a fragment of the vector with the passeste, containing the neo gene, MVM pause signal sequence, MC1 promoter, a diphtheria toxin A (DT-A) fragment and bluescript DNA. The neo gene has a PCK promoter just upstream of it, and the MVM pause signal and bluescript DNA are inserted between the neo gene and the MC1 promoter. This construct was used in the selection of a cell containing a genomic DNA gene which is deleted or reduced by homologous recombinantion with DT-A. The cassette is preferably expressed in embryonic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunosuppressant DNA and protein – useful for inhibition and treatment of autoimmune diseases caused by lymphoid cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 ialhsyepshdqdlgfekgeqlrileqsgewwkaqslttgq-egfipfnfvak 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 91; DB 39; Length 126;
Pred. No. 1.45e+00;
15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.6%; Score 90; DB 9; Length 48; Best Local Similarity 39.3%; Pred. No. 1.79e+00; Matches 11; Conservative 9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-1994 (first entry)
Vector pHFZprNeoDT junction fragment.
WWM pause signal sequence; cassette; neo gene; MCl prom diphtheria toxin A; DT-A; bluescript DNA; PCK promoter; homologous recombinantion; embryonic stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "fyn Aderived amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28..32
/note= "Linker amino acids"
33..48
/note= "Trp-lacZ amino acids"
                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. (MITU) MITSUBISHI CHEM CORP. WPI; 99-099029/09. N-PSDB; V62889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 15
R47126 standard; Protein; 48 AA.
R47126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.8%;
Best Local Similarity 30.2%;
Matches 16; Conservative
                              28-MAY-1997; 138905.
28-MAY-1997; JP-138905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J05328966-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE SUPPLY SEED OF THE SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY SUPPLY 
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ä

Gaps

1;

7; Indels

Search completed: Thu May 20 12:43:28 1999

1,

4 fvalydyearteddlsfekgekf-gmed 30 |:||||: || :|| :|: :|: 56 FLALYDFTARCGGELSVRRGDRLCALEE 83

쉱

Job time : 128 secs.

US-09-099-053-2-03.rpr

* * * * * * * * * * * * * * * * * * *	*****
*	
*	- * * * * * * * * * * * * * * * * * * *

*	* * * * * * * * * * * * * * * * * * * *
*	*****

* *	* * * * *

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:43:47 1999; MasPar time 6.59 Seconds Run on:

Tabular output not generated.

>US-09-099-053-2 (56-109) from US09099053.pep (3 of 6) 399

1 FLALYDFTARCGGELSVRRG.....ARRLSGQPSAGLVPITHVAK 54 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

116695 seqs, 37453910 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

Mean 35.494; Variance 59.968; scale 0.592 pir60 1:pirl 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	2.72e-44	4.07e-41	2.25e-10	4.93e-09	4.31e-08	1.56e-07	2.39e-07	8.52e-07	1.30e-06	1.97e-06	3.00e-06	4.54e-06	4.54e-06	4.54e-06	4.54e-06	4.54e-06	6.88e-06	6.88e-06	1.04e-05	1.04e-05	1.57e-05	1.57e-05	2.36e-05
		Description	srm - mouse	protein-tyrosinė kina	protein-tyrosine kina	protein-tyrosine kina		protein-tyrosine kina	p59(Xfyn) - Xiphophor	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina		protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina
		O.	156322	A56040	TVHAST	B34104	A34104	A39939	151592	S26420	138396	149552	B49114	S24547	TVCHS	TVFVS2	TVFVS1	TVFVPR	833569	I51593	TVHUHC	A45501	JQ1321	TVMSHC	A43807
		8	7	~	,	7	7	~	7	~	~	7	7	7	7	,	-	Н	7	~	-	~	7	Н	~
		Length DB	496	496	509	532	532	507	537	526	505	512	539	517	533	557	568	587	536	544	505	537	503	503	517
æ	Query	Match	73.2	69.7	ش	31.8			29.6	28.8	28.6	28.3	28.1			27.8			27.6		27.3	27.3	27.1	27.1	26.8
		Score	292	278	134	127	122	119	118	115	114	113	112	111	111	111	111	111	110	110	109	109	108	108	107
	Result	No.	٦	8	m	4	ഗ	ø	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

A56040 #type complete
protein-tyrosine kinase (EC 2.7.1.112) Srm, nonreceptor type
- mouse
#formal_name Mus musculus #common_name house mouse
01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
A56040

~

RESULT ENTRY TITLE

Kohmura, N.; Yagi, T.; Tomooka, Y.; Oyanagi, M.; Kominami, R.; Takeda, N.; Chiba, J.; Ikawa, Y.; Alzawa, S. Mol. Cell. Biol. (1994) 14:6915-6925
A novel nonreceptor tyrosine kinase, Srm: cloning and

A56040

ACCESSIONS REFERENCE #authors

ORGANISM DATE

#journal #title

7.79 e e e e e e e e e e e e e e e e e e e	u c	(ο΄ (ο΄
	ouse xt_change protein c protein gy	59 Gap: 13
protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina lyn protein-tyrosine kina lyn protein-tyrosine kina lyn protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina		/ 8 6 7 7 7
sine sine sine sine sine sine sine sine	numon_name house mousen 26-Jul-1996 #text_suka, F. 11:533-538 A clone encoding prokin. from GB/EMBL/DDBJ 11: PID:9684972 Thr or Tyr-specific glology; SH3 homology	nomcology flabel KLNN ATP-binding motif the 55731 #checksum DB 2; Length 496; 72e-44; thes 9; Indels 0 ARESGPPSTGLVPVTYLAK
protein-tyrosine protein-tyrosine	e } -115 EME EME HT - 8	y # labe ding mc l #che Length ; Inde STGLVPY
protein- protein- protein- protein- protein- protein- protein- protein- protein- lyn & prot lyn & prot lyn & prot protein- protein- protein- protein- protein- protein- protein-	26-Junar 26-Junar 26-Junar 233-5: 233-5: 210ne 210ne 210ne 210ne 210ne 210ne 210ne	0109y -bind 55731 2; L -44; -44; SGPPS SGPPS
	te evision 26-Jul-1 H.; Otsuka, F. 995) 21:533-538 el CDNA clone er fine skin. lated from GB/EN 19684971; PID:968 Ser/Thr or Tyr- se homology; SH3/,	ATP ght g DB 72e ches ches
ט	#type complete ame Mus musculus #common_n 96	kinase no kinase AT lar-weight e 292; DB . No. 2.72 Mismatche EEGDYIFAOR
A43806 A44991 TVHUSY A49114 A49114 TVHUG9 TVCHS S10808 TVFV60 OWFVPR OWFVR OWFVR TVHUSC 167811 167811 167811 167811 174905 S31568 S31645		ein Kil ein Kil ecular core 2' red. N 5; Mil 5; Mil 1
A43906 A449991 TV9US TV8US TV6US TV6US S20808 S20808 S20808 TVFV6 TVFV6 TVFUS	#type comple Mus muscu #sequence_98 Nakauchi, lon of a no kinase in m inary; tran lon of a no kunase in m inary; tran lon of a no with the label RES lon of a lon	protein) protein) protein) #molecule ; Score ; Pred. 5; N
	# # # # # # # # # # # # # # # # # # #	110 p 000 p 6 ## .28; .18; .18; .18c .18c
& & & & & & & & & & & & & & & & & & &	2 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	10ma egi 73 74 74 74 74 75 75 71 75 71 71
899988777777	156322 srm - mc #formal_ 26-711-1 156322 156322 156322 156322 156322 156322 156322 156322 160011fi 17009 17009 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320 186320	#1 #length Similarity 40; Conser LIXDFTARCAEE
00000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	# 1mil 0; XDFT YDFT
00000000000000000000000000000000000000	SM #form srm SM #form srm IONS 1563; UNCE 1563; UNCE Kawa LAOR 1563; Cession 1563; ##status	- m - m ()
4 N O C 8 O O O O O O O O O O O O O O O O O	1	4 <i>u</i> Hố no ru
00000000000000000000000000000000000000	EESULT 1 ENTRY PUTLE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title ##accession ##status ##status ##status ##status ##coss. CLASSIFICATION FEATURE 60-111	240-2 240-2 SUMMARY Query Best I Matche Db 6

```
ALTERNATE NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #introns
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                 #authors
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ഹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87-136
147-244
264-522
272-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                                                     #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                       DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily protein-tyrosine kinase src; protein kinase homology; S12 homology; ATP; autophosphorylation; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVHAST #type complete protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata formal_name Hydra attenuata 31-mar-1992 #sequence_revision 31-mar-1992 #text_change .05.sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase-related transforming protein (src); kinase-related
                                                                                       ##cross-references GB:D26186; NID:g529072; PID:d1005873; PID:g529073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                         *superfamily unassigned Ser/Thr or Tyr-specific protein
kinases; protein kinase homology; SH3 homology
ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E. #journal Mol. Cell. Biol. (1989) 9:4141-4151 structure and expression of STK, a src-related gene in simple metazoan Hydra attenuata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum 8721
                                                                                                                                                                                                               #domain SH3 homology #label SH3\
#domain protein Kinase homology #label KIN\
#ragion protein kinase APP-binding motif
#length 496 #molecular-weight 55593 #checksum 301
                                                                                                                                                                                                                                                                                                                                                                                       64 FVALYDYEARISEDLSFKKGERLQIINTADGDWWYARSLITN-SEGYIPSTYVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRALYDFTARCAEELSVSGGDRLYALKEEGDYIFAQRLSGPPSTGLVPVTYLAK 113
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase APP-binding motif\
#active_site Lys #status predicted\
#binding_site phosphate (TY) (covalent) (by
#ulopio_sphorylation) #status predicted
#length 509 #molecular-weight 56885 #checksum 87
                                                                                                                                                                                                                                                                                                   2; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 509;
                                                                                                                                                                                                                                                                                                 Score 278; DB 2; Length 496 Pred. No. 4.07e-41; 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 134; DB 1; Length 509
Pred. No. 2.25e-10;
11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
targeted disruption. A56040
                                                                     1-496 ##label KOH
                                   preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 40.7%; es 22; Conserved.
                                                                                                                                                                                                                                                                                                   69.78;
72.28;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.2%;
39; Conservative
                                                     ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frog
                                                                                                                         #map_position
                                                                         ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION
                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126-218
238-497
246-254
                                                                                                                                                                                                                             232-491
240-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66-115
                                                                                                                                                                                                               62-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                             KEYWORDS
                                                                                                           GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE
                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
*superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A34104 #type complete protein-tyrosine kinase (EC 2.7.1.112) src 1 - African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming protein (src) 1
#formal_name Xenopus laevis #common_name African clawed frog
30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change
20-Mar-1998
transforming protein (src) 2 #formal_name African clawed frog 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steele, R.E.; Chosn, R.; Ral, B.B.A.; Winokur, S.T.; Unger,
                                                                                                                                                                                                                                     each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                each
                                                                                                                                                                                                                                                                                                                   ##status preliminary; not compared with conceptual translation ##molecule_type mRNA ##residunary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status preliminary; not compared with conceptual translation ##molecule_type mRNA ##modes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. (1985) 13:1747-1761
Two divergent cellular src genes are expressed in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase-related transforming protein (src); kinase-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                  #authors Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
#journal J. Biol. Chem. (1989) 264:10649-10653
#title The two Xenopus laevis SRC genes are co-expressed and produces functional pp(60src).
#cross-references wild:89278134
#accession B34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-532 ##label STE ##cross-references GB:M24704; GB:J04822; NID:g214804; PID:g214805
                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-532 ##label STE
##cross-references GB:M23422; GB:J04822; NID:g214796; PID:g214797
NCE 151563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #checksum 7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 FVALYDYESRTETDLSFRKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B. J. Biol. Chem. (1989) 264:10649-10653

The two Xenopus laevis SRC genes are co-expressed a produces functional pp(60src).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 532 #molecular-weight 59736 #checksum 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 127; DB 2; Length 532; Best Local Similarity 38.9%; Pred. No. 4.93e-09; Matches 21; Conservative 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **status preliminary; translated from GB/EMBL/DDBJ
*##nolecule_type DNA
*##noniantal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references GB:M30858; NID:g214799; PID:g555569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439-492 ##label ST2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #cross-references MUID:89278134
#accession A34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:85215578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A34104; I51564
                                                                                                              B34104; I51563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steele, R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A34104
                                                                                                                                               A34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
```

m

```
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
241-499
249-257
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89-138
269-527
                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dene
                                                                                SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                     DATE
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                 *Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; phosphoprotein; phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. (1987) 84:8778-8782
Additional member of the protein-tyrosine kinase family: the
src-and lck-related protooncogene c-tkl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann
                                       #title Structural organization of a src gene from xenopus laevis.
#cross-references MUID:93064714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A39939
#type complete
protein-tyrosine kinase (EC 2.7.1.112) tkl - chicken
kinase-related transforming protein (tkl); T-cell surface
antigen associated protein tkl
#formal_name Gallus gallus #common_name chicken
06-Mar-1992 #sequence_revision 05-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status preliminary
##molecule_type mRNA
##residues 52-507 ##label STR
##cross_references GB:0103579; NID:g212712; PID:g212713

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
KEYWORDS ATP; lipoprotein; myristylation; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphotransferase; surface antigen; tyrosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-88 ##label CHO
##cross-references GB:M85043
##experimental_source thymus, spleen
##note sequence extracted from NCBI backbone (NCBIN:88831,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chow, L.M.; Ratcliffe, M.J.; Veillette, A. Mol. Cell. Biol. (1992) 12:1226-1233 tkl is the avian homolog of the mammallan lck tyrosine
                                                                                                                                                                                                                                                                                                                                           #domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase Arp-binding motif
#length 532 #molecular weight 59856 #checksum 7110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 FLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQPSAGLVPITHVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                          ##Status preliminary; translated from GB/EMBL/DDBJ##molecule_type DNA##residence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 122; DB 2; Length 532
Pred. No. 4.31e-08;
14; Mismatches 18; Indels
                                                                                                                                  ##residues 1.113 ##label ST2
##cross-references GB:M33646; NID:g214808; PID:g214810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3\
                                                                                                                                                                                                                                                                                 tyrosine-specific protein kinase
            Oncogene (1992) 7:2345-2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase gene.
#cross-references MUID:92186854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBIP:88833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *cross-references MUID:88097370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.6%;
Best Local Similarity 37.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A42126; A39939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A42126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A39939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A42126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A39939
                                                                                                                                        ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATE_NAMES
                                                                                                                                                                                                                       CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
#authors
                  #journal
                                                                                                                                                                                                     ntrons
                                                                                                                                                                                                                                                                                                                                       147-244
264-522
272-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66-114
125-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSIONS
                                                                                                                                                                                                                                                                                                                         87-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                              GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ς,
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature
form) #status predicted
#length 507 #molecular-weight 58011 #checksum 4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kashuba, V.I.; Rynditch, A.V.; Dostalova, V.; Hlozanek, I.; Zubak, S.V.; Kavsan, V.M. submitted to the EMBL Data Library, September 1992 Molecular cloning and DNA sequence analysis of duck-adapted variant of Rous sarcoma virus (da Pr-RSV-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hannig, G.; Ottilie, S.; Schartl, M.
Oncogene (1991) 6:361-369
Conservation of structure and expression of the c-yes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kashuba, V.I.; Serge, Z.V.; Rynditch, A.V.; Kavsan, V.M.; Hlozanek, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                   151592  #type complete
p59(Xfyn) - Xiphophorus helleri
#formal_name Xiphophorus helleri
04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
10-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Rous sarcoma virus
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 FVALYDYEARTEDDLSFRKGERFQILNSTEGDWWDARSLTT-GGSGYIPSNYVA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621
                                                                                                                                                                                                                                                            65 VALYDYEPTHDGDLGLKQGEKLRVLEESGEWWRAQSLTTGQ-EGLIPHNFVAM 116
                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN
#length 537 #molecular-weight 60447 #checksum
                                                                                                                                                       Score 119; DB 2; Length 507;
Pred. No. 1.56e-07;
15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1.537 ##label HAN
##cross-references EMBL:X54971; NID:g64481; PID:g64482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references EMBL:X68524; NID:g61903; PID:g61907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S26420 #type complete
protein-tyrosine kinase (EC 2.7.1.112) src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 2;
Pred. No. 2.39e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes in lower vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-526 ##label KAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:91187435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                       Query Match
Best Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 29.6%;
Best Local Similarity 38.9%;
Matches 21; Conservative
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-Dec-1997
S26420; S20676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151592
151592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S26420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S26417
```

US-09-099-053-2-03.rpr

148-245 265-523 273-281

SUMMARY

88-137

FEATURE

KEYWORDS

#gene

```
intestine.
#cross-references MUID:95251656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:U01350 CLASSIFICATION #superfamily prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary
                                                                                                                                                                                                                                                                                                           Ziemiecki, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.3%;
Best Local Similarity 40.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                          I48608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B49114
                                                                                                                                                                         I4955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION
                                                                                                                                                                                         ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                             #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
#journal
#title
                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123-215
239-501
247-255
                                 ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
                                                         REFERENCE
                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                  *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology;"SH3 homology ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T. Gene (1994) 138:247-251
Cloning of FRK, a novel intracellular SRC-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149552 #type complete protein-tyrosine kinase (EC 2.7.1.112) bsk/iyk - mouse intestinal tyrosine kinase #formal_name Mus musculus #common_name house mouse
                                                                                                                                                                                                                             #domain SH3 homology #label SH3\
#domain SH2 homology #label SH3\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif
#length 526 #molecular-weight 59212 #checksum 7994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN\
#region protein kinase Arb-binding motif
#length 805 #molecular weight 58254 #checksum 9379
                                                                                                                                                                                                                                                                                                                                                                                                                          86 FVALYDYESWTETDLSFKKGERLQIVNNTEGYWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
March 1990
                                                                                                                                                                                                                                                                                                                                           Score 115; DB 2; Length 526;
Pred. No. 8.52e-07;
16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.6%; Score 114; DB 2; Length 505; Best Local Similarity 46.2%; Pred. No. 1.30e-06; Matches 18; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
##residues 1-505 ##label RES
##cross-references EMBL:U00803; NID:9392887; PID:9392888
                                                                       ##residues 1-526 ##label KA2
##cross-references EMBL:X51861; NID:961896; PID:961897
submitted to the EMBL Data Library, $20676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 FVALFDYQARTAEDLSFRAGDKLQVLDTLHEGWWFARHL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase-encoding gene.
#cross-references MUID:94171047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references GDB:355675
#map_position 4q35-4q35
CLASSIFICATION #superfamily protei
                         ##molecule_type DNA ##residner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary
                                                                                                                                                                                                                                                                                                                                             Query Match 28.8%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB: FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATE_NAMES
#submission
                                                                                                                                                    CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                   #accession
```

REFERENCE #authors #journal

#title

ACCESSIONS

ORGANISM

RESULT

g ò ALTERNATE_NAMES ORGANISM

10

RESULT

දු

ô

232-494 240-248

SUMMARY

FEATURE 49-105

KEYWORDS

GENETICS

```
B49114  #type complete protein-tyrosine kinase (EC 2.7.1.112) fyk - Pacific electric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swope, S.L.; Huganir, R.L.
J. Biol. Chem. (1993) 208:25152-25161
Molecular cloning of two abundant protein tyrosine kinases in
Torpedo electric organ that associate with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; intestine; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
electric ray
10.Nov-1995 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                #authors Oberg-Welsh, C.; Welsh, M.
#journal Gene (1995) 152:239-242
#title Cloning of BSK, a murine FRK homologue with a specific pattern of tissue distribution.
#cross-references MUID:95137395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. (1995) 209:582-589 iyk, a novel intracellular protein tyrosine kinase differentially expressed in the mouse mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Torpedo californica #common_name Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #checksum 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                           Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 512 #molecular-weight 58891 #checksum 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-153,'T',155-236,'H',238-512 ##label REZ
##cross-references EMBL:248757; NID:9736263; PID:9736264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113; DB 2; Length 512
Pred. No. 1.97e-06;
12; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                    ##residues 1-512 ##label RES
##cross-references GB:L36132; NID:g556287; PID:g777773
NNCE 148608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 FVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKGTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain SH3 homology #label SH3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                  translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-539 ##label SWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
```

US-09-099-053-2-03.rpr

```
A41256
                                                                                                                                                                                                                                                                                                                          A32432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A90838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
                    #accession
                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#contents
                                                                                                                            #authors
#journal
                                                                                                                                                                                                                                                                                       ##note
                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88-137
148-245
265-523
273-281
                                                                                                           REFERENCE
                                                                                                                                                               #title
                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                 #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12,48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeya, T.; Hanafusa, H.
Cell (1983) 32:881-890
Structure and sequence of the cellular gene homologous to the
RSV sec gene and the mechanism for generating the
                                                                                                           ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology; SH2 homology; SH3 homology
ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *superfamily protein-tyrosine kinase src; protein kinase
                                                                                                           Gaps
                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) fgr - rat #formal_name Rattus norvegicus #common name Norway rat 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 19-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVCHS #type complete
protein-tyrosine kinase (EC 2.7.1.112) src - chicken
kinase-related transforming protein src
kinase-related transforming protein src
fromal_name Gallus gallus #common_name chicken
19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change
07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 517 #molecular-weight 58792 #checksum 9498
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 539 #molecular-weight 60720 #checksum 8770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 FVALYDYEARTGDDLTFTKGEKFHILNNTE-YDWWEARSLSS-GRTGYVPSNYVA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 FIALYNYDARTEDDLTFRKGEKFHIINSSEGDWWEARSLTT-GSTGYIPSNYVA 141
                                                                                                                                                                                                                                                                                                                                                                          Tue, C.C.
submitted to the EMBL Data Library, December 1990
S24547
                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111; .DB.2; .Length 512; Pred. No. 4.54e-06; 12; Mismatches 18; Indels
                                                                         Length 539;
                                                                     Score 112; DB 2; Length 539
Pred. No. 3.00e-06;
15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:X57018; NID:956145; PID:956146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Yue, C.C.
#journal Mol. Immunol. (1991) 28:399-408
#title Novel putative protein kinase clones f.
granular lymphocyte tumor cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##experimental_source lymphocyte cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A00630; A41256; A32432; C35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371-427 ##label YU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues 1-517 ##label YUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming virus.
                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.2%;
Matches 21; Conservative
                                                                     Query Match 28.1%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                         S24547; PT0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                             S24547
                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                              #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
#journal
#title
                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                               #authors
271-529
279-287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72-121
132-229
249-507
257-265
                                                                                                                                                                                                                                                                                                                                         ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENETICS
                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                      DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                             ò
```

```
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein kinase A) #status predicted\
#binding_site phosphate (Thr) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology alta homology alternative splicing; AFP; autophosphorylation; blocked umino end; lipoprotein; myristylation; phosphoprotein; phosphotransferase; proto-oncogene; tyrosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GB:M57290; NID:g212703; PID:g212706
##note alternatively spliced mRNA exclusively replaces the long
form in skeletal muscle shortly before hatching
this ORF appears not to be translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.
Cell (1989) 57:763-774
Purified maturation promoting factor phosphorylates pp60
(c-src) at the sites phosphorylated during fibroblast
                                                                                                                                                                                                                                  Dorai, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H. Mol. Cell. Biol. (1991) 11:4165-4176
Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oss-reterencession A32432
teession A32432
##molecule_type protein
##residues 2-88 ##label SHE
##residues 34-Thr, 46-Thr, and 72-Ser are phosphorylated during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Dorai, T.; Wang, L.H.
#authors Dorai, T.; Wang, L.H.
#journal Mol. Cell. Biol. (1990) 10:4068-4079
#title An alternative non-tyrosine protein kinase product of the c-src gene in chicken skeletal muscle.
#cross-references_MUID:90318371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the authors translated the codon CAG for residue 527
                                                                                                                                                                           Glu, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeya, T.; Hanafusa, H.
Cell (1983) 34:319
annotation; erratum, correct translation of residue 526
                                                                                                                                         AAC and CAG for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #active_site Lys #status predicted\
#binding_site phosphate (Tyr) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            experimental\
#binding_site phosphate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-182,'DP',185,'IPLPSCLC' ##label DO2
                                                                                            1-500, 'R', 502-533 ##label TAK
the authors translated the codons
residues 301 and 526 as Thr and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 484-533 ##label DOR
##cross-references GB:S43579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 experimental/
                                                                                                                                                                                                                                                                                                                                                              3' end of v-src.
A41256
*cross-references MUID:83155664
*accession A00630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #cross-references MUID:89249341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitosis
                                                             ##molecule_type DNA
##residues 1-5
```

```
FEATURE
88-137
148-245
265-523
273-281
                                                                                                                                                     KEYWORDS
                                                                         GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                                                                                                                                295
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP: autophosphorylation; blocked amino end; lipoprotein; myristylation; oncogene; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase
                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
                                                                                                                                                                                                                                                  TVFVS2 #type complete
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVFVS1 #type complete protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                        #formal_name avian sarcoma virus S2
31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change
07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name avian sarcoma virus S1
31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change
0'-Nov-1997
A25375
                                                                                                                                                                                                                                                                                                                                                                                                     Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, Toyoshima, K. Mol. Cell. Biol. 1986) 6:2420-2428
Activation of the cellular src gene by transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #active_site Lys #status predicted\
#binding_site phosphate (Tyr) (covalent) (by
autophosphorylation) #status predicted

th S7 #molecular weight 62582 #checksum 7810
predicted
#length 533 #molecular-weight 60023 #checksum 238
                                                                                                                                 86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                       86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toyoshima, K.
Mol. Cell. Biol. (1986) 6:2420-2428
Activation of the cellular src gene by transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
;;
                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111; DB 1; Length 557;
Pred. No. 4.54e-06;
15; Mismatches 19; Indels
                                                   Score 111; DB 1; Length 533;
Pred. No. 4.54e-06;
15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain SH2 homology #label SH2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession become ##molecule_type DNA ##molecule_type I-557 ##label IKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #cross-references MUID:87064539
                                                   7.8%;
Local Similarity 33.3%;
Local Similarity 33.3%;
Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 27.8%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 557
                                                                                                                                                                                                                                                                                        virus S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A25375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal
                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE 88-137 148-245 265-523 273-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE
                                                                                                                                                                       à
```

ò

```
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#active_site pys #status predicted\
#binding_site phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
#length 568 #molecular-weight 63632 #checksum 4430
                                                                                                                                                                *Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111; DB 1; Length 568 Pred. No. 4.54e-06; 15; Mismatches 19; Indels
                                                                                      1-568 ##label IKA
#cross-references MUID:87064539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.8%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                    #accession A25375
#molecule_type DNA
                                                                                      ##residues
                                                                                                                                                 #gene
```

Search completed: Thu May 20 12:45:34 1999 Job time: 107 secs.

?

******	(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:45:53 1999; MasPar time 4.06 Seconds375.926 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (56-109) from US09099053.pep (3 of 6) 399 1 FLALYDFTARCGGELSVRG.....ARRLSGQPSAGIVPITHVAK 54 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 36.365; Variance 52.725; scale 0.690 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Fred. No.	1.15e-51	2.07e-12	7.23e-11	8.78e-10	3.85e-09	6.29e-09	4.39e-08	7.10e-08	1.85e-07	1.85e-07	1.85e-07	1.85e-07	1.85e-07	2.98e-07	2.98e-07	4.78e-07	4.78e-07	7.66e-07	7.66e-07	1.23e-06	1.23e-06	1.96e-06	1.96e-06
	Describition	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN
£	10	SRM_MOUSE.	STK_HYDAT	SRC2_XENLA	SRC1_XENLA	LCK_CHICK	FYN_XIPHE	FRK_HUMAN	SRC_HUMAN	SRC_AVISR	SRC_CHICK	SRC_AVIST	SRC_AVISS	SRC_AVIS2	YRK_CHICK	YES_XIPHE	HCK_HUMAN	YES_XENLA	HCK_RAT	HCK_MOUSE	FGR_MOUSE	FYN_XENLA	FYN_MOUSE	FYN_HUMAN
9	9:	Н	Н	П	ч	٦	٦	Н	Н	ч	Н	Н	Н	Н	ч	Н	П	Н	Н	, - 1	Н	н	Н	Н
% Query Match formth pp		496	503	531	531	207	536	505	535	526	532	557	568	587	535	544	526	537	503	524	517	536	533	536
& Query	March					29.8	29.6		28.3			7	۲.		27.6	٠.	•	27.3	27.1	27.1	26.8	26.8	26.6	26.6
0,000	3001	292	134	127	122	119	118	114	113	111	111	111	111	111	110	110	109	109	108	108	107	107	106	106
Result		н	7	m	4	2	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.12e-06	4.906-00	4.96e-06	7.87e-06	1.25e-05	1.25e-05	1.25e-05	1.25e-05	3.10e-05	3.10e-05	7.65e-05	1.20e-04	1.20e-04	1.20e-04	1.87e-04	4.53e-04	4.53e-04	4.53e-04	4.53e-04	4.53e-04	7.02e-04	1.67e-03
PROTO-ONCOGENE TYROSIN	TIROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	NEURONAL PROTO-ONCOGEN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	ENTEROBACTIN SYNTHETAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN
YES_CHICK	SKC_KSVHI	SRC_RSVP	SRCN_MOUSE	LYN_MOUSE	LYN_RAT	FGR_HUMAN	YES_HUMAN	FYN_CHICK	YES_MOUSE	BLK_HUMAN	SRK1_SPOLA	SRK4_SPOLA	SRC_RSVSR	YES_AVISY	ABL_FSVHY	ABL_MOUSE	ABL1_HUMAN	ABL2_HUMAN	ENTF_ECOLI	YES_CANFA	LCK_HUMAN
д,	4	Н	Н	٦	Н	-	٦	Н	Н	Н	Н	Н	-	н	Н	Н	Н	Н	٦	-	Н
541	070	526	540	511	511	529	543	533	541	504	505	206	526	528	439	1123	1130	1182	1293	539	208
26.3	T . Q7	26.1	25.8	25.6	25.6	25.6	25.6	25.1	25.1	24.6	24.3	24.3	24.3	24.1	23.6	23.6	23.6	23.6	23.6	23.3	22.8
105	T C &	104	103	102	102	102	102	100	100	86	97	97	97	96	94	94	94	94	94	6	91
24	70	56	27	28	53	30	31	32	33	34	35	36	. 37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT	LT 1 SPM MOTISE STRANDARD. DRT. 496 AA
AC	62360;
DI	
DI	
ΕŪ	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
E	TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).
N S	SRMS OR SRM.
SO	
ဗ	
႘	RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN	[1]
RP	SEQUENCE FROM N.A.
R	
RX	MEDLINE; 97369678.
RA	KAWACHI Y., NAKAUCHI H., OTSUKA F.;
RT	encoding a t
RT	•
RL	EXP. DERMATOL. 21:533-538(1995).
RN	[2]
RP	SEOUENCE FROM N.A.
RC	TISSUE-LUNG;
RX	MEDLINE: 95021220.
RA	KOHMURA'N., YAGI T., TOMOOKA Y., OYANAGI M., KOMINAMI R., TAKEDA N.,
RA	
RT	"A novel nonreceptor tyrosine kinase, Srm: cloning and targeted
RT	1
RL	MOL. CELL. BIOL. 14:6915-6925(1994).
႘	-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
ပ္ပ	
ပ္ပ	
ပ္ပ	SRC
ပ္ပ	SIMILARITY: CONTAINS 1
ខ្ល	-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
ပ္ပ	
႘	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ပ္ပ	the European Bioinformatics Institute. There are no restrictions on its
ပ္ပ	
ပ္ပ	is not removed. Usage by and for commerc
ပ္ပ	
ပ္ပ	or send an email to license@isb-sib.ch).
႘	
DR	EMBL; D49427; G684972;
DR.	EMBL; D26186; G529073;
DR	MGD; MGI:101865; SRMS.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

a

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY.
         NAME TELETICAN SOLUTION SELECTION SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATH HOD DATE THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET THE TREET TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 90066418.

BOSCH T.C.G., UNGER T.F., FISHER D.A., STEELE R.E.;

Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuata.";

MOL. CELL. BIOL. 9:4141-4151(1989).

-! CATALITIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PROFENSINE PROSPHATE.

-! SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-! SIMILARITY: TO OTHER PROFEIN-TYROSINE KINASES IN THE CATALITIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 FRALYDFTARCAEELSVSRGDRLYALKEEGDYIFAQRLSGPPSTGLVPVTYLAK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).
EUKARYOTA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; ANTHOMEDUSAE;
HYDRIDAE; HYDRA.
                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION. 55 116 SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 292; DB 1; Length 496; Pred. No. 1.15e-51; 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STK_HYDAT STANDARD; PRT; 509 AA.

STK_HYDAT STANDARD; PRT; 509 AA.

01-AUG-1990 (REL. 15, CREATED)

01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)

01-CTT-1996 (REL. 34, LAST ANNOVATION UPDATE)

TYROSINE-PROTEIN KINASE STR (EC 2.7.1.112) (P57-STR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 R -> G (IN REF. 2).
238 LRK -> FGR (IN REF. 2).
78 N -> I (IN REF. 2).
55731 MW; FD44DEF6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO(107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO(109; PROTEIN_KINASE_IYR; 1.
PROSITE; PS50(011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50(001; SH2; 1.
PROSITE; PS50(002; SH3; 1.
PROSITE; PS00109; PROTEIN_KINASE_IYR; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1: PROSITE; PS50001; SH2; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.2%;
Best Local Similarity 74.1%;
Matches 40; Conservative
                                                                                                                                                                                 PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M25245; G159274; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
495
2495
354
3354
78
238
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00017; SH2; 1. PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A34094; TVHAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
234
240
262
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; P
PROSITE; P
PROSITE; P
PFAM; PF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

2012

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΩD
    DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DOR NO DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            ñ
                                                                                                                                                SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BHOSPHORYLATION (AUTO-) (BY SIMILARITY).
2B72ACE9 CR32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Two divergent cellular src genes are expressed in Xenopus laevis.";
NUCLEIC ACIDS RES. 13:1747-1761(1985).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 89278134.
STEELE R.E., UNGER T.F., MARDIS M.J., FERO J.B.;
"The two Xenopus laevis SRC genes are co-expressed and each produces
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                            TYROSINE PROTEIN KINASE; PROTO-ONCOGENE; PHOSPHORYLATION;
TRANSFERASE; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN.
LIPID 2 2 MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 FVALYDYEARISEDLSFKKGERLQIINTADGDWWYARSLITN-SEGYIPSTYVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,,
                                                                                                                                                                                                                                                                                                                                                        Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (REL. 13, CREATED)
1-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SANOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-2 (EC 2.7.1.112) (P60-SRC-2).
                                                                                                                                                                                                                                                                                                                                                     Score 134; DB 1; Pred. No. 2.07e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M23422; G214797; -.
EMBL; M30886; G555569; -.
EMBL; M30867; G555569; JOINED.
PIR; B34104; B34104.
PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
PROSITE: PS00119; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50001; S12; 1.
PROSITE: PS50002; S13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functional pp60src.";
J. BIOL. CHEM. 264:10649-10653(1989).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                        56885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 438-491 FROM N.A. IISSUE=ERYTHROCYTE; MEDLINE; 85215578.
                                                                                                                                                                                                                                                                                                                                                          33.6%;
                                                                                                                                                                                                                                                                                                                                   Guery Match
Best Local Similarity 40.7",
Best Local 22; Conservative
PFAM; PF00069; pkinase; 1. HSSP; P00523; 1PRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                126
246
246
268
360
390
509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 89278134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEELE R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRC2_XENLA
P13116;
                                                                                                                                                DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                              DOMAIN
```

```
PFAM; PF00069; pkinase; 1
   79
146
2265
271
2293
384
                                                                                                                                                                                                           LCK_CHICK
P42683;
                                 NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                 Query Match
   DOMAIN
                       DOMAIN
   ET ET ET ES
                                                                                                                                             음
                                                                                                                                                                 ò
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                              XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                              BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
C6ABE595 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                             STEELE R.E., UNCER T.F., MARDIS M.J., FERO J.B.;
"The two Xenopus laevis SRC genes are co-expressed and each produces functional pp60src.";
J. BIOL. CHEM. 264:10649.10653(1989).
-i- CATALIVILY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE IN TYROSINE - ADP +
                                                                                                                                                                                                 Gaps
                             MYRISTYLATION; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;

MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN.

INIT_MET 0 0 BY SIMILARITY.

DOMAIN 146 243 SH2.

DOMAIN 146 243 SH2.

DOMAIN 265 518 PROTEIN KINASE.

DOMAIN 271 279 ATP (BY SIMILARITY).

BINDING 293 293 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000523; 2PFK.
TRANSFERASE; AIP-BINDING; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                     84 FVALYDYESRTETDLSFRKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA-1-36
                                                                                                                                                                                                                                ñ
                                                                                                                                                                          Score 127; DB 1; Length 531; Pred. No. 7.23e-11;
                                                                                                                                                                                               13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                        01-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-1 (EC 2.7.1.112) (P60-SRC-1).
                                                  MYRISTATE (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
SH3.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
MYRISTATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                     531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A34104; A34104.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2 DOMAIN
                                                                                                                                                     59605 MW;
                                                                                                                                                                         31.8%;
larity 38.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN;
PF00018; SH3; 1.
PF00069; pkinase; 1.
P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M24704; G214805; -.
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                           140
243
518
279
384
                                                                                                                                                     531 AA;
                                                                                                                                                                                  Local Similarity
Hes 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 89278134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYRISTYLATION; SINIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                   4
SRC1_XENLA
P13115;
01-7
                                                                                                                              ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                          Query Match
           PFAM;
HSSP;
                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                          ö
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                        BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
AB0705D0 CRC32;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN TYROSINE PHOSPHATE.
-!- ENZYME REGULATION: REGULATED BY PHOSPHORYLATION ON TYR-348.
-!- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREBHARDT K., MULLINS J.I., BRUCK C., RUEBSAMEN-WAIGMANN H.;
"Additional member of the protein-tyrosine kinase family: the src-
and lok-related protooncogene c-tkl.";
PROC. NATL. ACAD. SCI. U.S.A. 84:8778-8782(1987).
-!- FONCTION: MAY PARTICIPATE IN ANYIGEN INDUCED T-CELL ACTIVATION.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN IYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92186854.
CHOW L., RATCLIFFE M., VEILLETTE A.;
"tkl is the avian homolog of the mammalian lck tyrosine protein
kinase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                              84 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLARSLSSGQT-GYIPSNYVA 136
                                                                                                                                                                                                                                                                                                                          .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALLUS GALLUS (CHICKEN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                            Score 122; DB 1; Length 531; Pred. No. 8.78e-10;
                                                                                                                                                                                                                                                                                                                       14; Mismatches 18; Indels
SH3.
SH2:
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M85043; G212533; -...
EMBL; J03579; G212713; ALT_INIT.
PROSITE; PS00107; PROTEIN_KINASE_ATP: 1.
PROSITE; PS00119; PROTEIN_KINASE_LOW; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
PROSITE; PS50012; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOL. CELL. BIOL. 12:1226-1233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                       59725 MW;
                                                                                                                                                                                                                                                            30.6%;
ilarity 37.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 46-507 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-88 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
     140
243
518
279
384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYROSINE KINASE C-TKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1
                                                                                                                                                                                                    531 AA;
                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88097370
```

```
PFAM; PF00069; pkinase; 1.
                                                                                                                            INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                  MOD_RES
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                LIPID
LIPID
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESCUENCE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF 
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ATHERINOMORPHA;
CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECILIIDAE; XIPHOPHORUS.
                     PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE;
ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
PHOSPHATIDYLINOSITOL 3-KINASE.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RIO LANCETILLA,
MEDLINE; 91187435.
HANNIG G., OTTILLE S., SCHARTL M.;
"Conservation of structure and expression of the c-yes and fyn genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (REL. 23, CREATED)
01-PEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||||: : |:|:::|::| |||:| ||: |: |: ||:| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VALYDYEPTHDGDLGLKQGEKLRVLEESGEWWRAQSLTTGQ-EGLIPHNFVAM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 119; DB 1; Length 507; Pred. No. 3.85e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                            MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in lower vertebrates.";
ONCOGENE 6:361-369(1991).
-!- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP
                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                       06C5A291 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                    SH2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54971; G64482; -
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; P50011; PROTEIN_KINASE_DOM; 1.
                                                                                                         PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                          MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.8%;
llarity 35.8%;
Conservative
                                                                                                                                                                                                   119
222
496
257
271
396
503
503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50001; SH2; 1
PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00017; SH2; 1.
PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XIPHOPHORUS HELLERI.
                                                                                                                                                                                                                                                                                                                                                                   392
503
507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                            LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYN_XIPHE P27446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; 1
PROSITE; 1
PROSITE; 1
                                                                                                                                                                                                                                                                                       NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                    INIT_MET
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                             LIPID
                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95210168.
CANCE W.G., CRAYEN R.J., BERGMAN M., XU L.H., ALITALO K., LIU E.T.,
"Rak, a novel nuclear tyrosine kinase expressed in epithelial cells.";
CELL GROWTH DIFFER. 5:1347-1355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DERIVED FROM TISSUES
  TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                  PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
BA03DB12 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRK_HUMAN STANDARD; PRT; 505 AA.
P42665; 013128;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE FRK (EC 2.7.1.112) (NUCLEAR TYROSINE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-i- TISSUE SPECIFICITY: RESTRICTED TO CELLS LINES DERIVED FROM TISS
OF LYMPHOID, BRAIN, BREAST, COLON AND BLADDER ORIGIN.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
-i- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 FVALYDYEARTEDDLSFRKGERFQILNSTEGDWWDARSLTT-GGSGYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEE J., WANG Z., LUOH S.-M., WOOD W.I., SCADDEN D.T.; "Cloning of FRK, a novel human intracellular SRC-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE, 93293373.

CANCE W.G., CRAYEN R.J., WEINER T.M., LIU B.T.;
CANCE Protein kinases expressed in human breast cancer.";
INT. J. CANCER 54:571-577(1993).
-!- CATALITIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                      PROTEIN KINASE.
PHOSPHORYLATION (BY PI
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 118; DB 1; I
Pred. No. 6.29e-09;
11; Mismatches 20;
                                                                         BY SIMILARITY.
MYRISTATE (BY S
PALMITATE (BY S
PALMITATE (BY S
                                                                                                                                                                                                  SH2
                                                                                                                                                                                                                                                                                                                                                                                            60316 MW;
PROTO-ONCOGENE; TRANSFERASE; ATP-BINDING; MYRISTYLATION; ELPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          29.6%;
llarity 38.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase-encoding gene.";
GENE 138:247-251(1994).
                                                                                                                                                                                                                                                                                            298
389
419
                                                                                                                                                                      142
245
523
11
284
                                                                                                                                                                                                                                                                                                                                                                                            536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LYMPHOID;
MEDLINE; 94171047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      276
298
389
419
530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASE RAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
```

```
MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
     the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
Q -> R. IN REF. 2).
C4226A83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 85213483.
ANDERSON S.K., GIBBS C.P., TANAKA A., KUNG H.-J., FUJITA D.J.;
"Human cellular src gene: uncleotide sequence and derived amino acid
"equence of the region coding for the carboxy-terminal two-thirds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 8/23/903.
TANARA A., GIBBS C.P., ARTHUR R.R., ANDERSON S.K., KUNG H.-J.,
FUJTA D.J.;
"DNA sequence encoding the amino-terminal region of the human c-src
protein: implications of sequence divergence among src-type kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 85187981.
PARKER R.C., MARDON G., LEBO R.V., VARMUS H.E., BISHOP J.M.;
"Isolation of duplicated human c-src genes located on chromosomes 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-07T-1989 (REL. 12, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 114; DB 1; Length 505;
Pred. No. 4.39e-08;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 FVALFDYQARTAEDLSFRAGDKLQVLDTLHEGWWFARHL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 AA
                                                                                                      EMBL; U00803; G392888; -.
EMBL; U2232; G732528; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTIEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PFAM; PF0017; SH2; 1.
PFAM; PF0018; SH3; 1.
PFAM; PF00169; PKinase; 1.
HSSP; P00523; 2PIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL. BIOL. 7:1978-1983(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOL. CELL. BIOL. 5:1122-1129(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 185-535 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 375-535 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.6%;
Best Local Similarity 46.2%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-184 FROM N.A. MEDLINE; 87257903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        491
262
262
354
387
1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 1
505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRC OR SRC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pp60c-src.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRC_HUMAN
P12931;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
MOD_RES
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE SOLUTION OF THE STATE OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Solution structure of the human pp60c-src SH2 domain complexed with a phosphorylated tyrosine pentapeptide.";
BIOCHEMISTRY 34:2107-2121(1995).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                   CHARIFSON P.S., SHEWCHUK L.M., ROCQUE W., HUMMEL C.W., JORDAN S.F. MOHR C., PACOFSKY G.J., PEEL M.R., RODRIGUEZ M., STERNBACH D.D., CONSLER T.G.;
                                                                                                                                                                                                                                                                                                                                     Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
                                                                                                       XU W., HARRISON S.C., ECK M.J.; "Three-dimensional structure of the tyrosine kinase c-Src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95161382.
XU R.X., WORD J.M., DAVIS D.G., RINK M.J., WILLARD D.H. JR.,
GAMPE R.T. JR.;
                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
                                                    X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 190090; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_IYR;
MOL. CELL. BIOL. 5:831-838(1985).
                                                                                                                                                                                                                                                                                                                                                                                  structural study.";
BIOCHEMISTRY 36:6283-6293(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, K03218, G338460; --
EMBL, M16237, G338460; --
EMBL, M16243; G338460; JOINED.
EMBL, M16244; G338460; JOINED.
EMBL, M16245; G338460; JOINED.
EMBL, K03212; G338460; JOINED.
EMBL, K03212; G338460; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 203-248
                                                                                                                                                              NATURE 385:595-602(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X03997; E303307; UX03998; E3033307; UX03999; E303307; UX04000; E303307; UX04000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E303307;
E303307;
E303307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K03214; G338460;
K03215; G338460;
K03216; G338460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G338460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, A26891; TVHUSC.
PDB; 1HCS; 15-SEP-95.
PDB; 1HCT; 15-SEP-95.
PDB; 1SHD; 26-JAN-95.
PDB; 1A07; 08-APR-98.
PDB; 1A07; 08-APR-98.
PDB; 1A09; 08-APR-98.
PDB; 1A18; 08-APR-98.
PDB; 1A18; 08-APR-98.
PDB; 1A18; 08-APR-98.
                                                                                                                                                                                                                                               MEDLINE; 97317069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X02647;
X03995;
X03996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K03217;
```

ဖ

```
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V-Src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
       음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          5
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH3; 1.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069; pkinase; 1.
PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 81220979.
MEDLINE: 81220979.
MEDLINE: 81220979.
MEDLINE: 81220979.
MOST D.K., SMART J.E.;
MOSTORE SPECIFICATION SITES IN transformation-specific gene products of distinct avian sarcoma viruses.";
NATURE 291:67-677 (1981).
- I- FUNCTION: THIS PHOSEPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSEPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of the viral and cellular src gene of chickens. 1. Complete nucleotide sequence of an EcoRI fragment of recovered avian Sarcoma virus which codes for gp37 and pp60src."; J. VIROL. 44:1-11(1982).
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIÀN SARCOMA VIRUS (STRAIN RASV1441).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              88 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQT-GYIPSNYVA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                      Length 535;
                                                                                                                                                                                                                                                                                                                                                                   Score 113; DB 1; Length 535
Pred. No. 7.10e-08;
14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        = ADP
                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION.
2C456535 CRC32;
                                                                                                                                                                                                   PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 83059858.
TAKEYA I., FELDMAN R.A., HANAFUSA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                  529 F
                                                                                                                                                                                                                                                                                                                                                                     h 28.3%;
Similarity 35.2%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                    144
247
522
283
297
388
419
                                                                                                                                                                                  833
150
269
297
388
4198
535 AA;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRC_AVISR
P00525;
                                                                                                                                                                                                       DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                  MOD_RES
SEQUENCE
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V-SRC.
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
   à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRC_CHTCK STANDARD, PRT; 532 AA.
P00523; Q91345; Q92013;
21-JUL-1986 (REL. 01, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAKETA T., HANAFUSA H.; "Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus."; CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ù
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAMPS M.P., TAYLOR S.S., SEFTON B.M.; "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites."; NATURE 310:589-592 (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; "Analysis of CDNAs of the proto-oncogene c-src: heterogeneity exons and possible mechanism for the genesis of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLUS GALLUS (CHICKEN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                     HSSP; POO523; 2PTK.
TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.85e-07;
15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY STMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84D2739D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111; DB 1;
                                                                                                                                                                                                                                                                                                                                                            MYRISTATE.
SH3.
SH2.
                                          PROSITE; PSO0107; PROTEIN_KINASE_ATP; PROSITE; PSO0109; PROTEIN_KINASE_IYR; PROGILI; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOL. CELL. BIOL. 11:4165-4176(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 33.3%;
18; Conservative
                                                                                                                                                                                                                                pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-18 FROM N.A. MEDLINE; 91304409.
EMBL; K00928; G210189; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAKEYA T., HANAFUSA H.;
CELL 34:319-319(1983).
                                                                                                                                                                                                                                                                                                                                  SH3 DOMAIN; SH2 DOMAIN
                                                                                                                                                                              PFAM; PF00017; SH2;
PFAM; PF00018; SH3;
PFAM; PF00069; pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83155664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 84270751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-BINDING
```

7

US-09-099-053-2-03.rsp

```
27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                         PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
244
519
111
280
294
415
                                                                                                       08-MAR-96.
07-FEB-95.
07-FEB-95.
07-FEB-95.
                                                                                                                                                                                                                  07-FEB-95
                                                                               08-MAR-96
                                                                                                                                                                                                                                           27-JAN-97
                                                                                                                                                                                                                                                                      27-JAN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
272
294
385
415
526
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID-STRUCTURE.
                                                                                                                                                           1PRM;
1RLP;
                                                                                                                                                                                                               1RLO;
1NLO;
  1SRL;
1SRM;
2PTK;
1QWE;
                                                                                                       1QWF;
                                                                                                                                   1PRL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRC_AVIST
P14085;
                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
MOD_RES
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
  PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                  PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
     SOUR SETTIFIED SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86151652.
COOPER J.A., GOULD K.L., CARTWRIGHT C.A., HUNTER T.;
"Tyr527 is phosphorylated in pp60c-src: implications for regulation.";
SCIENCE 231:1431-1434(1986).
                                                                                                                                                                                                     SMART J.E., OPPERVANN H., CZERNILOFSKY A.P., PURCHIO A.F.,
ERIKSON R.L., BISHOP J.M.;
Characterization of sites for tyrosine phosphorylation in the
transforming protein of Rous sarcoma virus (pp60v-src) and its normal
cellular homologue (pp60c-src).";
PROC. NATL. ACAD. SCI. U.S.A. 78:6013-6017(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
MEDLINE, 98070614.
WILLIAMS J.C., WEITLAND A., GONFLONI S., THOMPSON A.,
COURTNEIDGE S.A., SUPERTI-FURGA G., WIERENGA R.K.;
The 2.35 A crystal structure of the inactivated form of chicken Src:
a dynamic molecule with multiple regulatory interactions.";
J. MOL. BIOL. 274:757-775(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATRUCTURE BY NMR OF 76-139.
MEDLINE; 95063992.
FENG S., CHEN J.K., YU H., SIMON J.A., SCHREIBER S.L.;
FENG S., CHEN J.K., YU H., SIMON J.A., SCHREIBER S.L.;
Two binding orientations for peptides to the Src SH3 domain:
development of a general model for SH3-ligand interactions.";
SCIENCE 266:1241-1247(1994).
-: FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ENZYME REGULATION SECOMES ACTIVATED WHEN ITS MAJOR TYROSINE PHOSPHORYLATED. IT CAN ALSO BE PHOSPHORYLATED. IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL. AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.
-!- FOLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC--!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROPEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS AND MACROPHAGES.
                GOULD K.L., WOODGETT J.R., COOPER J.A., BUSS J.E., SHALLOWAY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU H., ROSEN M.K., SCHRELBEK S.L.;
"IH and 15N assignments and secondary structure of the Src SH3
                                                 HUNTER T.;
"Protein kinase C phosphorylates pp60src at a novel site.";
CELL 42:849-857(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 80-139. MEDLINE; 93279385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS LETT. 324:87-92(1993).
                                                                                                                                                         PHOSPHORYLATION AT TYR-415. MEDLINE; 82082387.
                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION AT TYR-526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; V00402; G63354; -.
EMBL; S43604; E75862; -.
EMBL; S43616; E75867; -.
EMBL; S43569; E75861; -.
EMBL; S43609; E75863; -.
EMBL; S43614; E75866; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S43609; E7586
EMBL; S43614; E7586
PIR; A00630; TVCHS.
MEDLINE; 86028181
```

```
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-JAN-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 87064539.
IKAWA S., HAGINO-YAMAGISHI K., KAWAI S., YAWAMOTO T., TOYOSHIWA K.;
"Activation of the cellular src gene by transducing retrovirus.";
"MUL. CELL. BIOL. 6:2420-2428(1986).
-I- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
KINANSE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-:- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
PIR; B25375; TVFVS2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIAN SARCOMA VIRUS (STRAIN S2).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                               PHOSPHORYLATION;
SH3 DOMAIN; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 111; DB 1;
Pred. No. 1.85e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59919 MW; 65406BF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557 AA
                                                                                                                                    PFAM: PF00017; SH2; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF000069; pkinase; 1.
TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE;
TRANSFERASE; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                  MYRISTATE.
PS00107; PROTEIN_KINASE_ATP; PS00109; PROTEIN_KINASE_TYR; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
```

ä

æ

```
LT 13
SRC_AVIS2
P15054;
 DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      V-SRC
                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                    g
   FFFFS
                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
7F8DAC50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKAWA S., HAGINO-YAMAGISHI K., KAWAI S., YAWAMOTO T., TOYOSHIMA K.; "Activation of the cellular src gene by transducing retrovirus."; MOL. CELL. BIOL. 6:2420-2428(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS5001; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIAN SARCOMA VIRUS (STRAIN S1).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                             86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |-|||||: | :| :| :|| :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :
                                                                                                                                                                                                                                                                                                                                                                                  Length 557;
                                                                                                                                                             TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION;
SH3 DOMAIN; SH2 DOMAIN.
LIPID 2 2 MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE; TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches 19; Indels
                                                                                                                                              TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                Score 111; DB 1; 1
Pred. No. 1.85e-07;
                                                                                                                                                                                                                   SH3.
SH2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              568 AA.
PROSITE; PS00109; PROTEÏN_KINASE_TYR; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. PROSITE; PS50001; SH2; 1. PROSITE; PS50002; SH3; 1. PFAM; PF00117; SH2; 1. PFAM; PF00018; SH3; 1. PFAM; PF00018; SH3; 1. PFAM; PF000018; SH3; 1. PFAM; PF000513; 2PTK.
   નંન
                                                                                                                                                                                              MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3.
                                                                                                                                                                                                                                                                                                                                               62582 MW;
                                                                                                                                                                                                                                                                                                                                                                                27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                     245
520
281
295
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SH2; 1
                                                                                                                                                                                                                                                                       273
295
386
416
557 AA;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 87064539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRC_AVISS
P14084;
                                                                                                                                                                                                                                                                                                          ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                       NP_BIND
BINDING
                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V-SRC.
AVIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          5;
                       ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORILARIDON (AUTO-) (BY SIMILARITY).

7F080D52 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCONNELL P.,
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (MAY-1997) TO THE PDB DATA BANK.
-!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
AND THE MAINTENANCE OF NEOPHASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN VITEO.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVIAN SARCOMA VIRUS (STRAIN PR2257).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERYK J., DEZELEE P., BARNIER J.V., SVOBODA J., NEHYBA J.,
KARAKOZ I., RYNDITCH A.V., YATSULA B.A., CALOTHY G.;
Transduction of the cellular src gene and 3' adjacent sequences
avian sarcoma virus PR257,";
J. VIROL. 63:481-492(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 146-249.
HOLLAND D.R., LUNNEY E.A., PLUMMER M.S., MUELLER W.T., MCCONNELL
PAVLOVSKY A., PARA K.S., SHAHRIPOUR A., HUMBLET C., SAWYER T.K.,
                                                                                                                                                                                                                                                                                                              86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                 .;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEĞUENCE FROM N.A.
YATSULA B.A., GERYK J., SVOBODA J., RYNDITCH A.V., CALOTHY
DEZELEE P.;
                                                                                                                                                                                               Length 568
                                                                                                                                                                                               Score 111; DB 1; Length 568
Pred. No. 1.85e-07;
15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (APR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
  PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>i - i - i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M21526; G210265; -.
EMBL; X51863; G394713; -.
PIR; A30174; TVFVPR.
PBB; BRL; C3-JUL-97.
PDB; LBKM; O7-JUL-97.
PROSITE; PSO0107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                           63632 MW;
                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  520
281
295
386
416
267
273
295
386
416
568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89094972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RUBIN J.R.;
```

```
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (C-YES).
                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
                                                                                                                                                   LIPID
                                                                                                                                 LIPID
                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                                                                                                           RESULT
            g
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i - FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS.
-i - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-i - TISSUE SPECIFICITY: THERE ARE ELEVATED LEVELS OF THIS PROTEIN IN
NEURAL AND HEMATOPOIETIC TISSUES.
                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 88DFD703 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel Yes-related kinase, Yrk, is expressed at elevated levels in neural and hematopoietic tissues."; ONCOGENE 8:823-831(1993).
                                                                                                                                                                                                                             15, Mismatches 19; Indels ... 2; Gaps
                                                                                                                                                                                                                                                                                                                                       Ö1-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YRK (EC 2.7.1.112) (P60-YRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: PHOSPHORYLATED.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO COTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                   86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                               EUKARYOTA; METÄZOA; CHÖRDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
PROSITE; PS50001; SH2; 1.

PRAM; PF00017; SH2; 1.

PFAM; PF00018; SH3; 1.

PFAM; PF00018; SH3; 1.

PFAM; PF000018; SH3; 1.

TROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE; TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN; 3D-STRUCTURE.

MYRISTATE.
                                                                                                                                                                                                         Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-BRAIN, AND KIDNEY;
MEDLINE; 91205395.
SUDOL M., GREULICH H., NEWMAN L., SARKAR A., SUKEGAWA J.,
YAMAMOTO T.;
                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                         Score 111; DB 1;
Pred. No. 1.85e-07;
                                                                                                                                                                                                                                                                                                                    535 AA
                                                                                                                                                   ATP (BY SIMIL
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                    65800 MW;
                                                                                                                                                                                                        27.8%;
llarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X67786; G63896; -.
                                                                                                                                                                                                                                                                                                                                                                                                       GALLUS GALLUS (CHICKEN).
                                                                                                         142
245
520
281
295
386
                                                                                                                                                                                                                                                                                                                                                                                   (YES RELATED KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; S29553; S29553.
; S29626; S29626.
; S33569; S33569.
                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                 148
267
273
295
386
416
587 AA;
                                                                                                                                                                                                                                                                                                                 YRK_CHICK
Q02977;
                                                                                                                                                            ACT_SITE
MOD_RES
SEQUENCE
                                                                                                        DOMAIN
DOMAIN
DOMAIN
NP_BIND
                                                                                                                                                    BINDING
          음
                                                                                                                                                                                                                                                                         ò
```

```
MEDLINE: 91187435.

HANNIG G., OTTILIE S., SCHARTL M.;

HANNIG G., OTTILIE S., SCHARTL M.;

"Conservation of structure and expression of the c-yes and fyn genes in lower vertebrates.";

ONCOGENE 6:361-386(1991).

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

PROTEIN TYROSINE PHOSPHATE.

-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ATHERINOMORPHA; CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECILLIDAE; XIPHOPHORUS.
                                                                                                                                                                        TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 FIALYDYEARTEDDLSFQKGEKFHIINNTEGDWWEARSLSS-GATGYIPSNYVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                           ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; DB 1; Length 535 Pred. No. 2.98e-07; 15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                  SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50B7CFF1 CRC32;
                                                                                                                                                                                                                                                                MYRISTATE (BY S
PALMITATE (BY S
PALMITATE (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 AA
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM: PF00017; SH2; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF00069; pkinase; 1.
PFSP: P06414; 1AOT.
PROTO-ONCOGENE; TRANSFERASE; TYROSINE-PROTE
                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54970; G64484; -. PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                          147 244

369 283

52 283

297 298

418

529

59871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
27.6%;
Best Local Similarity 35.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-RIO LANCETILLA;
MEDLINE; 91187435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XIPHOPHORUS HELLERI.
                                                                                                                                                                                                                                                                                                                                                          147
269
275
297
388
418
529
535 AA;
                                                                                                                                                                                                                      LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 15
YES_XIPHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
SEQUENCE
```

```
PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH2; 1.

PRAM: PF00017; SH3; 1.

R PFAM: PF00018; SH3; 1.

R PFAM: PF00018; SH3; 1.

R PRAM: PF00069; PKinase; 1.

R PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;

R PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;

R PRANSFRASE; ATP-BINDING; MYRISTATE (BY SIMILARITY).

T LIPID 2 153 MYRISTATE (BY SIMILARITY).

T DOMAIN 159 256 SH2.

T DOMAIN 278 531 PROTEIN KINASE.

T DOMAIN 278 531 PROTEIN KINASE.

T NP_BIND 284 292 ATP (BY SIMILARITY).

T ACT_SITE 397 BY SIMILARITY).

T ACT_SITE 397 BY SIMILARITY).

T MOD_RES 47 427 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.6%; Score 110; DB 1; Length 544; Best Local Similarity 35.8%; Pred. No. 2.98e-07; Matches 19; Conservative 10; Mismatches 24; Indels
```

97 FVALYDYEARTSDDLSFRKGDRFQIINNTEGDWWEARSINTGENGYIPSNYVA 149 g δy

ö

Gaps

; 0

Search completed: Thu May 20 12:46:07 1999 Job time: 14 secs.

•

*****	(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:46:26 1999; MasPar time 11.78 Seconds ... - 250.129-Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-099-053-2 (56-109) from US09099053.pep (3 of 6) 399 1 FLALYDFTARCGGELSVRG......ARRLSGQPSAGLVPITHVAK 54

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

sptremp19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 34.749; Variance 58.248; scale 0.597

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

Pred. No.	3.36e-09	6.32e-07	6.32e-07	1.48e-06	1.48e-06	3.47e-06	3.47e-06	3.47e-06	3.47e-06	3.47e-06	3.47e-06	8.04e-06	8.04e-06	8.04e - 06	1.85e-05	2.81e-05	2.81e-05	4.25e-05	6.41e - 05	6.41e - 05	
Description	DSRC41.	TYROSINE-PROTEIN KINAS	C-SRC TYROSINE KINASE.	B-CELL SRC-HOMOLOGY IY	B-CELL SRC-HOMOLOGY IY	NON-TYROSIN PROTEIN KI	F49B2.5 PROTEIN.	FGR MRNA.	C-SRC.	GENE C-SRC PRODUCING P	PROTEIN-TYROSINE KINAS	SRC-TYPE PROTEIN TYROS	NEURAL PRECURSOR CELL	ENHANCER OF FILMENTATI	GARDNER-RASHEED FELINE	P59FYN.	PROTO-ONCOGENE FYN.	SRC RELATED TYROSINE K	PP60-SRC PROTEIN (FRAG	(RECOVERED INSERTION M	
ei H	094879	007461	091952	061745	061364	090993	045539	063206	090992	098915	064817	077050	035177	014511	061404	016248	062844	062662	085730	085476	
DB	5	14	13	11	1	13	S	11	13	13	14	'n	디	4	11	4	11	11	14	14	
ouery Match Length DB	517	526	527	512	512	193	496	517	533	533	587	517	833	834	517	534	537	506	204	285	
Query Match	31.8	28.8	28.8	28.3	28.3	27.8	27.8	27.8	27.8	27.8	27.8	27.3	27.3	27.3	26.8	26.6	26.6	26.3	26.1	26.1	
Score	127	115	115	113	113	111	111	111	111	111	111	109	109	109	107	106	106	105	104	104	
Result No.		7	М	4	Ŋ	φ	7	ထ	6	10	11	12	13	14	15	16	17	18	19	20	

41e-	. 66e-0 . 66e-0 . 66e-0	9.66e-05 1.45e-04 1.45e-04	.31	7.31e-04 1.09e-03	1.09e-03 1.09e-03	•	n on	1.09e-03 1.62e-03	. 62	S.	S.	3.57e-03	3.57e-03
VIRAL SEQUEN	PP6USRC PROTEIN (SRC-1 SRC ONCOGENE (ISOLATE EMBRYONAL FYN-ASSOCIAT	EFS1. TYROSINE KINASE (FGR P LYN PROTEIN TYROSINE K	SH3 ADAPTOR PROTE RECEPTOR PROTEIN	BLK-PROTEIN TYROSINE K SRC.	(SCHMIDT-RUPPIN D STRA TYROSINE KINASE.	\circ	I NOSTNE	PP62V. HYPOTHETICAL 25.1 KD P		MURINE		PROTO-ONCOGENE TYROSIN	SH3-CONTAINING PROTEIN
092806 Q60567 Q85464	091851 085465 064355	043281 P78453 013064	055032	Q16291 Q85477	Q64994 Q64993	093080	086362	Q86363 O53200	085466	25	013692	386	035413
4114	13	446	11	14	14		14	14		7	4	4	11
525 526 73	113 128 560	561 177 488	377	505 523	526 526	526	545	546 238	812	206	284	1149	1196
26.1 25.1 25.8	ນ ທ ທ ໝ ໝ ໝ	0 0 C	6.6	9.4	e. e.	ω.		۳. بر	4	3.6	3.6	3.6	3.6
0000	N 101 101	0 0 0	NN	'n'n	N N	Č,	Ň	άÑ	Ñ	7	7	7	7
104	103 103 103	103	866	98	97	97	97	97 96	96	94	94	94	94
222	4.2.2 4.0.5	228 288	30	33	3.4 3.5	36	38	e 4 0 0	41	42	43	44	45

ALIGNMENTS

RESULT 1 O94879 PRELIMINARY; PRT; 517 AA.		DSRC411.		PIERYGOTA; DIPIERA; BRACHYCERA; MUSCOMORPHA; EPHYDROI	•	SEQUENCE FROM	STRAIN=CANTON S; MEDLINE: 96268448.	TAKAHASHI F., ENDO S., KOJIMA I., SAIGO K.;	"Regulation of cell-cell contacts in develor		GENES DEV. 10:1645-1656(1996).		PFAM: PF00017; SH2: 1.	PFAM; PF00018;	PFAM; PF00069; pkinase; 1.	SEQUENCE SI/ AA;	Query Match 31.8%; Score 127; DB 5; Length 517; Best Local Similarity 40.0%; Pred. No. 3.36e-09; Matches 22; Conservative 11; Mismatches 20; Indels 2; Gaps	68 FVALYDYDARTDE	: : : :	Sui	007461;	01-NOV-1996 (TREMBLREL. 01,	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-SRC).	
E C	3555	SEC	38	86	Ś 🛣	RP	2 X	RA	R	RI	R.	אַ ה ה	D E	DR	E C	กั		qq	ΩŽ	E C	A P	D	2 2	DE DE	ซี

ä

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  g
                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID DATE OF SERVICE STATE OF SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                            STRAIN=PR-RSV-C;
MEDLINE; 93254440.
RASHUBA V.I., KANSAN V.M., RYNDICH A.V., LAZURKEVICH Z.V., ZUBAK S.V.,
POPOV S.V., DOSTALONA V., HLOZANEK I.;
"Complete nucleotide sequence of Rous sarcoma virus variants adapted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XIPHOPHORUS XIPHIDIUM.
BUKARYOTA, METAZOA, CHRDATA, VERTEBRATA, ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: BUTELEOSTEI; ACRAYHOPPERYGII; ATHERINOMORPHA;
CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECILLIDAE; XIPHOPHORUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-PR-RSV-C;
KASHUBA V. I., SERGE Z.V., RYNDITCH A.V., KAVSAN V.M., HLOZANEK I.;
SUBMITTED (APPR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
KINASE THAI CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES IN
                                                                                                                                                                                                                                                                                       A.V., LAZURKEVICH 2.V., ZUBAK S.V., I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51861; G61897; --
EMBL; X68524; G61907; --
EMBL; PFOMO, SPOOLOT; SH2; 1.
PFAM; PFOOLO18; SH3; 1.
PFAM; PFOOLO69; pkinase; 1.
TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE; TRANSFERASE;
PHOSPHORYLATION; ATP-BINDING; MXRISTYLATION; SH3 DOMAIN; SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).

MYRISTATE (BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

DA81EC07 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
ROUS SARCOMA VIRUS.
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYROSINE PHOSPHATE.
SIMILARITY: BELONGS TO THE SRC FAMILY OF TYROSINE KINASES.
SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 FVALYDYESWTETDLSFKKGERLQIVNNTEGYWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 115; DB 14; Length 52
Pred. No. 6.32e-07;
16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
                                                                                                                                                                                                                                                                    STRAIN-PR-RSV-C;
KASHUBA VI., I., KAVSAN V.M., RYNDICH
POPOV S.V., DOSTALOVA V., HLOZANEK
MOL. BIOL. 27:269-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                       BIOL. MOSK. 27:436-450(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 33.3%;
Somilarity 33.3%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 PRELIMINARY;
091952;
01-00V-1996 (TREMBLREL. 0:
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
C-SRC TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (MAR-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 AA;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PR-RSV-C;
                                                                                                                                                                                        duck cells."
                                                                                                                                                                                                                                                                                                                                                                                                              ZUBAK S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XSRC.
                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
δ
```

```
ä
                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALBYC; TISSUE-MAMMARY GLAND;
MEDLINE; 95251656
THUVESON M., ALBREEHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
THUVESON M., ALBREEHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
THUYESON M., ALBREEHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;

"iyk, a novel intracellular protein tyrosine kinase differentially
expressed in the mouse mammary gland and intestine.";
BIOCHEM. BIOCHYS. RES. COMMUN. 209:582-589(1995).
EMBL. Z48757, G73624.
PROCHEM. BIOCHYS. FKY.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE; 95137395.
OBERG-WELSH C., WELSH M.;
"Cloning of BSK, a murine FRK homologue with a specific pattern tissue distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
B-CELL SRC-HOMOLOGY TYROSINE KINASE (INTESTINAL TYROSINE KINASE)
                                                                                                                                                                                                                                                                                                                                          80 FVALYDYESRTETDLSFKKGERLQILNNTEGDWWLANSLTT-GKSGYIPSNYVA 132
                                                                                                                                                                                                                                                                                                                                                                                       56 FLALYDFTARCGGELSVRRGDRLCALEEG-GGYIFARRLSGQPSAGLVPITHVA 108
                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
..
SEQUENCE FROM N.A.
STRAIN=SSP.F1, RIO SOTO LA MARINA, MEXICO;
RAULF F., SAM S., ROBERTSON S.M., MAEUELER W., SCHARTL M.;
SUBMITTED (FEB.1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X64658; G65305; -.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00068; PKINASS; 1.
SEQUENCE 527 AA; 59078 MW; 40D366A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 512;
                                                                                                                                                                                                                                             Length 527;
                                                                                                                                                                                                                                        Score 115; DB 13; Length 52
Pred. No. 6.32e-07;
13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 113; DB 11; Length 5:
Pred. No. 1.48e-06;
12; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 FVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKGTGL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 512 AA; 58928 MW; 808D1612 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                          Query Match 28.8%;
Best Local Similarity 35.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.3%;
Best Local Similarity 40.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRK OR IYK.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00017; SH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 4
Q61745
Q61745;
Q1-NOV-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ir 5
Q61364
Q61364;
```

2

,; ;;

Length 496;

SORRES

g ò

```
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTAING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDES D., SHOWNKEEN IS MALDON N., SMITH A., SONHAAMER E., STABEN R., SULSTON J.,
THERRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nuclectide sequence from chromosome III of C.
elegans.";
NATURE 368: 32-38 (1994).
EMBL: S1146996;
EMBL: S1146996;
SEQUENCE 496 AA; 56307 MW; C766F63E CRC32;
                                                                                                                                                                                                                                                                                62 FVALFQYDARTDDDLSFKKDDILEILNDTQGDWWFARH-KATGRTGYIPSNYVAR 115
                                                                                                                                                                                                                                                                                                   70 FVALYDYEARTGDDLTFTKGEKFHILNNTE-YDWWEARSLSS-GRTGYVPSNYVA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.8%; Score 111; DB 11; Le Best Local Similarity 38.2%; Pred. No. 3.47e-06; Matches 21; Conservative 12; Mismatches 18;
                                                                                                                                                                                                            Score 111; DB 5;
Pred. No. 3.47e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00069; pkinase; 1.
NCE 517 AA; 58792 MW; 285CE487 CRC32;
                                                                                                                                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-F344; TISSUE-LEUKEMIA;
YUE C.C., LABASH J.D., JAXE M.;
YUE C.C. CAPASH J.D., OA(1990).
EMBL: X57018; G56146; -
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                  D1T 8 063206 PRELIMINARY; 063206; 063206; 0603206; 01.NOV-1996 (TREMBLREL. 01, C. 01.NOV-1998 (TREMBLREL. 08, L. 01.NOV-1998 (TREMBLREL. 08, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01,
01,
08,
                                                                                                                                                                                                             27.8%;
32.7%;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL. (
(TREMBLREL. (
(TREMBLREL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ę.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 83155664.
TAKEYA T., HANAFUSA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase
                                                                                                                                                                                             Query Match
Best Local Similarity 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGR MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HANAFUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090992
090992;
                                                                                                                                                                                                                                                                                                                                                                      RESULT
       g
                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDCLINE; 90318371.

DORAI T., WANG L.H.;

LOCKAI T., WANG L.H.;

LOCKAI SKeletal muscle.";

MOL. CELL. BIOL. 10:4068-4079(1990).

EMBL; MP5290; G212706; -..

PFAM; PF00017; SH2; 1.

SEQUENCE 193 AA; 21180 MW; 85B7D527 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COULSON A.,
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 94150718.
MULSON R., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                           Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 193;
                                                                                                                                                                                                                                                                 54 FVALFDYQARTAEDLSFRAGDKLQVLDTSHEGWWLARHLE-KKGTGL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KERSHAW J.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                        Score 113; DB 11; I
Pred. No. 1.48e-06;
12; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111; DB 13; I
Pred. No. 3.47e-06;
15; Mismatches 19;
                                                                              PRAMI PF00017; SH2; 1
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 512 AA; 58891 MW; DECF53C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                  PRT; ... 1:93 A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496 AA
GENE 152:239-242(1995).

EMBL; L36122; G777773; --
MGD; MGI:103265; FRK.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 08, LAST AN NON-TYROSIN PROTEIN KINASE (C-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
,
,
,
,
,
,
,
,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%;
                                                                                                                                                                          28.3%;
                                                                                                                                                                                          Local Similarity 40.4%;
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 PRELIMINARX;
045539;
04-5539;
01-JUN-1998 (TREMBLREL. 0
01-JNN-1999 (TREMBLREL. 0
01-JAN-1999) (TREMBLREL. 0
F49B2.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                LT 6
Q90993;
Q90993;
```

Matches

g ö

RESULT

ë,

4

Indels

Length 517;

```
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                        01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 12
077050
077050;
                                                                                                                                                           064817;
                                                                                                                     LT 11.
Q64817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACSRC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                  엄
                                                                                                                                                                                                                                                                .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97008971.
WEIJLAND A., NEUBAUER G., COURTREIDGE S.A., MANN M., WIENERGA R.;
"The purification and characterization of the catalytic domain of Src
expressed in Schizosaccharomyces pombe. Comparison of
unphosphorylated and tyrosine phosphorylated species.";
EUR. J. BIOCHEM. 240:756-764(1996).
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 8315564.
TAKEYA T., HANAFUSA H.;
"Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";
CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 484-533 FROM N.A.
MEDLINE: 91304409.
DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.;
"Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
exons and possible mechanism for the genesis of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Structure and sequence of the cellular gene homologous to the RSV is gene and the mechanism for generating the transforming virus.";
                                                                                                                                                                                                                                                                                                                             86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE C-SRC PRODUCING PROTEIN PP60-C-SRC.
THIS GENE IS HOMOLOGOUS TO THE ROUS SARCOMA VIRUS GENE V-SRC (PP60C-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 533;
                                                                                                                                                                                                                          Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVI
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEILAND A.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                      Score 111; DB 13; L
Pred. No. 3.47e-06;
15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111; DB 13; I
Pred. No. 3.47e-06;
15; Mismatches 19;
                                                                                                         PROSITE, DECORATE TO THE PEAM; PF00017; SH2; 1. PFAM; PF00018; SH3; 1. PFAM; PF00069; pkinase; 1. SEGUENCE 533 AA; 60038 MW; 8E987D6B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase; 1.
AA; 60010 MW; 0D446FF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA.
              src gene and the mechanism for generating CELL 32:881-890(1983).
EMBL. J00844; G901820; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              нiн
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOL. CELL. BIOL. 11:4165-4176(1991).
EMBL; V00402; E281134; -..
EMBL; V00402; E1181088; -..
EMBL; S43579; E97011; -..
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.8%;
larity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02,
02,
08,
                                                                                                                                                                                                                          27.8%;
                                                                                                                                                                                                                                             Larity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00017; SH2; 1
                                                                                                                                                                                                                                       Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         LT 10
Q98915 PREL
Q98915; Q91343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-SRC OR C-SCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V-src.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                DDACOOS SAN THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE T
                                                                                                                                                                                                                                                                                                                                                δŏ
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA; EUECHINOIDEA;
ECHINACEA; ECHINOIDA; ECHINOMETRIDAE; ANTHOCIDARIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Origin and evolution of the c-src-transducing avian sarcoma virus PR2257.";
J. GEN. VIROL. 75:2777-2781(1994).
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                            AVIAN SARCOMA VIRUS.
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

ONODERA H., KOBARI K., SAKUMA M., SATO M., SUYEMITSU T., YAMASU
Expression of a src-type protein tyrosine kinase gene, AcSrcl,
the sea urchin embryo.";
DEV. GROWTH DIFFER. 0:0-0(1999).
EMBL; AB016815; D1034710; -.
SEQUENCE 517 AA; 58568 MW; 5A72B5C9 CRC32;
                         86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 FVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQT-GYIPSNYVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95016532.
XATSOLA B.A., GERYK J., SVOBODA J., RYNDITCH A.V., CALOTHY
DEZELEE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111; DB 14; I
Pred. No. 3.47e-06;
15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 27.3%; Score 109; DB 5; I. Local Similarity 38.7%; Pred. No. 8.04e-06; les 12; Conservative 11; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65778 MW; A02F2A78 CRC32;
                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517
                                                                                                                                      587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 YIALYDYDARSESDLSFKKGEKLEILNNTDG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::||||: || ::|| ::|::| |:: |
FLALYDFTARCGGELSVRRGDRLCALEEGGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTHOCIDARIS CRASSISPINA (SEA URCHIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TREMBLREL. 08, CREAT
OL-NOV-1998 (TREMBLREL. 08, LAST
01-NOV-1998 (TREMBLREL. 08, LAST
SRC-TYPE PROTEIN TYROSINE KINASE.
                                                                                                                                                                                01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 Match 27.8%;
Local Similarity 33.3%;
Local Similarity 33.3%;
Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
TYROSINE-PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                  (TREMBLREL.
                                                                                                                                                                                                                             (TREMBLREL
                                                                                                                                                                                                                                                    PROTEIN-TYROSINE KINASE
                                                                                                                                                                                                       (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587 AA;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-PR2257/16;
```

```
: 179 secs
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time
                          g
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                       KUMAR S., TOMOOKA Y., NODA M.; "Identification of a set of genes with developmentally down-regulated expression in the mouse brain."; BIOCHEM. BIOPHYS. RES. COMMUN. 185:1155-1161(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRUH G., GOLEMIS E.A.;
BANKS.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                  01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NEURAL PRECURSOR CELL EXPRESSED DEVELOPMENTALLY DOWNREGULATED NEDD9
                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 109; DB 11; Length 833;
larity 35.3%; Pred. No. 8.04e-06;
Conservative 14; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ALYDNVPECAEELAFRKGDILTVIEQNTGGLEGWWLCSLHGRQGIVPGNRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and function of Cas-L, a 105-kD Crk-associated substrate-related protein that is involved in beta 1 integrin-mediated signaling in lymphocytes.";
J. EXP. MED. 184:1365-1375(1996).
EMBL; L43821; G1280212; ---
EMBL; L43821; G1280787; ---
EMBL; W67317; G1490787; ---
SEQUENCE 834 AA; 92860 MW; 3F3CF55D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
MEDLINE; 97033512.
MINEGISHI M., TACHIBANA K., SATO T., IWATA S., NOJIMA Y.,
MORIMOTO C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.04e-06;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                      10 ALYDNVPECAEELAFRKGDILTVIEQNTGGLEGWWLCSLHGRQGIVPGNRV
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-SPLEEN;
HARVEY K.F., FITTER S., KUMAR S.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BYBL, AF009366; G454523; -.
PFAM; PF00018; SH3; 1.
SEQUENCE 833 AA; 92973 MW; 41A6A250 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
LAW S.F., ESTOJAK J., WANG B., MYSLIWIEC T.H.,
SUBMITIED (APR-1996) TO EMBL/GENBANK/DDBJ DATA
 PRT; 833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109;
                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 14
014511
014511;
01-00V-1996 (TREMELREL. 01, CR
01-NOV-1996 (TREMELREL. 01, LA
01-NOV-1998 (TREMELREL. 08, LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%;
35.3%;
                        (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.3%;
Best Local Similarity 35.3%;
Matches 18; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 18; Conser
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                TISSUE=SPLEEN;
MEDLINE; 92328780.
                        01-JAN-1998
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
유
                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
RESULT 15

RESULT 15

Octobrow 1996 (TREMELEE. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELEE. 01, LAST SEQUENCE UPDATE)
DE GARDER-PASHEED FELINE SARCOMA VIRAL (FGR) ONCOGENE HOMOLOG
CC-FCR MENA)

DE GARDARYOR, METAZOA, CHORDATA, VERTEBRATA; MANMALIA; EUTHERIA; RODENTIA;
CC EUKARYOTH; MURIDAE; MURINAE; MUS.
RX MEDLINE; 90191719.
RX MEDLINE; 90191719.
RA KING F.J. COLE M.D.;
RY MOLOGENE SI37-344 (1990).
DR PASH SEQUENCE FROM N.A.
RY MOLOGENE SI37-344 (1990).
DR PROSITE; PRO0109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PRO0109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM; PRO0101; SH2; 1.
DR PRAM
```

Search completed: Thu May 20 12:49:25 1999

***************************************		安全专家安全的安全的安全的 医克克克氏试验检尿病 医克格氏氏征 医克克克氏氏征 医克克克氏氏征 医克克氏氏 医克克氏虫虫 医克克氏氏 医克克氏氏征 医克克氏征 医克克氏征 医克克氏征 计记录器
******	<u> </u>	******

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:50:50 1999; MasPar time 11.20 Seconds 176.653 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-09-099-053-2 (120-212) from USO9099053.pep (4 of 6) 699 1 WYFSGVSRTQAQQLLLSPPN......LLTYYKANWKLIQNPLLQPC Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing:

summaries Minimum Match 0% Listing first 45

Database:

a-geneseg35
1:part1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 20:part10 11:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 29.030; Variance 115.410; scale 0.252 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	. :		ıc			m	~	~	~	~	~	<u>~</u>	~	~	<u>~</u>	m	m	
	N.	-61	9-15	1.5	-1	3-13	2-13	2-1	-13	9-13	3-13	3713	9-13	-1	9-13	-1-6	-13	
	Pred.	8.52e-6	.62e-	.62e-1	.62e-	.20e-	.20e-]	.20e-1	.20e-1	.20e-1	206	1.51e-1	.89e-1	.65e-	.65e-1	.83e-1	.30e-	
	2	ω.	۲	1	Ч	٦	7	Т	П	٦	Н	7	٦	4	4	Ŋ	7	
	Description	Human SAD.	Megakaryocyte kinase	Protein tyrosine-kina	pTK gene LpTK-2 prod.	Human p56-lck protein	DET1-DET2-spacer-ek-1	Human lck SH2 domain	DET1-DET2-spacer-ek-1	DET1-DET2-spacer-ek-1	FKBP-LCK: SH2 fusion p	Breast tumor kinase,	Amino acid sequence o	Amino acid sequence o	Chicken pp60 c-src pr	Amino acid sequence o	Human GRBP protein.	
)																		
	QI	W89248	R84183	R85929	R41941	W31184	W02120	W19624	W03982	W11286	W14788	R63088	W59760	W59756	R39705	W59763	W76830	
	DB	39	15	14	ω	56	18	24	21	23	21	12	33	33	œ	33	37	
	Query Match Length DB	488	298	502	502	101	134	134	134	134	224	451	86	86	533	86	330	
	ch	0.	?	?	7	'n	ī.	ī,	r.	ທ	Ŋ	34.3		33.6	33.6	.5	۳.	
dР	Ouery	100.0	37	37	37	34	34	34	34	34	34	34	34	33	m	m	m E	
	Score	669	260	260	260	241	241	241	241	241	241	240	239	235	235	234	233	
	Result No.	Н	7	m	4	ហ	φ	7	ω	თ	10	11	12	13	14	15	16	

77 7 7 7 7 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9	.78e-0 .34e-0 .34e-0
ino acid sequence k SH2 region. Tal oacid sequence man src SH2 domain T1-DET2-spacer-ek-T1-DET2-spacer-ek-T1-DET2-spacer-ek-T1-DET2-spacer-ek-T2-EK-T	SH2 domain from human SH2 domain from human Human protein-tyrosin
W59757 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090 W72090	თ თ თ თ
10000000000000000000000000000000000000	101
102 102 130 130 130 130 130 130 106 106 106 117 1114 1217 1217 1217 1217 1217 1217	117 112 593
	27 27 27
22222222222222222222222222222222222222	თთთ
11112222222222222222222222222222222222	

ALIGNMENTS

RESI ID AC	RESULT 1 ID W89248 standard; Protein; 488 AA. AC W89248;
H	10-MAR-1999 (first entry)
ΩE	Human SAD.
ΚW	PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
ΚW	type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
ΚW	neurodegenerative disease; neuronal survival; Alzheimer's disease;
X	Parkinson's disease; Huntington's disease.
SO	Homo sapiens.
PN	WO9849317-A2.
D D	
ΡF	-
PR	
PR	-
P.R	
PR	
PR	11-JUN-1997; US-049756.
PR	18-JUN-1997; US-049914.
ΡA	(SUGE-) SUGEN INC.
ΡI	App H, Clary D, Courtneidge SA, Hui TH, Jallal B,
ΡI	Markby D, Onrust S, Peles E, Plowman GD;
DR.	WPI; 99-009434/01.
DR	N-PSDB; V81743.
Εď	New nucleic acid encoding specific protein tyrosine phosphatases -
Τď	
ΡŢ	prevention of cancer and neurodegenerative disease
PS	Claim 2; Page 154-155; 193pp; English.
ပ္ပ	The present invention describes isolated, enriched or purified nucleic
ပ္ပ	acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
8	present sequence represents human SAD. The above proteins, other than
<u> </u>	ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
ပ္ပ	substances that modulate their activity (i.e. agonists and antagonists,
ပ္ပင္ပ	including NBP) in vivo or in vitro. These substances are used to treat
2	or prevent diseases associated with abnormal signal transduction
ပ္ပင္ပ	pathways that involve the proteins, particularly cancer (e.g. leukaemia
2 5	and lymphomal, while modulators of ALK-/ (which is a type I receptor
ع ر	Setting Unitedizing Aliasof ale used. To promice mentions and vivat, particularly for treating Aliabeims's Darkinson's or Huntington's
) כ	diseases Nucleic acid fragments to the bolynucleotides encoding the
)	

a

```
14-FEB-1996 (first entry)
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                    116 wffgaigrsdaekqllysenktgsfliresesqkgefslsvldgavvkhyrikrldeggf 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New POLY: nucleotide(s) encoding megakaryocyte tyrosine kinase(s) - used to develop prods. for the treatment and diagnosis of kinase related signal transduction abnormalities.

Claim 19; Fig 3A; 82pp; English.

Human megakaryocyte kinase MKK3 (R84183) is a 58 kDa cytosolic tyrosine kinase showing 47% homology with fyn. Recombinant MKK3 can be produced in host calls by expression of encoding cDNA (T00618), and used in the treatment and diagnosis of e.g. leukaemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                 ö
                                                                                                                         Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoplasmic tyrosine kinase; leukaemia; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 260; DB 15; Length 29
Pred. No. 1.62e-15;
23; Mismatches 23; Indels
                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Catalytic_domain
/note= "N.B. the sequence is incomplete;
Fig 3B is missing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-RN-1995; U05008.
22-ARR-1995; US-232545.
21-APR-1995; US-426509.
21-APR-1995; US-426509.
(SUGE-) SUGEN INC.
(SUGE-) SUGEN INC.
(SIGE-) SUGEN INC.
MPI: 95-382959/49.
N-PSDB; T00618.
                                                                                                                       Score 699; DB 39;
Pred. No. 8.52e-61;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56..113
/label- SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123..202
/label= SH2_domain
247..305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 3
R85929 standard; Protein; 505 AA.
R85929;
                                                                                                                                                                                                                                                                                                                                                                                77 2
R84183 standard; Protein; 298 AA.
R84183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Megakaryocyte kinase MKK3.
Megakaryocyte kinase-3, MKK3.
cellular signal transduction;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%;
larity 41.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 fltrrrifstlnefvshy 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 YLQKGRLFPGLEELLTYY 197
                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 32; Conserv
                                                                                 488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9529185-A1
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                    SOURCE SELECTER SERVICE SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
  866666
                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                              ô
```

```
N-PSDB; T03097.

N-PSDB; T03097.

Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation Disclosure; Pages 56-58; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. A LpTK2 gene (T03097) was isolated from lymphocytic and megakaryocytic cell libraries. The encoded novel pTK, LpTK2 (R65929), shows homology to known pTKs, and can be used to design drugs that modulate pTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 wffgaigrsdaekgllysenktgsfliresesqkgefslsvldgavvkhyrikrldeggf 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pTK; protein tyrosine kinase; catalytic domain; c-kit; megakaryocyte;
lymphocyte; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein tyrosine kinase genes and proteins encoded by genes are of human mega-karyocytic origin claim 3; fig 5; 60pp; English.

Claim 3; Fig 5; 60pp; English.

PTK genes were identified using two sets of degenerative oligonucleotide primers: a first set which amplifies all pTK DNA segments (Q4974-44), and a second set which amplifies highly conserved sequences present in the catalytic domain of the c-kit subgroup of pTKs (Q4974-66). The pTK genes identified are described in Q49747-57 and R41897-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The LpTKs are expressed in lymphocytic cells, as well as megakaryocytic cells. The partial and full-length LpTK2 gene sequences are given in Q49749 and Q49784 respectively. The protein sequence corresp. to Q49749 is claimed (claim 7) and stated as given in the specification, however is missing from the publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 260; DB 14; Length 505;
Pred. No. 1.62e-15;
23; Mismatches 23; Indels
               Protein tyrosine-kinase; PTK; LpTK2; agonist; cell growth; differentiation.
                                                                                                                                                                                                                                                                       SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                          Matthews W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowley S, Groopman J, Scadden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
                                                                                                                                                                                                                                                                          Lee JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
Protein tyrosine-kinase LpTK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 4
R41941 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%;
Local Similarity 41.0%;
Les 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 fltrrrifstlnefvshy 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| : |:|: |:|: |
180 YLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R41941;
10-MAR-1994 (first_entry)
                                                                                                                                             12-OCT-1995.
04-APR-1995; U04228.
04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1993.
22-JAN-1993; U00586.
22-JAN-1992; US-826935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pTK gene LpTK-2 prod.
pTK; protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 93-320330/40.
N-PSDB; Q49754.
                                                                                                                                                                                                                                                                                                                                   WPI; 95-366160/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA;
                                                                                    Homo sapiens.
WO9527061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9315201-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avraham H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

Ö,

"defined epitope tag from HIV-1 gp120/160"

Location/Qualifiers

2..12 /label= DET1

'note-

"hexahistidine tag'

note-

19..21 /label- Spacer /label DET2

22..26 /label= EK .130

/note= "enterokinase cleavage site"

 \sim

```
Homo sapiens;
synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-727211-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1996
      Chimeric F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                           region
                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                  Key
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of autoimmune oisease and for T and B cell proliferation,
T. Feathert of autoimmune oisease and for T and B cell proliferation,
This sequence represents the B56-lck SH2 binding domain which is
Capable of binding the p62 sequences represented in W3182 and
Capable of binding the p62 sequences represented in W3182 and
W3183 in a phosphotyrosine (P7) independent manner. Such p62
CC Gapable of modulating T or B cell
CC Gativity. They are also capable of modulating degradation of Lck
CC activity. They are also capable of modulating expression of
CC cativity. They are also capable of modulating expression of
CC cativity. They are also babble of modulating expression of
CC cativity. They are this is benefit and arresting cell cycle
CC cativity. They are also benefit benefit and arresting cell cycle
CC protection at specific boundaries to thereby modulate cell
CC proliferation. As p62 acts to boost B cell response and may be used to
CC treat disorders where this is benefitial, e.g. infections pathogenic
CC expand T cell populations for treating infectious diseases or cancer,
CC expand T cell populations for treating infectious diseases or cancer,
CC e.g. the resulting cells may be transduced to render them resistant to
CH IV infection. Inhibitors of p62 can be used to reduce B or T cell
CC responses and may be used to treat a variety of autoimmune diseases, e.g.
CANNOT All and CONNOT All and 
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulation;
p56-lck;
                                                                                                                   116 wffgaigrsdaekqllysenktgsfliresesqkgefslsvldgavvkhyrikrldeggf 175
                                                                                                                                                    120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| :|| :|| :|| :|| ||:|| || || || ||: ||:||||| ||: ||:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 wffknlsrkdaergllapgnthgsfliresestagsfslsvrdfdqnqgevvkhykirnl 60
                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .28-OCT-1996 (first entry)
DETI-DETI-Spacer-ek-1ck SH2 construct.
Bone resorption disease; Osteoporosis; src SH2 domain antagonist; src homology 2 domain; lck SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wallew;
11-MAR-1998 (first entry)
11-Man p56-lck protein SH2 domain.
p62; cytoplasmic; T cell; B cell; development; activation; r
cellular response; cell proliferation; autoimmune disease; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 241; DB 26; Length 101;
Pred. No. 1.20e-13;
21; Mismatches 31; Indels '
Length 505;
                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-1996; U19944.
19-DEC-1995; US-574959.
(DAND ) DANA FARBER CANCER INST INC.
Joung I, Shin J, Strominger JL, Vadlamudi RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 260; DB 8; 1
Pred. No. 1.62e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 98
                                                         23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  T
W31184 standard; Protein; 101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 6
W02120 standard; Protein; 134 AA.
                                                                                                                                                                                                                                                                  :| : |:|: |:|: |
180 YLQKGRLFPGLEELTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%;
                                                                                                                                                                                                                                    176 fltrrrifstlnefvshy 193
Query Match
Best Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 40.4%;
Matches 40; Conservative
                                                            32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-341351/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9722255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W02120;
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K K B B B B B
                                                                                                                   셤
                                                                                                                                                                             ö
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA----QAKVC-HYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 wffknlsrkdaergllapgnthgsfliresestagsfslsvrdfdqnggevvkhykirnl 90
                                                                                                                                                                                                                                                                         WPI; 96-372674/38.
Use of selective src SH2 domain ligand - to prepare medicament for treating bone resorption disease
Example 11; Page 28-29; 47pp; English.
Construct DET1-DET2-spacer-ek-1ck SH2 (W02120) was obtd. by
Inserting a PCR fragment (see also T36190-91) coding for human lck
SH2 domain into a vector contg. a tagged chicken src gene
DET1-DET2-spacer-SH2 (see also T36186-87). The construct can be
expressed in E. coli and used, together with similar constructs (see
also W02119-21 and W02124-27), in binding assays to determine the
specificity of cpds. to inhibit SH2 domains; cpds. that selectively
inhibit the human src SH2 domain are useful in treating bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W19624;
27-007-1997 (first entry)
Human lck SH2 domain fusion protein.
Stat 5; Signal Transduction and Activation of Transcription;
Src homology domain; SH2; erythropoiesis enhancing; anaemia;
fusion protein; ek; entercokinase; epitope; antibody production;
detection; HIV; human immunodeficiency virus type 1; gpl20;
glycoprotein 120; selective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "defined epitope tag 1 from HIV gp120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13..18
/note= "hexahistidine sequence tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 241; DB 18; L. Pred. No. 1.20e-13; 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resorption diseases such as osteoporosis. Sequence 134 AA;
/label- lck-SH2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                        07-FEB-1996; 200270.
10-FEB-1995; US-386381.
07-MAR-1995; US-400220.
30-JUN-1995; US-497357.
11-OCT-1995; US-541080.
29-DEC-1995; US-5810868.
(SMIK.) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W19624 standard; Protein; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19..21
/label= spacer
22..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.4%;
Matches 40; Conservative
                                                                                                                                                                                                                                                          Dunnington DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
```

4

```
peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                               Matches
                                                                                                                                 셤
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                            Enhancing erythropolesis with specific activator of human Stat 5 SH2 domain - has very low binding affinity to other SH2 domains so free domain - has very low binding affinity to other SH2 domains so free cost side effects, particularly for treating anemia Example 11; Page 54-55; 91pp; English.

W19624 is a fusion protein of formula DET1-DET2-Sp-ek-SH2, where DET1 is a defined epitope tag from HIV-1 gpl20, DET2 is a hexalistidine sequence tag (binds to nickel-containing resins, used for purification). Sp is a spacer, ek is an enterokinase protease recognition site and SH2 is the human lck SH2 domain. DET1 is included so that antibodies against the epitope can be used to detect the recombinant expression of the fusion protein and hence the SH2 domain. The fusion proteins are used for identifying compounds that bind the SH2 domain causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 28-29; 46pp; English.

This sequence represents the DETI-DETI-spacer-ek-lck SH2 construct encoded by the sequence amplified by the primers given in T37297-98. This protein fragment was used in the isolation of a compound for improving erythropoiesis. The compound may be used for the treatment of anamaia or to enhance haematopoiesis. The isolated compound antagonises the hcp SH2 domain without side effects caused by non-specific inhibition of other SH2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 wffknlsrkdaerqllapgnthgsfliresestagsfslsvrdfdqnqgevvkhykirnl 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of selective antagonist of haematopoietic acid phosphatase SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain - with no significant affinity for other SH2 domains, to increase erythropoiesis and haematopoiesis, esp. for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerase chain reaction; PCR; amplify; primer; chicken; src; SH2 domain; DET1; DET2; erythropolesis; anaemia; haematopolesis;
"enterokinase protease recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241; DB 24; L/Pred. No. 1.20e-13; 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1997 (first entry)
DET1-DET2-spacer-ek-lck SH2 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1996.
07-FEB-1996; 200269.
10-FEB-1995; US-386381.
07-MAR-1995; US-400220.
30-JUN-1995; US-497357.
11-OCT-1995; US-540680.
29-DEC-1995; US-581089.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                        30-JUN-1995; US-497357.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W03982 standard; Peptide; 134 AA
                          27..134
/note= "lck SH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 40.4%;
Matches 40: Concomment
   /note=
                                                                                                                                                         28-JUN-1996; U11158.
38-FEB-1996; US-598715.
                                                                                                                                                                                                                                                                                       Dunnington DJ;
WPI; 97-108736/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96-386024/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP-728482-A2.
                                                                                         WO9702024-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunnington DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anaemia
                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
   ò
```

```
Example 11: Page 51-52: 88pp; English.

Example 11: Page 51-52: 88pp; English.

Wil285-Wil288 represent fusion proteins containing Src homology 2 (SH2)

Wil285-Wil288 represent fusion proteins containing Src homology 2 (SH2)

Comains. These sequences are used to identify a compound that targets the human Stat (signal transduction and activation of transcription) 6 SH2

Commain. The identified compound activation of transcription) 6 SH2

Compound has an affinity for the human Stat5

SH2 GM2 SH2, Src SH2, Ick SH2 or Fyn SH2 of more than 50 (preferably 100) times lower than its affinity for hcg SH2, SH-PPP2 SH2, p85

COMPOUND SH2, Src SH2, Ick SH2 or Fyn SH2 of more than 50 (preferably 100) times lower than its affinity for Stat 6 SH2. SH2 domains are conserved non-catalytic sequences found in a variety of signaling molecules, such as non-receptor protein tyrosine kinases, and in occopanic proteins. The compounds identified using the fusion proteins

Comcogenic proteins. The compounds identified using the fusion proteins are used as the administered compound in the method of the invention for treating allergic reactions. Administration of the compound avoids the side effects (e.g. reduced erythrocyte production) associated with consecution inhibition of SH2 domains rather than all 60 known domains. Companies are be used for the treatment of asthma and allergic rhintits, but can also be used to treat atopic dermatitis. Inhibition of the human companies in terleuxin-4 (iL-4) or IL-13.
                                                                                                                                                                                                                                                                                                                                           DET.-DET2-spacer-ek-lck SH2 fusion protein.

DET1-DET2-spacer-ek-lck SH2 fusion protein.

HIV-1; gpl20; defined epitope tag; DET1; envelope protein; human; Stat 6; signal transduction and activation of transcription; Src homology 2; signalling molecule; protein tyrosine kinase; oncogenic protein; hcp SH2; signalling molecule; protein tyrosine production; inhibitor; p85 SH2; asthma; allergic rhinitis; atopic dermatitis; IgE receptor; SH-PTP2 SH2; interleukin-4; IL-4; SH2 domain; Stat5 SH2; src SH2; lck SH2; fyn SH2;
                                                                                                               31 wffknlsrkdaergllapgnthgsfliresestagsfslsvrdfdqnggevvkhykirnl 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "enteroprotein kinase recognition sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating allergies with specific inhibitor of human Stat 6 SH2 domain - having very low binding affinity to panel of other SH2 domains so free of side effects, specifically for asthma and
                                            7;
  Length 134;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "defined epitope tag 1 (DET1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "defined epitope tag 2 (DET2)"
                                               31;
                                                                                                                                                                          91 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 128
                                                                                                                                                                                                     Pred. No. 1.20e-13;
21; Mismatches 31
    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "human lck SH2 domain"
    Score 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                       W11286 standard; peptide; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK) SMITHKLINE BEECHAM CORP. Dunnington DJ; WPI; 97-108735/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL-13; therapy; fusion protein.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "spacer"
h 34.5%;
Similarity 40.4%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27..134
/note= "1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
22..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1996; US-598716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1995; US-49735
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-1997.
28-JUN-1996; U11074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergic rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9702023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
```

Query Match

요 ò g ò

```
W59760;
W59760;
M2-OCT-1998 (first entry)
Amino acid sequence of the SH2 domain src mutant M2.
SH2 domain; signal transduction protein; cancer; SH2 domain src; tumour;
phosphorylation; breast cancer; ovarian cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1998.
16-SEP-1994; UG-308086.
16-SEP-1994; UG-308086.
(UNIW ) UNIV WASHINGTON SCHOOL MED.
Shaw A, WASKman G;
WPI: 98-46608/37.
Modified SH2 domains of intracellular proteins - useful for inactivating signal transduction proteins in the treatment of e.g. cancer, or for targetting specific SH2 domains for diagnostics Example 2; Column : 22pp; English.
This is the amino acid sequence of a SH2 domain src mutant M2, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 wffgcisrseavrrlqaegnatgaflirvsekpsadyvlsvrdtqavrhykiwrraggrl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 29-31; 52pp; English.

A brk (breast tumor kinase) cDNA fragment was used to screen a cDNA library prepared from human breast tumor cell line T-47D. 2 cDNAs were isolated. The silghtly longer clone lambda-t2 (Q8189) encoded brk (R63088), which was identified as a novel putative non-receptor kinase of use as a prognostic/diagnostic of breast
                                                                                                                                                                                                                                                                                                                                                           /note= "potential regulatory tyrosine equivalent to Tyr-527 of c-src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel protein tyrosine kinase and its DNA - isolated from huma breast tumour, useful for diagnosis and prognosis of cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                            /note= "corresponds to the strong indicator sequence of PTK specificity in subdomain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
                                                                                                                                                                                                                                                                                                   /note= "putative autophosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 240; DB 12; Length 451
Pred. No. 1.51e-13;
16; Mismatches 39; Indels
                                                       .203
:e= "putative ATP binding domain"
                                  "similar to PTK SH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kamalati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 hlneavsflslpelvnyhrag-slshglrlaapc 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 YLOKGRLFPGLEELLTYYKANWKLION-PLLOPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CANC.) CANCER RES INST.
(WELL.) WELLCOME FOUND LTD.
Barker KT, Crompton MR, Gusterson BA,
Mitchell PJ, Page MJ, Spence P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "SH2 domain src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥Ÿ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       т 12
W59760 standard; peptide; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.4%;
Matches 37; Conservative
                                                                                                    /note= "F
312..317
78..169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JAN-1995.
08-JUL-1994; G01479.
09-JUL-1993; GB-014233.
11-MAR-1994; GB-004817.
                                      /note-
                                                                                                                                                                                                                                                                                                                                   misc_difference 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 95-066901/09.
N-PSDB; 081189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor metastasis
                                                              binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9502057-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5786454-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergies.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                    domain
   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport 10.75 (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75) (10.75
                                                                                                                                                                      125 wffknlsrkdaergllapgnthgsfliresestagsfslsvrdfdqnggevvkhykirnl 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA----QAKVC-HYRVSMA 174
                                                                                                                             31 wffknlsrkdaergllapgnthgsfliresestagsfslsvrdfdqnggevvkhykirnl 90
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W14788;
20-JUN-1997 (first entry)
FKBP-LCK:SH2; Fusion protein; SH2 domain; Src homology 2;
Fusion protein; high throughput assay; signal transduction; ligand;
microscintillation.
                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 241; DB 21; Length 22
Pred. No. 1.20e-13;
21; Mismatches 31; Indels
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1995 (first entry)
Breast tumor kinase, DrK.
Breast tumor kinase, DrK.
protein-tyrosine-kinase; PTK;
breast cancer; metastasis; prognosis; diagnosis; T-47D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "similar to PTK SN3 domain"
                                                                  21; Mismatches 31;
                                                                                                                                                                                                                                                                 91 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 dnggfyi-spritfpglhelvrhytnasdglctrlsrpc 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                               175 ADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
Score 241; DB 23;
Pred. No. 1.20e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-1997.
11-SEP-1996. U14567.
15-SEP-1995. US-003819.
12-MAR-1996. GB-005210.
(MERI ) MERCK & CO INC.
Marcy A, Sallowe SP, Wisniewski D;
WPI: 97-202171/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .T 11
R63088 standard; Protein; 451 AA.
R63088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W14788 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.5%;
34.5%;
40.4%;
                                                                  40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 4
                           Best Local Similarity
Matches 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9710253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
```

A COUNTY OF THE PART OF THE PA

domain

RESULT ID R6 AC R6 DT 12 DDE BI KW BI KW DI KW DI CS HC FT GC

엄

ò

ò

ä

Gaps

```
in the treatment of e.g. cancer, or for targetting specific SH2 domains in the treatment of e.g. cancer. Or for targetting specific SH2 domains for diagnostics. The modified Src SH2 domain is useful as a research tool to study signal transduction in general and for a variety of applications such as diagnostics, therapeutics, and drug design. It detects aberrant phosphorylation events including those associated with tumnour progression of breast and ovarian carcinomas for tumnour to treat disorders resulting from aberrant signal transduction pathways to treat disorders resulting from aberrant signal transduction pathways to treat associated by the signal transduction protein prevents further transmission of the signal transduction protein prevents curve binds to an aberrant signal transduction protein thereby blocking the binding of the wild type SH2 domains, or inactivates the phosphorylated signal transduction protein by removing a phosphate group. This sequence is not given in the specification, but is created using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and staging. It interferes with signal transduction pathways to treat disorders resulting from aberrant signal transduction pathways such as cancer, autoimmune disease, and allergies. Interference with the signal generated by the signal transduction protein prevents further transmission of the signal to other components of the cell. It also binds to an aberrant signal transduction protein thereby blocking the binding of the wild type SH2 domains, or inactivates the phosphorylated signal transduction protein by removing a phosphate group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W59756 standard; peptide; 98 AA.
W59756,
12-0cT-1998 (first entry)
12-0cT-1998 (first entry)
And no acid sequence of the SH2 domain src.
SH2 domain; signal transduction protein; cancer; SH2 domain src; tumour; phosphorylation; breast cancer; ovarian cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                     1 wyfgkitrreserlllnpenprgtflvresettkgayclsvsdfdnakglnvkhykirkl 60
                                                                                                                                                                                                                                                                                                                                                               Gaps
method of the invention to inactivate signal transduction
                                                                                                                                                                                                                                                                                                                            Length 98;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                             28; Mismatches 30;
                                                                                                                                                                                                                                                                                                                            Score 239; DB 33;
Pred. No. 1.89e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ADGSLYLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 dsggfyitsrtqfsslqqlvayyskhadlachrltnvc 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..98
/note= "SH2 domain src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                           and information provided
                                                                                                                                                                                                                                                                                                                            34.2%;
35.7%;
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 35.7%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5786454-A.
28-JUL-1998.
16-SEP-1994; 308086.
                                                                                                                                                                                                                                                                                           98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergies
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                        W59756,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
5555555555555555555
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δŏ
```

```
ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1998 (first entry)
Amino acid sequence of the SH2 domain src mutant M3.
SH2 domain; signal transduction protein; cancer; SH2 domain src; tumour; phosphorylation; breast cancer; ovarian cancer; autoimmune disease;
                                                                                                                                                    148 wyfgkitrreserllInpenprgtflvresettkgayclsvsdfdnakglnvkhykirkl 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn bisclosure; Page 64-66; 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46687) is used to transform endothelial have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angloplasty, heart bypass surgery, vessel graft and stent
                                                                                                                  1 wyfgkitrreserlllnpenprgtflvresettkgayclsvsdfdnakglnvkhykirkl 60
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
.,
                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 235; DB 8; Length 533;
Pred. No. 4.65e-13;
26; Mismatches 20; Indels
Length 98,
                                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1993 (first entry)
Chicken pp60 c-src protein.
Endothelial, tyrosine kinase protein, pp60 c-src; ss.
                                 Pred. No. 4.65e-13;
   DB 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bell L, Luthringer DJ, Madri JA, Warren SL;
WPI; 93-243209/30.
                                                         26; Mismatches
Score 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "SH2 domain src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 dsggfyitsrtqfsslqqlvayy 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                   T 14
R39705 standard; Protein; 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .r 15
W59763 standard; peptide; 98
                                                                                                                                                                                                                                     61 dsggfyitsrtqfsslqqlvayy
                                                                                                                                                                                                                                                                         175 ADGSLYLQKGRLFPGLEELLTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%;
   33.6%;
38.6%;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1998.
16-SEP-1994; 308086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus.
WO9314193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R39705
                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5786454-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         R39705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W59763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
ID WS
MD WS
DT 122
DE AM
KW PH
KW PH
KW AB
CS SY
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF RE
FF R
                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                               δλ
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
```

```
Parameter of for transduction proteins - useful for modified SH2 domains of intracellular proteins - useful for modified SH2 domains of intracellular proteins in the treatment of e.g. rancer, or for targetting specific SH2 domains for diagnostics cancer, or for targetting specific SH2 domains for diagnostics. The method of the invention to inactivate signal transduction proteins to the method of the invention to inactivate signal transduction proteins in the treatment of e.g. cancer, or for targetting specific SH2 domains of for diagnostics. The modified Src SH2 domain is useful as a research tool to study signal transduction in general and for a variety of applications such as diagnostics, therapeutics, and drug design. It capplications such as diagnostics, therapeutics, and drug design. It capplications such as diagnostics, therapeutics, and drug design. It capplications are aberrant phosphorylation events including those associated with tumour progression of breast and ovarian carcinomas for tumour cumour progression of breast and ovarian carcinomas for tumour cumour progression of breast and ovarian carcinomas for tumour cumour progression of breast and ovarian tansduction protein prevents such as cancer, autoimmune disease, and allocation protein thereby blocking the binding of the wild type SH2 domains, or inactivates the call of the wild type SH2 domains, or inactivates the phosphorylated signal transduction protein by removing a phosphate group. This sequence is not given in the specification, but is created using Sequence 18 AA;
16-SEP-1994; US-308086.
(UNIW ) UNIV WASHINGTON SCHOOL MED.
Shaw A, Waksman G;
```

ώ, 1 wyfgkitrreserlllnpenprgtflvresettkgayclsvsdfdnakglnvkhykirkl 60 Score 234; DB 33; Length 98; Pred. No. 5.83e-13; 26; Mismatches 20; Indels 5; Gaps Query Match 33.5%; Best Local Similarity 38.6%; Matches 32; Conservative q

61 dsggfyfssrtqfsslqqlvayy 83 අ

ò

175 ADGSLYLQKGRLFPGLEELLTYY 197

δ

Search completed: Thu May 20 12:53:20 1999 Job time : 150 secs.

*		*
* * * * *	(MI)	*****
* * * *		****
****	<u> </u>	*****
******		*******
***************************************		*************************************
****		******
*****		*******
****	[*****
****		******
* * *		***

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 12:53:40 1999; MasPar time 9.55 Seconds 364.544 Million cell updates/sec Tabular output not generated. Run on:

Title:

>US-09-099-053-2 (120-212) from US09099053.pep (4 of 6) 699 1 WYFSGVSRTQAQQLLLSPPN......LLTYYKANWKLIQNPLLQPC 93 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

116695 seqs, 37453910 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 39.723; Variance 76.072; scale 0.522 Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	61e-	kina 8.61e-1	kina 1.29e-	kina 3.	kina 6.	kina 1.	kina 7.	kina 1.	se 2.94e-26	kina 2.	kina 1.10e-2	ine kina 1.10e-25	ine kina 1.10e-25	kina 1.10e-2	kina 2.	kina 2.64e-2	ine kina 4.09e-25	kina 4.	ine kina 9.81e-25	ine kina 9.81e-25	ine kina 1.52e-24	- Rous 1.52e-24	1 500.0
0	Description		protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	p56-tck - mouse	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	pp62v protein	2000
	ΩI	156322	A56040	I49552	S24553	S24550	I38396	OKHULK	849016	I48845	A23639	TVFV60	TVCHS	TVFVS2	TVFVPR	TVHUHC	I51593	TVHAST	TVFVS1	A40092	JQ1321	TVFVMT	S52313	252211
	DB	7	~	~	7	7	~	Н	7	7	7	,	Н	Н	н	H	7	Н	Н	~	~	Н	~	c
	Length	496	496	512	206	505	505	509	451	509	509	526	533	557	587	505	544	509	568	499	503	523	545	276
эÞ (Query	89.4	89.4	39.5	38.5	37.5	37.2	34.5	34.3	34.0	•	•	33.6	33.6		•	33.3			٠	32.9	ς.	'n.	32 8
	Score	625	625	276	269	262	260	241	240	238	238	235	235	235	235	233	233	232	232	230	230	229	229	229
	No.	н	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

	32.5 503 1 TVWSHC protein-tyrosine kina 3 63e-24 32.5 528 1 TVCHYS protein-tyrosine kina 3 63e-24 32.3 526 1 TVCHYS protein-tyrosine kina 3 63e-24 32.3 526 2 S2008 protein-tyrosine kina 5 62e-24 32.3 526 1 OKEVYR protein-tyrosine kina 5 62e-24 32.2 537 2 A45501 protein-tyrosine kina 8 69e-24 32.2 541 2 TVHUSC protein-tyrosine kina 8 69e-24 32.0 529 1 TVHUSC protein-tyrosine kina 8 69e-24 32.0 529 1 TVHUSC protein-tyrosine kina 1.34e-23 31.9 507 2 A39939 protein-tyrosine kina 2.07e-23 31.9 526 2 S15582 protein-tyrosine kina 2.07e-23 31.8 228 2 S25730 sem-5 protein-tyrosine kina 2.07e-23 31.6 541 2 A5152 protein-tyrosine kina 2.07e-23 31.5 543 1 TVHUYS protein-tyrosine kina 7.62e-23 31.5 543 1 TVHUYS protein-tyrosine kina 7.62e-23 31.3 1123 2 A59562 protein-tyrosine kina 1.18e-22 31.3 1130 1 TVHUA SH2-SH3 adaptor protein 1.18e-22 31.3 1130 1 TVHUA SH2-SH3 adaptor protein 1.18e-22 31.0 217 2 A55962 protein-tyrosine kina 2.79e-22 31.0 1182 2 A35962	ALIGNMENTS	15632 #type complet. srm - mouse #formal_name Mus musculu 26-Jul-1996 #sequence_re 156322 156322 Kawachi, Y.; Nakauchi, H J. Invest. Dermatol. (19 Identification of a nove tyrosine kinase in mur	IS63 Ltype Ltype steren #sup ki	Similarity 82.8%; Pred. No. 8.61e-106; 77; Conservative 11; Mismatches 5; Indels 0; Gaps 0; SGISRAQAQQLLLSPANAPGAFLIRPSESSIGGYSLSVRAQAKVCHYRICMAPSGSL 183 : : : : :	LOEGOLFPSLDALLAYYKTNWKLIQNPLLOPC 216 - -	A56040 #type complete protein-tyrosine kinase (EC 2.7.1.112) Srm, nonreceptor type - mouse #formal_name Mus musculus #common_name house mouse 01-bc-1995 #sequence_revision 01-bc-1995 #text_change 12-un-1998 A56040 A56040
SUM PER SUM PACC CLA PER SUM PACC CLA PER SUM PACC CLA PER SUM PACC PACC PACC PACC PACC PACC PACC PAC	420180040445018004644		ESULT NTRY ITLE RGANISN ATE CCESSIC EFERENC # jour #tit]	#accessic ##stat ##stat ##cros LASSIFICATI 62-111 232-491 240-248	Ouery Match Best Local Matches 124 WYF	184 Y 180 Y	ESULT NTRY ITLE RGANISM ATE CCESSIONS

~

```
ö
Kohmura, N.; Yagi, T.; Tomooka, Y.; Oyanagi, M.; Kominami, R.; Takeda, N.; Chiba, J.; Ikawa, Y.; Aizawa, S. Mol. Cell. Bioll. (1994) 14:6915-6925
A novel nonreceptor tyrosine kinase, Srm: cloning and
                                                                                                                                                                      ##residues 1-496 ##label KOH
##cross-references GB:D26186; NID:9529072; PID:d1005873; PID:9529073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 WYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGYSLSVRAQAKVCHYRICMAPSGSL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ziemiecki, A.
Biochem. Biophys. Res. Commun. (1995) 209:582-589
iyk, a novel intracellular protein tyrosine kinase
differentially expressed in the mouse mammary gland and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        src; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       *superfamily unassigned Ser/Thr or Tyr-specific protein
kinases; protein kinase homology; SH3 homology
ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149552 *type complete protein-tyrosine kinase (EC 2.7.1.112) bsk/iyk - mouse intestinal tyrosine kinase (EC 4.7.1.112) bsk/iyk - mouse intestinal tyrosine knowse *common_name house mouse 02.jul-1996 *sequence_revision 02-Jul-1996 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Oberg-Welsh, C.; Welsh, M.
#journal Gene (1995) 152:239-242
#title Cloning of BSK, a murine FRK homologue with a specific pattern of tissue distribution.
#cross-references MUID:95137395
                                                                                                                                                                                                                                                                                                                                          #domain SH3 homology #label SH3\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif
#length 496 #molecular-weight 55593 #checksum 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148608
Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-512 ##label RES
##cross-references GB:L36132; NID:9556287; PID:9777773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily protein-tyrosine kinase si
homology; SH2 homology; SH3 homology
ATP; intestine; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 625; DB 2; Le
Pred. No. 8.61e-106;
11; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 YLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 YLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                     targeted disruption
                                                                                                                                                                 1-496 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:95251656
#accession I48608
                                                                                                                            preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149552; 148608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residues 1-153
                                                                                                                                                    ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                         A56040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149552
                                                                                                                                                                                                                                   #map_position 2
CLASSIFICATION #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #gene
CLASSIFICATION
                                                                                                                                 ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSIONS
REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m
  authors
                                           #journal
                                                                                                                                                                                                                                                                                                                                          62-111
232-491
240-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
56-112
                                                               #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                             GENETICS
                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
S24550 #type complete
protein-tyrosine kinase (EC 2.7.1.112) 1 - freshwater sponge (Spongilla lacustris)
src-type tyrosine kinase 1
#formal_name Spongilla lacustris
07.May-1993 #sequence_revision 07-May-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                       $24553 #type complete protein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sponge (Spongilla lacustris) src-type tyrosine kinase 4
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                            123 WFFGAIKRADAEKQLLYSENQTGAFLIRESESQKGDFSLSVLDEGVVKHYRIRRLDEGGF 182
                                                                                                                                                                                                                  120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 WFFGQVKRVDAEKQLMMPFNNLGSFLIRDSDTTPGDFSLSVRDIDRVRHYRIKKLENGTY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Spongilla lacustris
07-May-1993 #sequence_revision 07-May-1993 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif
th 512 #molecular-weight 58891 #checksum 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raulf, F.
submitted to the EMBL Data Library, September 1991
$24550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library, September 1991
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 506 #molecular-weight 57561 #checksum 9
                                                                                                Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 506
                                                                                                Score 276; DB 2; Length 512
Pred. No. 1.29e-33;
26; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 269; DB 2; Length 506
Pred. No. 3.01e-32;
24; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-506 ##label RAU
##cross-references EMBL:X61604; NID:g10155; PID:g10156
                                                                                                                                                                                                                                                                             180 YLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC
                                                                                                                                                                                                                                                      183 FLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 FVTR-RLTFQSIQELVAYY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: : || | :::||::||
180 YLQKGRL-FPGLEELLTYY 197
                                                                                                39.5%;
ilarity 37.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.5%;
Best Local Similarity 40.5%;
Matches 32; Conservative
                                        #region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $24550
Raulf, F.
submitted t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
                                                                                                                    Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S24553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
#submission
#accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #gene
CLASSIFICATION
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
  123-215
239-501
247-255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122-214
238-496
246-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSIONS
                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 - 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                          SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ENTRY
TITLE
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                              g
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
ALTERNATE_NAMES ORGANISM
                                                                                                                                                                                                                                                                                                                                                #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                             ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #title
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                      RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                               #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                           122 WFLGKIKRVEAEKMLNQSFNQVGSFLIRDSETTPGDFSLSVKDQDRVRHYRVRRLEDGSL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 WFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKHYRIKRLDEGGF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GDB:355675 .........##cross-references GDB:355675 .......##map_position 4q35-4q35 ..........#map_position 4q35-4q35 .............#superfamily protein-tyrosine kinase src; protein kinase homology; SH3 homology; SH3 homology; AH3 homology ATP: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T. #journal Gene (1994) 138:247-251
#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.
#cross-references MUID:94171047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                   #domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ArP-binding motif\
#active_site Lys #status predicted
#length 505 #molecular-weight 57693 #checksum 3389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 505 #molecular weight 58254 #checksum 9379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138396 #type complete
protein-tyrosine kinase (EC 2.7.1.112) FRK - human
FYN-related kinase (FRK)
#formal_name Homo sapiens #common_name man
15.Mar-1996 #sequence_revision 15-Mar-1996 #text_c)
                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                     Score 262; DB 2; Length 505; Pred. No. 6.94e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:U00803; NID:g392887; PID:g392888
                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches 23; Indels
                                         ##cross-references EMBL:X61601; NID:g10149; PID:g10150
                                                                                                                                                                                #domain SH3 homology #label SH3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 260; DB 2;
Pred. No. 1.70e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 YLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 FVTRRSTFQILHELVDHYKIETDGLCCKLLYPC 214
##molecule_type mRNA
##residues 1-505 ##label RAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-505 ##label RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 FLTRRRIFSTLNEFVSHY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| : |:|: |:|: |
180 YLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-Apr-1998
138396
138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDB: FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATE_NAMES
ORGANISM
                                                                                                   CLASSIFICATION
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                   122-214
238-496
246-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232-494
240-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                  61-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49-105
                                                            GENETICS
                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #dene
                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

```
S07822
Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. (1988) 38:117-126
Structure and expression of lck transcripts in human lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.
Mol. Cell. Biol. (1989) 9:2173-2180
Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
#journal Blochim. Biophys. Acta (1986) 888:286-295
#title Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.

Bur. J. Immunol. (1986) 16:1643-1646

A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.;
Rosen, N.
#journal Oncogene Res. (1987) 1:357-374
#title Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines.
#cross-references MUID:88217332
OKHULK #type complete
protein-tyrosine kinase (EC 2.7.1.112) lck - human
kinase-related transforming protein (lck)
#formal_name Homo sapiens #common_name man
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                            J00152; S07822; S07200; S01879; S07143; A32797; I57636
J00152
                                                                                                                                                                                                                                                                          Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R. Gene (1989) 44-105-113 Structure of the human lck gene: differences in genomiscretus of the human lck genes affect only organisation within src-related genes affect only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-315, Asaitri', 212-257, RCGW', 262, 'ITI', 266, 'T'
268-281, 'AGRLP', 287-503, 'STA' ##label KOG
##cross-references EMBL:X05027; NID:936807; PID:936808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
##residues 1-86,'P',88-509 ##label PER
##cross-references EMBL:X13529; NID:g34294; PID:g34295
SNCE S07200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 'A',376-509 ##label TRE
##cross-references EMBL:X04476; NID:g35779; PID:g35780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cession JQ0152
##molecule_type DNA
##residues 1-509 ##label ROU
##cross-references EMBL:X14053
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #cross-references MUID:89123626
#accession S07822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:87133831
#accession S07200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title
```

```
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                              15-67
78-170
189-448
197-205
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
68-116
243-501
251-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
REFERENCE
                                         #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
DATE
                                                                                                                                                                                                                 GENETICS
                                                                                                                                                                                                                                         #dene
                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                අ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S49016
Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalyzes the phosphorylation of a peptidyl tyrosine residue by \ensuremath{\mathrm{ATP}}
                                                                                                                                             #authors Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
#journal Mol. Cell. Biol. (1988) 8:3058-3064
#title Structure of the murine lck gene and its rearrangement in a murine lymphoma cell line.
#cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *product protein-tyrosine kinase lck *status predicted *label MAT.
** #domain SH3 homology *|label SH3\/
** #domain SH2 homology *|label SH2\/
** #domain SH2 homology *|label SH2\/
** #domain SH2 homology *|label SH2\/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #map_position 1p35-1p34.3
#introns 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 31ntrons 399/1; 443/1
                                                                                                                                                                                                                                                                                                                ##cross-treferences GB:M21510; NID:g187031; PID:g553522
##cross-references GB:M21510; NID:g187031; PID:g553522
TProtein tyrosine kinases play important roles in the control of cell growth and differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology homology; SH2 homology; SH2 pre-type blocked amino end; lipoprotein; myristylation; phosphoprotein; phosphotransferase; thiolester bond; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA----QAKVC-HYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #active_site_Lys_#status predicted\
#binding_site_phosphate(Tyr)(covalent)(by
autophosphorylation) #status predicted\
#binding_site_phosphate (Tyr) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             form) #status predicted\
#binding_site palmitate (Cys) (covalent) #status
predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #molecular-weight 58000 #checksum 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase (EC 2.7.1.112) brk - human #formal_name Homo sapiens #common_name man 07-may-1995 #sequence_revision 21-Jul-1995 #text chsquare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.5%; Score 241; DB 1; Length 509; Best Local Similarity 40.4%; Pred. No. 7.83e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches 31; Indels
                                                                                                   ##cross-references GB:M26692; NID:9341523; PID:9349702
NCE I57636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 ADGSLYLOKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 DNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPC 224
                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                            ane GDB:LCK
##cross~references_GDB:119360; OMIM:153390
                                                       ##molecule_type DNA
##residues 1-35 ##label TAK
in T cells.
#cross-references MUID:89313764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
#length 509 #mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Conservative
                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                                                                                                                                                                                           I57636
                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #description
                                                                                                                                                                                                                                                                               ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68-116
127-224
243-501
251-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
2-509
                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                 #gene
                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273
394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
```

Ø

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Voronova, A.F.; Sefton, B.M.
#journal Nature (1986) 319:682-685
#title Expression of a new tyrosine protein kinase is stimulated retrovirus promoter insertion.
#cross-references MUID:86146842
                                                                                                                                                                                                                                                                                                                                                                         *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 WFFGCISRSEAVRRLQAEGNATGAFLIRVSEKPSADYVLSVRDTQAVRHYKIWRRAGGRL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B.A.; Crompton, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-509 ##label RES
##cross-references EMBL:X03533; NID:g54813; PID:g54814
FICATION #superfamily protein tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Mus musculus #common_name house mouse 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Apr-1998 148845 148845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                        cDNAs encoding a novel brk, expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 451 #molecular-weight 51834 #checksum 5817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 509 #molecular-weight 57942 #checksum 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 240; DB 2; Length 451; Pred. No. 1.22e-26; 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 238; DB 2; Length 509;
Pred. No. 2.94e-26;
22; Mismatches 31; Indels
                                                                                                                                                                                                                             ##residues 1-451 ##label MIT
##cross-references EMBL:X78549; NID:9515025; PID:9515026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3 | #domain SH2 homology #label SH2 |
Lowe, P.N.; Page, M.J.; Gusterson,
Oncogene (1994) 9:2383-2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 DNGGFYI-SPRITFPGLHDLVRHYTNASDGLCTKLSRPC 224
                                                     Cloning and characterisation of non-receptor tyrosine kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 HLNEAVSFLSLPELVNYHRAQ-SLSHGLRLAAPC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 YLQKGRLFPGLEELLTYYKANWKLION-PLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #type complete
                                                                                                                                                                                                                                                                                                                                              ##cross-references GDB:378058
                                                                                                                                                         ##molecule_type mRNA
##residno
                                                                                                                breast tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.0%;
Best Local Similarity 39.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.3%;
Best Local Similarity 39.4%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p56-tck - mouse
                                                                                                                                                                                                                                                                                                                   GDB: BRK
                                                                                                                                              849016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I48845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I48845
```

```
148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88-137
148-245
265-523
273-281
                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                              A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czernilofsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman, H. Muture (1983) 301:736-738

Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Voronova, A.F.; Adler, H.T.; Sefton, B.M.
#journal Mol. Cell. Biol. (1987) 7:4407-4413
#title Two lck transcripts containing different 5' untranslated regions are present in t cells.
#cross-references Mull:88142832
#accession 157629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #rocecute_type und
#residues
#ross-references GB:M18098; NID:g198766; PID:g198767
#cross-references GB:M18098; NID:g198766; PID:g198767
#CATION #superfamily protein-tyrosine kinase src; protein kinase
homology: SH2 homology; SH3 homology;
S ATP; autophosphorylation; kinase-related transforming
protein; phosphoprotein; phosphotransferase;
tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                     #formal_name Mus musculus #common_name house mouse
29_Aug-1987_#sequence_revision 29-Aug-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Rous sarcoma virus
22-Way-1981 #sequence_revision 17-Dec-1982 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 509 #molecular-weight 57952 #checksum 3251
                                                                               A23639 #type complete
protein-tyrosine kinase (EC 2.7.1.112), lymphocyte
                                                                                                                                                                                                                                  Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, Cell (1985) 43:393-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 238; DB 2; Length 509
Pred. No. 2.94e-26;
22; Mismatches 31; Indels
  212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 DNGGFYI-SPRITFPGLHDLVRHYINASDGLCTKLSRPC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ADGSLYLOKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
175 ADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A38017; A00631; S02726; A38018
                                                                                                                                                                                                                                                                                                                                                                                                       -509 ##label MAR ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #cross-references MUID:83141780
#accession A38017
                                                                                                                                                                                                                                                                                                                                           #cross-references MUID:86079521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.08;
39.48;
                                                                                                                                                                                                 A23639; I57629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 39.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-Mar-1998
                                                                                                                                                                              28-Feb-1997
                                                                                                                      lck protein
                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A23639
                                                                                                                                                                                                                                                                                                                                                             A23639
                                                                                                                                                                                                                                                                                                                                                                                                                          I57629
                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
                                                                                                                    ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                          10
                                                                                                                                                                                                                                                              #journal #title
                                                                                                                                                                                                                      REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127-224
243-501
251-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                   ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
68-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARY
                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

```
Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. (1982) 44:1-11
DNA sequence of the viral and cellular src gene of chickens:
I. Complete nucleotide sequence of an EcoRI fragment of recovered avian sarcoma virus which codes for gp37 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mature
                                                                                                               #authors Takeya, T.; Hanafusa, H.
#journal Cell (1983) 32:881-890
#title Structure and sequence of the cellular gene homologous to RSV sec gene and the mechanism for generating the transforming virus.
#cross-references_MUID:83155664
                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source strain Schmidt-Ruppin
$02726
$02726
#authors
Barnier, J.V.; Dezelee, P.; Marx, M.; Calothy, G.
#journal Nucleic Acids Res. (1989) 17:1252
#title Nucleotide sequence of the src gene of the Schmidt-Ruppin
#cross-references MUID:89160256
#accession $02726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; oncogene; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature (1981) 291:675-677
Homologous tyrosine phosphorylation sites in
transformation-specific gene products of distinct avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-9,'G',11-62,'D',64-123,'V',125-319,'K',321-495,'S' 497-526 ##label BAR ##cross-references EMBL:X13745; NID:961908; PID:961909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##residues 1-15,'C',17-94,'RT',97-116,'D',118-337,'T',339-526
                                                                                                                                                                                                                                                                                                                                                                           1-62,'D',64-95,'T',97-123,'V',125-300,'N',302-526
##label TAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            form) #status predicted\
#active_site Lys #status predicted\
#binding_site phosphate (Tyr) (covalent) (by
autophosphorylation) #status experimental
#length 526 #molecular-weight 58984 #checksum 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #contents annotation; phosphorylation site
MENT The sequence from the Schmidt-Ruppin strain is shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235; DB 1; Length 526;
Pred. No. 1.10e-25;
26; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references GB:K00928; NID:g210187; PID:g210189
##molecule_type DNA
##residues
1-526 ##label CZE
##experimental_source strain Schmidt-Ruppin
MCE A00630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##experimental_source strain rASV1441
REFERENCE A38019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sarcoma viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #cross-references MUID:83059858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:81220979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.6%;
Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A38018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A38018
                                                                                                                                                                                                                                                                                                              A00631
                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION
                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
```

```
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                      88-137
148-245
265-523
273-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88-137
148-245
265-523
273-281
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                          34,46
                                                                                                                                                                                                                                           12,48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgene
                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                         #authors Takeya, T.; Hanafusa, H.
#journal Cell (1983) 32:881-890
#title Structure and sequence of the cellular gene homologous to the RSV sec gene and the mechanism for generating the transforming virus.
#cross-references MUID:83155664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-182,'DP',185,'IPLPSCLC' ##label DO2
##cross-references GB.M57290; NID:9212703; PID:9212706
##note alternatively spliced mRNA exclusively replaces the long
form in skeletal muscle shortly before hatching
##note this ORF appears not to be translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.
Cell (1989) 57:763-773
Purified maturation promoting factor phosphorylates pp60 (c-src) at the sites phosphorylated during fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A41256
Dorai, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
Mol. Cell. Biol. (1991) 11:4165-4176
Malysis of coNAs of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the A41256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Dorai, T.; Wang, L.H.
#journal Mol. Cell. Biol. (1990) 10:4068-4079
#title An alternative non-tyrosine protein kinase product of the cross-references MUID:90318371
120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLĞGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the authors translated the codon CAG for residue 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
##residues 1-500, R',502-533 ##label TAK
##rote the authors translated the codons AAC and CAG for
##note residues 301 and 526 as Thr and Glu, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily protein-tyrosine kinase src; protein kinase
                                                                                                                                                                             TVCHS #type complete
protein-tyrosine kinase (EC 2.7.1.112) src - chicken
kinase-related transforming protein src - chicken
kinase-related transforming protein src - chicken
#formal_name Gallus qallus #common_name chicken
19-Feb-1984 #sequence_revision 07-oct-1994 #text_change
07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type protein
##molecule_type protein
##residues 2-88 ##label SHE
##rote 34-Thr, 46-Thr, and 72-Ser are phosphorylated
##note mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeya, T.; Hanafusa, H.
Cell (1983) 34:319
annotation; erratum, correct translation of
                                                                                                                                                                                                                                                                                                     A00630; A41256; A32432; C35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 484-533 ##label DOR ##cross-references GB:S43579
                                                          208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                   #cross-references MUID:89249341
#accession A32432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A32432
                                                                                                                                                                                                                                                                                                                          A00630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A90838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A00630
                                                                                                                                                                                                                      ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                        REFERENCE
#authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #contents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
#title
                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal
                                                                                                                                                                                                                                                                                                   ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                              DATE
                                                                                                 á
```

```
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH3\
#domain protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#rodified_site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein kinase A) #status predicted\
#binding_site phosphate (Thr) (covalent) #status experimental\
#binding_site phosphate (Ser) (covalent) #status
#binding_site phosphate (Ser) (covalent) #status
#pinding_site phosphate (Ser) (covalent) #status
homology; SH2 homology; SH3 homology alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphotransferase; proto-oncogene; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myristylation; oncogene; phosphoprotein;
phosphotransferase; transforming protein; tyrosine-specific
protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif.
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#active_site Lys #status predicted\
#active_site phosphate (Tyr) (covalent) (by

    avian sarcoma

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophorylation; blocked amino end; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name avian sarcoma virus S2
31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change
07-Nov-1997
B25375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #active_site Lys #status predicted\
#binding_site phosphate (Tyr) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 60023 #checksum 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamo-Toyoshima, K.
MOI. Cell. Biol. (1986) 6:2420-2428
Activation of the cellular src gene by transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 235; DB 1; Length 533. Pred. No. 1.10e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.10e-25;
26; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVFVS2 #type complete
protein-tyrosine kinase (EC 2.7.1.112) src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-557 ##label IKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|:
175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:87064539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
#length 533 #mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
33.6%;
Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B2537
```

```
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                  #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal
#title
                                                                         #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                 REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64-112
123-220
239-497
247-255
ACCESSIONS
                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
2-505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology APP: autophosphorylation; blocked amino end; lipoprotein; myristylation; oncogene, phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geryk, J.; Dezelee, P.; Barnier, J.V.; Svoboda, J.; Nehyba, J.; Karakoz, I.; Rynditch, A.V.; Yatsula, B.A.; Calothy, G. J. Virol. (1989) 63:481-492
Transduction of the cellular src gene and 3' adjacent sequences in avian sarcoma virus PR2257.
                                                                                           ю
М
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#region protein kinase homology #label KIN\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#active_site Lys-#status predicted\
#binding_site phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
#length 587 #molecular-weight 65800 #checksum 2040
                                                                                                                                                                                                                                                                                                                  TVFVPR #type complete
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma
                                                                                                                                                   120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                             148 WYFGKITRRESERLLLUPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 WYFGKITRRESERLLLUPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                     TVHUHC #type complete
protein-tyrosine kinase (EC 2.7.1.112) hck - human
fformal_name Homo sapiens #common_name man
31.Dec-1989 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                 #checksum 7810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                      Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 235; DB 1; Length 587; Pred. No. 1.10e-25;
autophosphorylation), #status predicted
#length 557 #molecular-weight 62582 #checks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Mismatches 20; Indels
                                                    Score 235; DB 1; Le
Pred. No. 1.10e-25;
26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##rocidues 1-587 ##label GER
                                                                                                                                                                                                     208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                          175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein kinase
                                                    33.6%;
ilarity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-May-1998
                                                                     Local Similarity
les 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148-245
265-523
273-281
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
               SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTRY
                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                             DATE
                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                  ô
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
##residues 1-505 ##label QUI
##cross-references GB.M16591
##note the codon given for 3-Cys (TCG) is inconsistent with the
authors' translation
A27811; A27812; JC1149; C38268; S31103
A27811
Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Diaz, M.O.; Rowley, J.D.
M.J.; Le Beau, M.M.; Diaz, M.O.; Rowley, J.D.
Mol. Cell. Biol. (1987) 7:2267-2275
Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and is expressed in hemopoletic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H. Gene (1992) 113:275-280
The genomic locus of the human hemopoletic-specific cell protein tyrosine kinase (PTK) encoding gene (HCK) confirms conservation of exon-intron structure among human PTKs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalyzes the phosphorylation of a peptidyl tyrosine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
#binding_site palmitate (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8913-8917
Putative tyrosine kinases expressed in K-562 human leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *product protein-tyrosine kinase hck *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myristylation; phosphoprotein; phosphotransferase;
thiolester bond; transforming protein; tyrosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M. #journal Mol. Cell. Biol. (1987) 7:2276-2285
#title Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin.
#cross-references MID:87257943
#accession A27812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; autophosphorylation; blocked amino end; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GB:M16592; NID:g183913; PID:g306833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #map_position 20q11-20q12
#introns 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #label MAT\
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references GDB:119303; OMIM:142370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 157-505 ##label HRA
##cross-references EMBL:X59741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residues 362-417 ##label PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the src family #cross-references MUID:92241680 #accession JC1149
                                                                                                                                                                                                                                                                  #cross-references MUID:87257942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cross-references MUID:91062389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase
                                                                                                                                                                                                                                                                                                       cession A27811
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDB: HCK
                                                                                                                                                                                                                                              cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A27812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A38268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C38268
```

```
Query Match 33.3%; Score 233; DB 1; Length 505; Best Local Similarity 41.4%; Pred. No. 2.64e-25; Matches 41; Conservative 24; Mismatches 27; Indels 7; Gaps
SUMMARY
                                                                                                 δ
                                                                                                                   පු
```

ς;

Search completed: Thu May 20 12:55:42 1999 Job time : 122 secs.

*****	(TM)
****	·======
****	<u> </u>

*******	. []

******	<u> </u>
*****	1

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar Time 5.35 Seconds 491.220 Million cell updates/sec Thu May 20 12:56:02 1999; Tabular output not generated. Run on:

>US-09-099-053-2 (120-212) from US09099053.pep (4 of 6) 699 Description: Perfect Score:

1 WYFSGVSRTQAQQLLLSPPN.....LLTYYKANWKLIQNPLLQPC Sequence:

PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 Database:

Mean 40.582; Variance 67.112; scale 0.605 1:swissprot Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SECTION STATE ST	Score 625 269	Ouery Match	Length DB	DB 1	ID SRM_MOUSE SRM_ SPOLA	Description TYROSINE-PROTEIN KINAS	Pred. No. 2.01e-122
34.0 509 1 LCK_HUMAN PROTO-ONCOGENE TYROSIN 34.0 508 1 LCK_HUMAN PROTO-ONCOGENE TYROSIN 34.0 508 1 LCK_HUMAN PROTO-ONCOGENE TYROSIN 33.8 552 1 SRC1_DROME TYROSINE-PROTEIN KINAS 33.6 526 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.6 537 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.6 557 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.2 569 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.2 569 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_AMT TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 KES-KSVHI TYROSINE-PROTEIN KINAS 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN		37.5	500		SRK1_SPOLA	TYROSINE-PROTEIN KINAS	6.09e-36
34.0 508 1 LCK_MOUSE PROTO-ONCOGENE TYROSIN 53.8 552 1 SRC_LDROME TYROSINE-PROTEIN KINAS 33.6 526 1 SRC_AVISR TYROSINE-PROTEIN KINAS 33.6 526 1 SRC_AVISR TYROSINE-PROTEIN KINAS 33.6 557 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.5 557 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.8 503 1 RC_AVIST TYROSINE-PROTEIN KINAS 32.8 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_RSVHI TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_RSVHI TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_RSVHI TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_RSVHI TYROSINE-PROTEIN KINAS 32.3 52.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN		34.5	508 508		FKK_HUMAN LCK_HUMAN	TYROSINE-PROTEIN KINAS PROTO-ONCOGENE TYROSIN	1.71e-35 2.83e-31
33.6 526 1 SRC_RSVSR TYROSINE-PROTEIN KINAS 33.6 526 1 SRC_RAVISR TYROSINE-PROTEIN KINAS 33.6 537 1 SRC_AVISR TYROSINE-PROTEIN KINAS 33.6 587 1 SRC_AVIS2 TYROSINE-PROTEIN KINAS 33.6 587 1 SRC_AVIS2 TYROSINE-PROTEIN KINAS 33.3 526 1 HCK HUMAN TYROSINE-PROTEIN KINAS 33.2 541 1 YES_XIPHE PROTOCONCOGENE TYROSIN 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 523 1 SRC_RSVPA TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRICK TYROSINE-PROTEIN KINAS 32.2 555 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS			508		LCK_MOUSE	PROTO-ONCOGENE TYROSIN	1.30e-30
33.6 526 1 SRC_AVISR TYROSINE-PROTEIN KINAS 33.6 532 1 SRC_CHICK PROTO-ONOGGENE TYROSIN 33.6 587 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_AMT TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_AMT TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRAYI TYROSINE-PROTEIN KINAS 32.5 542 1 SRC_RSVH TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRAYI TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRAYI TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRAYI TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CRAYI TYROSINE-PROTEIN KINAS 32.7 552 1 SRC_RSVH TYROSINE-PROTEIN KINAS 32.7 552 1 SRC_RSVH TYROSINE-PROTEIN KINAS 32.7 552 1 SRC_RSVH TYROSINE-PROTEIN KINAS 32.7 552 1 SRC_RSVH TYROSINE-PROTEIN KINAS			526	-	SRC_RSVSR		5.92e-30
33.6 532 1 SRC_CHICK PROTO-ONCOGENE TYROSIN 33.6 557 1 SRC_AVIST TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KINAS 33.2 509 1 YES_XIPHE PROTO-ONCOGENE TYROSIN 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_ANT TYROSINE-PROTEIN KINAS 32.8 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN		33.6	526	Н	SRC_AVISR		5.92e-30
33.6 557 1 SRC_AVIST TYROSINE-PROTEIN KIRAS 33.3 544 1 YES_XIPHE PROTEIN KIRAS 33.3 544 1 YES_XIPHE PROTO-ONCOGENE TYROSIN 33.2 509 1 STC_HYDAT TYROSINE-PROTEIN KIRAS 33.2 509 1 STC_HYDAT TYROSINE-PROTEIN KIRAS 33.2 498 1 STC_AVISS TYROSINE-PROTEIN KIRAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KIRAS 32.9 531 1 HCK_MOUSE TYROSINE-PROTEIN KIRAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_KIRK TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_KIRK TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_KIRK TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_KIRK TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_KIRK TYROSINE-PROTEIN KIRAS 32.5 551 1 STC_HUMAN PROTO-ONCOGENE TYROSIN		33.6	532	Н	SRC_CHICK	PROTO-ONCOGENE TYROSIN	5.92e-30
33.6 587 1 SRC_AVIS2 TYROSINE-PROFEIN KIRAS 33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KIRAS 33.2 509 1 STK_HYDAT TYROSINE-PROTEIN KIRAS 33.2 568 1 STK_HYDAT TYROSINE-PROTEIN KIRAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KIRAS 32.9 523 1 SRC_AVISS TYROSINE-PROTEIN KIRAS 32.8 523 1 SRC_RSVPA TYROSINE-PROTEIN KIRAS 32.5 524 1 HCK_RAT TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_CHICK PROTOGENE TYROSIN 32.3 541 1 YES_CHICK PROTOGENE TYROSIN 32.3 551 SRC_RSVHT TYROSINE-PROTEIN KIRAS 32.2 542 1 SRC_RSVHT TYROSINE-PROTEIN KIRAS 32.3 543 1 SRC_RSVHT TYROSINE-PROTEIN KIRAS 32.3 541 1 YES_CHICK PROTOGENE TYROSIN		33.6	557	Н	SRC_AVIST		5.92e-30
33.3 526 1 HCK_HUMAN TYROSINE-PROTEIN KIRAS 33.3 544 1 YES_XIPHE PROTO-OCGGENE TYROSIN 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KIRAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KIRAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KIRAS 32.9 503 1 HCK_ANT TYROSINE-PROTEIN KIRAS 32.9 524 1 HCK_MOUSE TYROSINE-PROTEIN KIRAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KIRAS 32.5 541 1 YES_CRVHI TYROSINE-PROTEIN KIRAS 32.3 551 1 SRC_RSVHI TYROSINE-PROTEIN KIRAS 32.3 552 1 SRC_RSVHI TYROSINE-PROTEIN KIRAS 32.3 551 1 SRC_RSVHI TYROSINE-PROTEIN KIRAS 32.2 535 1 SRC_RSVHI TYROSINE-PROTEIN KIRAS			587	Н	SRC_AVIS2		5.92e-30
33.3 544 1 YES_XIPHE PROTO-ONCOGENE TYROSIN 53.2 509 1 STK_HYDAT TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_RAT TYROSINE-PROTEIN KINAS 32.8 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_KSYHT TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_KSYHT TYROSINE-PROTEIN KINAS 32.3 52.1 SRC_KSYHT TYROSINE-PROTEIN KINAS 32.3 52.5 1 SRC_KSYHT TYROSINE-PROTEIN KINAS 32.3 52.5 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 52.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN			526	~	HCK_HUMAN		1.62e-29
33.2 509 1 STK_HYDAT TYROSINE-PROTEIN KINAS 33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_RAT TYROSINE-PROTEIN KINAS 32.8 523 1 SRC_RSVPA TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 32.3 535 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS 32.2 535 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS		33.3	544	-	YES_XIPHE	PROTO-ONCOGENE TYROSIN	1.62e-29
33.2 568 1 SRC_AVISS TYROSINE-PROTEIN KINAS 32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 523 1 SRC_RSVPA TYROSINE-PROTEIN KINAS 32.8 524 1 HCK_RAT TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 32.3 551 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS 32.2 535 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS	~	33.5	509	-	STK_HYDAT	TYROSINE-PROTEIN KINAS	2.69e-29
32.9 498 1 BLK_MOUSE TYROSINE-PROTEIN KINAS 32.9 503 1 HCK_RAT TYROSINE-PROTEIN KINAS 32.8 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 YES_CHICK PROTO-ONOGENE TYROSIN 32.3 526 1 SRC_RSWHI TYROSINE-PROTEIN KINAS 32.2 535 1 SRC_RSWHI TYROSINE-PROTEIN KINAS 32.3 526 1 SRC_RSWHI TYROSINE-PROTEIN KINAS	~	33.2	568	Н	SRC_AVISS		2.69e-29
32.9 503 1 HCK_RAT TYROSINE-PROTEIN KINAS 32.8 523 1 SRC_RSVPA TYROSINE-PROTEIN KINAS 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.5 541 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 32.3 556 1 SRC_RCHY PROTO-ONCOGENE TYROSIN 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN	_	32.9	498	Н	BLK_MOUSE		7.36e-29
32.8 523 1 SRC_RSVPA TYROSINE-PROTEIN KINAS 1 32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 3 32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 3 32.2 535 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS 3 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 9	_	32.9	503	Н	HCK_RAT		7.36e-29
32.5 524 1 HCK_MOUSE TYROSINE-PROTEIN KINAS 3 32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 3 32.2 535 1 SRC_RSWH TYROSINE-PROTEIN KINAS 3 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 5	σ.	32.8	523	П	SRC_RSVPA		1.22e-28
32.5 541 1 YES_CHICK PROTO-ONCOGENE TYROSIN 3 32.3 526 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS 5 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 9	_	32.5	524	H	HCK_MOUSE		3.33e-28
32.3 526 1 SRC_RSVH1 TYROSINE-PROTEIN KINAS 5 32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 9		32.5	541	-	YES_CHICK	PROTO-ONCOGENE TYROSIN	3.33e-28
32.2 535 1 SRC_HUMAN PROTO-ONCOGENE TYROSIN 9	ın		\sim	Н	SRC_RSVH1	TYROSINE-PROTEIN KINAS	5.49e-28
		32.2	535	٦	SRC_HUMAN		9.06e-28

EMBL; D49427; G684972; -.
EMBL; D26186; G528073; -.
MGI: 101865; SRMS;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

9.06e-28	9.06e-28	1.50e-27	2.47e-27	2.47e-27	4.07e-27	6.70e-27	1.10e-26	1.82e-26	1.82e-26	1.82e-26	2.99e-26	4.91e-26	4.91e-26	4.91e-26	4.91e-26	8.08e-26	1.33e-25	1.33e-25	3.58e-25	3.58e-25	5.87e-25
PROTO-ONCOGENE TYROSIN	NEURONAL PROTO-ONCOGEN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	SEX MUSCLE ABNORMAL PR	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTEIN E(SEV)2B (SH2-	GROWTH FACTOR RECEPTOR	GROWTH FACTOR RECEPTOR	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	GROWTH FACTOR RECEPTOR	1-PHOSPHATIDYLINOSITOL	PROTO-ONCOGENE TYROSIN
YES_XENLA	SRCN_MOUSE	FGR_HUMAN	LCK_CHICK	SRC_RSVP	SEMS_CAEEL	YES_MOUSE	YES_HUMAN	ABL_MLVAB	ABL_MOUSE	ABL1_HUMAN	DRK_DROME	GRB2_HUMAN	GRB2_MOUSE	ABL_FSVHY	ABL2_HUMAN	FGR_FSVGR	SRC2_XENLA	SRC1_XENLA	GRB2_XENLA	PIP5_HUMAN	FGR_MOUSE
н	Н	н	Н	Н	Н	Н	Н	-	-	-	-	Н	Н	н	-	-	(Н	-1	-	П
537	540	529	507	526	228	541	543	746	1123	1130	211	217	217	439	1182	545	531	531	217	1252	517
32.2	32.2	32.0	31.9	31.9	31.8	31.6	31.5	31.3	31.3	31.3	31.2	31.0	31.0	31.0	31.0	30.9	30.8	30.8	30.5	30.5	30.3
225	225	224	223	223	222	221	220	219	219	219	218	217	217	217	217	216	215	215	213	213	212
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 95021220.
KOHMURA N., YAGI T., TOMOOKA Y., OYANAGI M., KOMINAMI R., TAKEDA N., CHIBA J., IKAWA Y., AIZAWA S.;
"A novel nonreceptor tyrosine kinase, Srm: cloning and targeted
                                                                                                                                                                                                                                                            KAWACHI Y., NAKAUCHI H., OTSUKA F.; ^{\circ} Isolation of a cDNA encoding a tyrosine kinase expressed in murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOL. CELL. BIOL. 14:6915-6925(1994).

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.

-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; ROBENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                              Q62270; Q62360;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70)
                   496 AA
                   PRT;
                                                                                                                                                                                                                                                                                              skin.";
EXP. DERMATOL. 21:533-538(1995).
                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-THYMUS;
MEDLINE; 97369678.
                   STANDARD;
                                                                                                                      SRMS OR SRM.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    disruption.
                 SRM_MOUSE
RESULT
```

```
PS50002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLICING
                                                                                                                                                                                                                                                                                                                                                    SRK1_SPOLA
P42686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; E
PROSITE; E
PROSITE; E
                                                                                                                                 DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                       DOMAIN
  SETTTT TETT SO
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                ö
                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
R -> G (IN REF. 2).
LRK -> FOR (IN REF. 2).
N -> I (IN REF. 2).
W+> FD44DEF6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92334872.
OTTILE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
OTTILIE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
Multiple src-related kinase genes, srk1-4, in the fresh water sponge Spongilla lacustris.":
ONCOGENE 7:1625-1630(1992).
                                                                                                                                                                                                                                                                                                  124 WYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGYSLSVRAQAKVCHYRICMAPSGSL 183
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-! - SUBCELLULAR LOCATION: CYPOLASMIC (PROBABLE).
-! - ALTERNATIVE PRODUCTS: SRK1 AND SRK4 MAY ARISE BY ALTERNATIVE
                                                                                     TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.

55 116 SH3.
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                           Score 625; DB 1; Length 496; Pred. No. 2.01e-122;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                    SRK4_SPOLA STANDARD; PRT; 506 AA. P42690; PRL-32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANOLATION UPDATE)
                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE-PROTEIN KINASE SRK4 (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                 184 YLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPC 216
                                                                                                                                                                                                                                                                                                                                           180 YLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X61604; G10156; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
                                                                                                       116
124
216
234
40
52
40
262
4
384
78
78
1238
1.
278
N
55731 MW; b
                                                                                                                                                                                                                                           89.4%;
                               PROSITE; PS50002; SH3; 1.
PFAM: PF00017; SH2; 1.
PFAM: PF00018; SH3; 1.
PFAM: PF000069; pkinase; 1.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                Conservative
           PS50011; PROTEIN
PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                                                                                                                     496 AA;
                                                                                                                                                                                                                                                      Best Local Similarity
Matches 77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
 PS00109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN.
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                ACT_SITE
MOD_RES
                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                 DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                             Query Match
                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                g
 δ
                                                                                                                                                                                                                                                                                                                                                       ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92334872.
OTTILIE S., RAUDE F., BARNEKOW A., HANNIG G., SCHARTL M.;
"Multiple src-related kinase genes, srkl-4, in the fresh water sponge
Spongilla lacustris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 WFFGQVKRVDAEKQLMMPFNNLGSFLIRDSDTTPGDFSLSVRDIDRVRHYRIKKLENGTY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONCOGENE 7:1625-1630(1992).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYPOPLASMIC (PROBABLE).
-!- ALTERNATIVE PRODUCTS: SRK1 AND SRK4 MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                               TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2.DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.

SH3.

DOMAIN 54 116 SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 269; DB 1; Length 506;
Pred. No. 1.64e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
807A71D0 CRC32;
                                                                                                                                                                                                                                                                                           SH2.
PROTEIN KINASE.
ATP (BY SIMILARI
ATP (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SKRI (EC 2 7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 AA.
     4
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PRAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X61601; G10150; -
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      359 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 FVTR-RLTFOSIOELVAYY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: : || | :::||::||
180 YLQKGRL-FPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.5%;
Best Local Similarity 40.5%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                   214
493
254
268
                                                                                                                                                                                                                                                                                                                         240
246
268
359
506 AA;
```

```
DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOGA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEOUENCE FROM N.A.
MEDLINE; 95210168.
CANCE W.G., CRAVEN R.J., BERGMAN M., XU L.H., ALITALO K., LIU E.T.;
RAK, a novel nuclear tyrosine kinase expressed in epithelial cells.";
CELL GROWTH DIFFER. 5:1347-1355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE, 93293373.

CANCE W.G., CRAVEN R.J., WEINER T.M., LIU E.T.;

CANCE W.G., CRAVEN R.J., WEINER T.M., LIU E.T.;

"Novel protein kinases expressed in human breast cancer.";

INT. J. CANCER 54:571-577(1933).

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PHOSPHATE.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

-!- TISSUE SPECIFICITY: RESTRICTED TO CELLS LINES DERIVED FROM TISSUES

OF LYMPHOID, BRAIN, BREAST, COLON AND BLADDER ORIGIN.

-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

-!- SIMILARITY: CONTAINS I SH2 DOMAIN.

-!- SIMILARITY: CONTAINS I SH3 DOMAIN.
                                                                                                                                                                                                                 122 WFLGKIKRVEAEKMLNQSFNQVGSFLIRDSETTPGDFSLSVKDQDRVRHYRVRRLEDGSL 181
                                                                                                                                                                                                                                                                                                               FRK_HUMAN STANDARD; PRT; 505 AA.
P42685; 013128;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
YFROSINE-PROTEIN KINASE FRK (EC 2.7.1.112) (NUCLEAR TYROSINE PROTEIN KINASE RAK).
                                                                                                                                                                                 Gaps
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000069; pkinase; 1.
HSSP; P00523; 2PTK.
TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEE J., WANG 2., LUOH S.-M., WOOD W.I., SCADDEN D.T.; "Cloning of FRK, a novel human intracellular SRC-like tyrosine
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                         Length 505;
                                                                                                                                                        Score 262; DB 1; Length 505
Pred. No. 6.09e-36;
21; Mismatches 35; Indels
                                                                                                   ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                         BY SIMILARITY.
3AE3DF34 CRC32;
                                                                             SH2.
PROTEIN KINASE
                                                                                                                                                                                                                                                               180 YLQKGRLFPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                                182 FVTRRSTFQILHELVDHYKIETDGLCCKLLYPC 214
                                                                 116 SF
214 SF
493 PF
254 AT
268 AT
359 AT
57693 MW;
                                                      SH3 DOMAIN; PHOSPHORYLATION.
DOMAIN 54 116
DOMAIN 122 214
                                                                                                                                                        37.5%;
39.8%;
                                                                                                                                               Ouery Match
Best Local Similarity 39.00,
37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase-encoding gene.";
GENE 138:247-251(1994).
                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-LYMPHOID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94171047.
                                                                                                 246
268
359
505 #
                                                                                                                         ACT_SITE
SEQUENCE
                                                                                      DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                      RESULT
    DAN WENT THE THE SO
                                                                                                                                                                                                    ద
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                    ò
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 WFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKHYRIKRLDEGGF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87133831.
CACCIA N., TOYONAGA B., SPOLSKI R., YANAGI Y., YOSHIKAI Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7.1.112) (P56-LCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAK T.W.;

A human T cell-specific cDNA clone (YT16) encodes a protein with

"A human to a family of protein-tyrosine kinases.";

EUR. J. IMMUNOL. 16:1643-1646(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE: 89123626.
PERIMITER R.M., MARTH J.D., LEWIS D.B., PEET R., ZIEGLER S.F., WILSON C.B., "Structure and expression of lck transcripts in human lymphoid
                                                                                                                                                                                                                                                        PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000618; Dkinase; 1.
HSSP; P00523; ZPTK.
TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 90108697.
ROUER E., VAN HUYNH T., DE SOUZA S.L., LANG M.C., FISCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260; DB 1; Length 505
Pred. No. 1.71e-35;
23; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G -> R.
P -> A (IN REF. 2).
C4226A83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCK_HUMAN STANDARD; PRT; 508 AA. P06239; P07100; 01-JAN-1988 (REL. 06, CREATED) 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC. (LSK) (T CELL-SPECIFIC PROTEIN-TYROSINE KINASE)
                                                                                                                                        EMBL; U00803; G332588; -.
EMBL; U22322; G732528; -.
PROSITE; PSO0107; PROTEIN_KINASE_ATP;
PROSITE; PSO0109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS50011; SH2; 1.
PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL. BIOCHEM. 38:117-126(1988).
                                                                                                                                                                                                                                                                                                                                                                                              116 208
134 491
40 248
2 262
3 54
3 87
1 122
1 15
5 8 2 5 4 W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| : |:|: |:|: |
180 YLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 FLTRRRIFSTLNEFVSHY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.2%;
Best Local Similarity 41.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
122
115
505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
```

Mon May 24 07:23:56 1999

```
"Structure of the human lck gene: differences in genomic organisation within src-related genes affect only N-terminal exons."; GENE 84:105-113(1989).
                                                                                   VEILLETTE A., FOSS F.M., SAUSVILLE E.A., BOLEN J.B., ROSEN N.;
"Expression of the lok tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines.";
ONCOGENE RES. 1:357-374(1987).
                                                                                                                                                                                                       Human T lymphocytes express a protein-tyrosine kinase homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAMAGÜCHI H., HENDRICKSON W.A.;
"Structural basis for activation of human lymphocyte kinase Lck upon
tyrosine phosphorylation.";
MATURE 384:484-489(1996).
                                                                                                                                                                                                                                                                  MEDLINE; 89096891.
GARVIN A.M., PAWAR S., MARTH J.D., PERLMUTTER R.;
"Structure of the murine lck gene and its rearrangement in a murine
                                                                                                                                                                                                                                                                                                                                                                   MEDIALIS; 03-27-27-04.

MINIMARY T., LEUGN S., GERNONE A., KOGA Y., TAKIHARA Y.,

MINIMANOTO N.G., MAK T.W.;

MINIMARY OF G., MAK T.W.;

MINIMARY OF G., MAK T.W.;

MINIMARY OF TWO PROMOTERS OF The human lck gene: differential accumulation of two classes of lck transcripts in T cells.";

MOL. CELL. BIOL. 9:2173-2180(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIKOL V., BAUMANN G., KELLER T.H., MANNING U.M., ZURINI M.G.M.;
"The crystal structures of the SH2 domain of p561ck complexed with
two phosphonopeptides suggest a gated peptide binding site.";
"MOL. BIOL. 246:344-355(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.
MEDLINE; 96177765.
TONG L., WARREN T.C., KING J., BETAGERI R., ROSE J., JAKES S.;
"Crystal structures of the human p561ck SH2 domain in complex with two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";
J. MOL. BIOL. 256:601-610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECK M.J., ATWEELL S.K., SHOELSON S.E., HARRISON S.C.; "Structure of the regulatory domains of the Src-family tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN TYROSINE PHOSPHATE.
ENZYME REGULATION: REGULATED BY PHOSPHORYLATION ON TYR-504
                                                                                                                                                                            FREVILLYAN J.M., LIN Y., CHEN S.J., PHILLIPS C.A., CANNA C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
MEDLINE; 95173978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500. MEDLINE; 97100952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
                                                                                                                                                                                                                               BIOCHIM. BIOPHYS. ACTA 888:286-295(1986)
                                                                                                                                                                                                                                                                                                         .ymphoma cell line.";
                                                             SEQUENCE OF 367-508 FROM N.A. MEDLINE; 88217332.
                                                                                                                                                      SEQUENCE OF 374-508 FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-34 FROM N.A. MEDLINE; 89313764.
                                                                                                                                                                                                                                                        SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase Lck.";
NATURE 368:764-769(1994).
                                                                                                                                                                87000726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94203291
                                                                                                                                                                                           LINNA T.J
                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [10]
```

CD4 OR CD8.
SIMILARITY: CONTAINS 1 SH2 DOWAIN.
SIMILARITY: CONTAINS 1 SH3 DOWAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION.
PHOSPHORYLATION.
TO SERVICE STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTO-ONCOGENE: TYROSCINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE; ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; PALMITATE; LIPOPROTEIN; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 241; DB 1; Length 508
Pred. No. 2.83e-31;
21; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDAFL -> AGRLP (IN REF. 2)
T -> A (IN REF. 5).
L -> H (IN REF. 4).
QYQPQP -> STA (IN REF. 2).
10E545CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 DNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFO0017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE.
                                                                                                                                                                                                                                        L; M36881; G187034; -..
L; X04476; G35780; -..
L; X14055; G825687; JOINED.
L; X14054; G825687; JOINED.
L; X05369; G34289; -..
L; X05369; G34289; -..
L; M21510; G553522; ALT_TERM.
L; M21510; G553522; ALT_TERM.
L; M20152; OKHULK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508
57869 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                     EMBL; X13529; G34295; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-96.
08-MAR-96.
08-MAR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1LCJ; 15-OCT-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503
508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2544
2722
3363
3363
364
364
205
205
205
205
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1CWE;
1LKK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3LCK;
1CWD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1LKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1LCK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
LIPID
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

```
HERENE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE
                                                                                                                                                                                                                                                                                                                MEDIINE; 86079521.
MARTH J.D., PEET R., KREBS E.G., PERLMUTIER R.M.;
A lymphocyte-specific protein-tyrosine Kinase gene is rearranged and overexpressed in the murine I cell lymphoma LSTRA.";
CELL 43:393-404(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88142832.
VORONOVA A.F., ADLER H.T., SEFTON B.M.;
"Two lck transcripts containing different 5' untranslated regions are present in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABRAHAM K.M., LEVIN S.D., MARTH J.D., FORBUSH K.A., PERLMUTTER R.M.; "Thymic tumorigenesis induced by overexpression of p561ck."; PROC. NATL. ACAD. SCI. U.S.A. 88:3977-3981(1991).
                                                                  P06240: 061794; 061795; 062320; 01-7NY-1988 (REL. 06, CREATED) 01-FBE-1994 (REL. 38, LAST SEQUENCE UPDATE) 01-NOY-1997 (REL. 35, LAST SEQUENCE UPDATE) PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (P56-LCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 89096891.
GARVIN A.M., PAWAR S., MARTH J.D., PERLMUTTER R.M.;
"Structure of the murine lck gene and its rearrangement in a murine
l'ymphoma cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Creation and characterization of temperature-sensitive mutants of the lck tyrosine protein kinase."; J. VIROL. 66:7406-7413(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABRAHAM N., MICELI M.C., PARNES J.C., VEILLETTE A.;
Enhancement of T-cell responsiveness by the lymphocyte-specific
tyrosine protein kinase p561ck.";
NATURE 350:62-66(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cells:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           φ
                                                                                                                                                                                             LCK ÓR LSK-T.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VORONOVA A.F., SEFTON B.M.;
Expression of a new tyrosine protein kinase is stimulated
retrovirus promoter insertion.";
NATURE 319:682-685(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMREIN K.E., SEFTON B.M.;
"Avian reovinus mRNAs are nonfunctional in infected moue translational basis for virus host-range restriction.";
PROC. NATL. ACAD. SCI. U.S.A. 85:4257-4261(1988).
                                                        508 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93133805.
CARRERA A.C., ALEXANDROV K., ROBERTS T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93059694.
HURLEY T.R., AMREIN K.E., SEFTON B.M.;
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MÖL. CELL. BIOL. 8:3058-3064(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOL. CELL. BIOL. 7:4407-4413(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-10 FROM N.A.
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF TYR-504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF TYR-504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF LYS-272. MEDLINE; 91163633.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 86146842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91219495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 88248001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS
                                                      LCK_MOUSE
                                                                                                                                                                            (LSK)
                                     RESULT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4 OR CD8.
--- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND AT A B ELEYATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOWA) CELLS.
--- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE.
-!- ENZYME REGULATION: REGULATED BY PHOSPHORYLATION ON TYR-504.
-!- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
                                                                                                                                                                                                                                                                                                                                                                                                            KOBGL M., ZLATKINE P., LEY S.C., COURTNEIDGE S.A., MAGEE A.I.;
"Palmitoylation of multiple Src-family kinases at a homologous N-terminal motif.";
BIOCHEM, J. 303:749-753(1994).
-i- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE
"The conserved lysine of the catalytic domain of protein kinases is actively involved in the phosphotransfer reaction and not required for anchoring ATP.";
                                                                                                                                                                      MEDLINE; 94019312.
SHENNY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LUBLIN D.M.;
"Palmitylation of an amino-terminal cysteine motif of protein
tyrosine kinases p561ck and p59fyn mediates interaction with
glycosyl-phosphatidylinositol-anchored proteins.";
MOL. CELL. BIOL. 13:6385-6392(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-CELL ONTOGENY.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROPEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; PALMITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYRISTATE (BY SIMILARITY).
PALMITATE.
PALMITATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                           PROC. NATL. ACAD. SCI. U.S.A. 90:442-446(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P06239; 1LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X03533; G54814; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95071286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                             PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPID
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL).
K->N: REDUCED ACTIVITY.
A->S: REDUCED ACTIVITY.
V->A: REDUCED ACTIVITY.
V->A: REDUCED ACTIVITY.
K->R: LOSS OF ACTIVITY.
K->N: REDUCED ACTIVITY.
K->N: REDUCED ACTIVITY.
K->N: REDUCED ACTIVITY.
K->N: REDUCED ACTIVITY.
K->N: REDUCED ACTIVITY.
K->N: REDUCED ACTIVITY.
K->V: REDUCED ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :|| :|| :|| ||:|| || ||:||| || ||: ||||| ||: ||:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE: 84082064.

HOFFMANN F.M., FRESCO L.D., HOFFMAN-FALK H., SHILO B.-Z.;
HOFFMANN F.M., FRESCO L.D., HOFFMAN-FALK H., SHILO B.-Z.;
"Nucleotide sequences of the Drosophila src and abl homologs:
conservation and variability in the src family oncogenes.";
CELL 35:393-401(1983).

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 86028179. SIMON M.A., DREES B., KORNBERG T., BISHOP J.M.; The nucleotide sequence and the tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; ARTHROPODA; TRÁCHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 238; DB 1; Length 508;
Pred. No. 1.30e-30;
22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                      >>F: CAUSES THYMIC TUMORS.
> -> DA (IN REF. 2).
70423E50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 DNGGFYI-SPRITFPGLHDLVRHYTNASDGLCTKLSRPC~223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
1-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC64B (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 AA
                                                                                                                                                                                                                                                                                                      Y->F:
VP ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                                                                                                                                               MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 249-552 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M11917; G158501; -.
EMBL; K01043; G157304; -.
PIR; A00634; TVFFS.
FLYBASE; FBGn0003501; Src64B.
363
393
393
204
269
270
271
272
274
274
275
583
57821
                                                                                                                                                                                                                                                                                                                                                                                                                     34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           39.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila c-src.";
CELL 42:831-840(1985).
                                                                                                                                                                                                                                                                                                                             282
508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRC1_DROME
P00528;
                                                                                                           MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                               MOD_RES
MOD_RES
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORIATION:

RPQ -> ASI (IN REF. 2).

MWDL -> TAAADVGF (IN REF. 2).

E -> Q (IN REF. 2).

L -> VV (IN REF. 2).

L -> VV (IN REF. 2).

C -> R (IN REF. 2).

E -> A (IN REF. 2).

G -> R (IN REF. 2).

D -> N (IN REF. 2).

G -> N (IN REF. 2).

AS -> TT (IN REF. 2).

AS -> TT (IN REF. 2).

AS -> TT (IN REF. 2).

C -> Q (IN REF. 2).

AS -> TT (IN REF. 2).

C -> R (IN REF. 2).

C -> R (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).

C -> C (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 WFFENVLRKEADKLLLAEENPRGTFLVRPSEHNPNGYSLSVKDWEDGRGYHVKHYRIKPL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRC_RSVSR STANDARD; PRT; 526 AA.
P00524;
21-JUL-1986 (REL. 01, CREATED)
01-JUL-1889 (REL. 11, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDIJNE; 89160256.
BARNIER J.V., DEZELEE P., MARX M., CALOTHY G.;
BARNIER Sequence of the src gene of the Schmidt-Ruppin strain of
Rous sarcoma virus type E. ",
NUCLEIC ACIDS RES. 17:1252-1252(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROUS SARCOMA VIRUS (STRAIN SCHMIDT-RUPPIN).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                         PFAM: PF00069; pkinase; 1.
HSSP; P11362; 1FGI.
TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; PHOSPHORYLATION;
TRANSFERASE; ATP-BINDING; SH3 DOMAIN; SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 236; DB 1; Length 552
Pred. No. 3.57e-30;
22; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 DNGGYYIATNQTFPSLQALVMAYSKNALGLCHI-LSRPC 259
PROSITE; PSO0107; PROTEIN_KINASE_ATP;
PROSITE; PSO0109; PROTEIN_KINASE_TYR;
PROSITE; PSS00011; PROTEIN_KINASE_DOM;
PROSITE; PSS0001; SH2; 1.
PROSITE; PSS0002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.8%;
Best Local Similarity 38.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63018
                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
MEDLINE; 83141780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 AA;
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V-SRC.
                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A PACTOR OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVI
```

^

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 MEDLINE; 81220979.

NEIL J.C., GHYSDAEL J., VOGT P.K., SMART J.E.;
"Homologous tyrosine phosphorylation sites in transformation-specific gene products of distinct avian sarcoma viruses.";
NATURE 291:675-677(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93201600.
WAKSHAN G., SHOELSON S.E., PANT N., COMBURN D., KURIYAN J.;
Binding of a high affinity phosphotyrosyl peptide to the Src SH2
domain: crystal structures of the complexed and peptide-free forms.";
CELL 72:779-790(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLUMMER M.S., HOLLAND D.R., SHAHRIPOUR A., LUNNEY E.A., FERGUS J.H., MARKS J.S., MCCONNELL P., MUELLER W.T., SAWYER T.K.;
"Design, synthesis, and cocrystal structure of a nonpeptide Src SH2 domain ligand.";
J. MED. CHEM. 40:3719-3725(1997).
-!- FUNCTION. THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPPLASTIC TRANSFORMATION. IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                   WAKSMAN G., KOMINOS D., ROBERTSON S.C., PANT N., BALTIMORE D., BIRGE R.B., COWBURN D., HANAFUSA H., MAYER B.J., OVERDUIN M., RESH M.D., RIOS C.B., SILVERNAN L., KURIYAN J.; "Crystal structure of the phosphotyrosine recognition domain SH2 of v-src complexed with tyrosine-phosphorylated peptides."; NaTURE 358:646-653(1992).
                                                                                                              TAKEYA T., HANAFUSA H.; "Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus."; CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
              ISCHER E., GOODMAN H.;
Corrections to the nucleotide sequence of the src gene of Rous
                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 144-247 (SH2 DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 146-247 (SH2 DOMAIN).
MEDLINE; 98038574.
                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1:5 ANGSTROMS) OF 148-245 (SH2 DOMAIN)
CZERNILOFSKY A.P., LEVINSON A.D., VARMUS H.E., BISHOP J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                       PHOSPHORYLATION AT TYR-416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L29199; G459677; -. EMBL; X13745; G61909; -. EMBL; V01169; G61499; -.
                                          Sarcoma virus.";
NATURE 301:736-738(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1SHA; 31-0CT-93.
PDB; 1SHA; 31-0CT-93.
PDB; 1SHB; 31-0CT-93.
PDB; 1SPR; 31-MAX-94.
PDB; 1SPR; 31-JUL-94.
PDB; 1SPS; 31-JUL-94.
                                                                                    SEQUENCE FROM N.A. MEDLINE; 83155664.
                                                                                                                                                                                                                                                                                                         MEDLINE; 92357140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN VITRO.
```

```
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIAN SARCOMA VIRUS (STRAIN RASV1441).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ις
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 235; DB 1; Length 526;
Pred. No. 5.92e-30;
26; Mismatches 20; Indels
                                                                                                        TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION;
SH3 DOMAIN; SH2 DOMAIN; 3D-STRUCTURE.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50007; SH3; 1.
PFAM; PF00017; SH2; 1.
PFAM; PF00017; SH3; 1.
PFAM; PF00018; SH3; 1.
TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
                                                                                                                                                                                                                                                                                                                                     3
3
3
                                                                                                                                                                                                                   ATP (D1 ) D1 SIMILARITY.

PHOSPHORYLATION (AUTO-).

'TN REF. 2 AND 3).
                                                                                                                                                                                                                                                        (IN REF. 2 AND 3
(IN REF. 2).
(IN REF. 3).
(IN REF. 2).
(IN REF. 2 AND 3
(IN REF. 2 AND 3
                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58953 MW; D110C9D9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 AA
                                                                                                                                      MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 83059858.
TAKEYA T., FELDMAN R.A., HANAFUSA H.;
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 DSGGFYITSRIQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.6%;
Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
195
206
209
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
244
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V-SRC.
AVIAN SARCOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRC_AVISR
P00525;
                                                                                                                                                                                                                         ACT_SITE
MOD_RES
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                               NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
HELIX
                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                    TURN
                                                                                                                                                                                                                                                                                                                                                                                                                             IURN
                                                                                                                                                                                                                                                                                                                                                                                                                                            rurn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rurn
```

'n

œ

```
MEDLINE; 91304409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93279385.
                                                                SEQUENCE FROM N.A. MEDLINE; 83155664.
                                                                                                                                                                                                                                                                                                MEDLINE; 84270751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95063992
                                                                                                                                                                                                                                                                                      ATP-BINDING SITE
                                                                                                                                                REVISION TO 525
                                                                                                                                                                                                                                                                                                                                                                                                     HUNTER T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ж
Э
                                                                                       "Homologous tyrosine phosphorylation sites in transformation-specific gene products of distinct avian sarcoma viruses."; NATURE 291:675-677(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete nucleotide sequence of an EcoRI fragment of recovered avian sarcoma virus which codes for gp37 and pp60src.", J. VIROL. 44:1-11(1982).
                                                                                                                         -!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DNA sequence of the viral and cellular src gene of chickens. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 235; DB 1; Length 526; Pred. No. 5.92e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-).
84D2739D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE.
SH3.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
---ATP - (BY--SIMILARITY).
                                                    PHÓSPHORYLATION AT TYR-416.
MEDLINE; 81220979.
NEIL J.C., GHYSDAEL J., VOGT P.K., SMART J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                             DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                      PIR; A00631; TVFV60.
PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ULT 10
SRC_CHICK STANDARD; PR'
P00523; 091345; 092013;
21-JUL-1986 (REL. 01, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUE
15-JUL-1998 (REL. 36, LAST ANNOT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ADGSLYLOKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
245 SH
217 PR
517 AT
295 ...-AT
386 ...-AT
58878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00069; pkinase; 1. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                             EMBL; K00928; G210189; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        PF00017; SH2; 1.
PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
267
273
295
386
416
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                           IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
ID SE
AC PC
DT 21
DT 01
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
MEDLINE; 86151652.
COOPER J.A., GOULD K.L., CARTWRIGHT C.A., HUNTER T.;
"Tyr527 is phosphorylated in pp60c-src: implications for regulation.";
SCIENCE 231:1431-1434(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken Src:
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in 5'
                                                                                                                                                                                                                                                                                     the cellular gene homologous to the RSV for generating the transforming virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAMPS M.P., TAYLOR S.S., SEFTON B.M.;
"Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
dependent protein kinase have homologous ATP-binding sites.";
NATURE 310:589-592(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the Src SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exons and possible mechanism for the genesis of the 3' end of v-src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., CHEN J.K., YU H., SIMON J.A., SCHREIBER S.L.;
binding orientations for peptides to the Src SH3 domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
MEDLINE; 86028181.
GOULD K.L., WOODGETT J.R., COOPER J.A., BUSS J.E., SHALLOWAY
                                                                                               AVES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Protein kinase C phosphorylates pp60src at a novel site.";
CELL 42:849-857(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART J.E., OPPERMANN H., CZERNILOFSKY A.P., PURCHIO A.F., ERIKSON B.L., BISHOP J.M., "Characterization of sites for tyrosine phosphorylation in transforming protein of Rous sarcoma virus (pp60v-src) and
                                                           GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVI
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98070614.
WILLIAMS J.C., WEIJLAND A., GONFLONI S., THOMPSON A., COURTNEIDGE S.A., SUPERTI-FURGA G., WIERBRAA R.K.;
The 2.35 A crystal structure of the inactivated form of a dynamic molecule with multiple regulatory interactions. J. MOL. BIOL. 274:757-775(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; "Analysis of cDNAs of the proto-oncogene c-src: hetero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular homologue (pp60c-src).";
PROC. NATL. ACAD. SCI. U.S.A. 78:6013-6017(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fu H., ROSEN M.K., SCHREIBER S.L.;
"IH and 15N assignments and secondary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL. BIOL. 11:4165-4176(1991).
                                                                                                                                                                                                                                                       TAKEYA T., HANAFUSA H.; "Structure and sequence of src gene and the mechanism CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS LETT. 324:87-92(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHÓSPHORYLATION AT TYR-415.
MEDLINE; 82082387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION AT TYR-526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 80-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 76-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-18 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKEYA T., HANAFUSA H
CELL 34:319-319(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FENG
```

σ

```
IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                     T 11
SRC_AVIST
P14085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                     RSGL
PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO PHODO P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                g
                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    -i- FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS
                                                                                                                                                                                                          -!- ENZIME REGULATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE PHOSPHORYLATED IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.
-!- POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROFEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.
-!- SIMILARITY: TO OTHER SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH3 DOMAIN; SH2 DOMAIN;
development of a general model for SH3-ligand interactions."; SCIENCE 266:1241-1247(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 235; DB 1; Length 532; Pred. No. 5.92e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION;
                                                                                                                                                                CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION.
65406BF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE;
TRANSFERASE; ATP-BINDING; MYRISTYLATION;
TO 0 0
LIPID 1 1 MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -; -; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE.
SH3.
SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_IYR; PROSITEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 F
59919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00402; G63354; --
EMBL; S43604; E75862; --
EMBL; S43616; E75867; --
EMBL; S43587; E75861; --
EMBL; S43609; E75863; --
EMBL; S43614; E75866; --
PIR; A00630; TVCHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
280
294
385
415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-94.
31-MAY-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00017; SH2;
                                                                                                                                     AND MACROPHAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415
526
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A00630; PDB; ISRL; 3 PDB; ISRL; 3 PDB; 2PTK; 2 PDB; IQWE; C PDB; IQWE; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; IRLP; C PDB; C PDB; IRLP; C PDB; C PDB; C PDB; C PDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
MOD_RES
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
```

```
'n
120 WYFSGVSTTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                          01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 7F8DAC50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 87064539.
IKAWA S., HAGINO-YAMAGISHI K., KAWAI S., YAWAMOTO T., TOYOSHIMA K.;
"ACLIVATION of the cellular src gene by transducing retrovirus.";
MOL. CELL. BIOL. 6:2420-2428(1986).
-!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_LOM; 1.
PROSITE; PS00110; PROTEIN_KINASE_LOM; 1.
PROSITE; PS0011; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                  V-SRC.
AVIAN SARCOMA VIRUS (STRAIN S2).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ς,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 235; DB 1; Length 557;
Pred. No. 5.92e-30;
26; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 AA.
                                                                                                                                                                                                                557 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYRISTATE
                                                                                                                                                                                                                PRT;
                                                                   207 DSGGFYITSRTQFSSLQQLVAYY 229
                                                                                                208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62582 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%;
ilarity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3 DOMAIN; SH2 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
267
273
273
295
295
386
386
416
557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
ID SRC_AVIS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

PRT;

STANDARD;

ë

Gaps

26; Mismatches 20; Indels

32; Conservative

පු

147 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 206

```
Query Match
Best Local Similarity
                              Matches
                                                             요
                                                                                           ò
                                                                                                                          d
                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 88DFD703 CRC32;
                                                                                                                                                                                                                      Ţ
                                                                                                                                                                                                                                                                                                                                                                           W.T., MCCONNELL P.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (MAY-1997) TO THE PDB DATA BANK.
-!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                       AVIÀN SARCOMA VIRUS (STRAIN PR2257).
VIRUSES: RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                    GERYK J., DEZELEE P., BARNIER J.V., SVOBODA J., NEHYBA J.,
KARAKOZ I., RYNDITCH A.V., YATSULA B.A., CALOTHY G.;
Transduction of the cellular src gene and 3' adjacent sequences
avian sarcoma virus PR2257.";
J. VIROL. 63:481-492(1989).
                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 146-249.
HOLLAND D.R., LUNNEY E.A., PLUMMER M.S., MUELLER W.T., MCCONNELL
PAVLOVSKY A., PARA K.S., SHAHRIPOUR A., HUMBLET C., SAWYER T.K.,
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
YATSULA B.A., GERYK J., SVOBODA J., RYNDITCH A.V., CALOTHY
DEZELEË P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00069; pkinase; 1. TRANSFORMING PROTEIN; ONCOGENE; TRANSFERASE; PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE; TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                             SUBMITTED (APR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1BKL; 23-JUL-97.
PDB; 1BKM; 07-JUL-97.
PDB; 1BKM; 07-JUL-97.
PPDS; 1EKM; 07-JUL-97.
PPOSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M21526; G210265; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X51863; G394713; -. PIR; A30174; TVFVPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
245
520
281
295
386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
267
273
295
386
416
587 AA;
                                                                                                                                                                     MEDLINE; 89094972.
                                                                                                                                                        FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PROSITE; P
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                   V-SRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPID
```

```
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 87257942.
QUINTRELL N., LEBO R., VARMUS H., BISHOP J.M., PETTENATI M.J.,
LE BEAU M.M., DIAZ M.O., ROWLEY J.D.;
"Identification of a human gene (HCK) that encodes a protein-tyrosine
kinase and is expressed in hemopoietic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 87257943.
ZIEGLER S.F., MARTH J.D., LEWIS D.B., PERLMUTTER R.M.;
"Novel protein-tyrosine kinase gene (hck) preferentially expressed in
cells of hematopoietic_origin.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98239731.
HORITA D.A., BALDISSERI D.M., ZHANG W., ALTIERI A.S., SMITHGALL T.E., GMEINER W.H., BYRD R.A.;
"Solution structure of the human Hck SH3 domain and identification of its ligand binding site.";
J. Mol. BIOL. 278:253-265(1998).
                                                                                          120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                      148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
MEDLINE; 91342636.
LOCK P., RALPH S., STANLEY E., BOULET I., RAMSAY R., DUNN A.R.;
"Two isoforms of murine hok, generated by utilization of alternative translational initiation codons, exhibit different patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHANG W., SMITHGALL T.E., GMEINER W.H.;
"Sequential assignment and secondary structure determination for the Src Chomology 2 domain of hematopoietic cellular kinase.";
FEBS LETT. 406:131-135(1997).
                                     Gaps
                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P59-HCK AND P60-HCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUMAS C.,
                                     5.
                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97177106.
SICHERI F., MOAREFI I., KURIYAN J.;
"Crystal structure of the Src family tyrosine kinase Hck.";
                                     20; Indels
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AROLD S., O'BRIEN R., FRANKEN P., STRUB M.P., HOH F.,
Score 235; DB 1; 1
Pred. No. 5.92e-30;
26; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
MEDLINE: 97177106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137
                                                                                                                                                                                                                                                        526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subcellular localization.";
MOL. CELL. BIOL. 11:4363-4370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. CELL. BIOL. 7:2276-2285(1987).
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOL. CELL. BIOL. 7:2267-2275(1987).
                                                                                                                                            208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                  01-AUG-1988 (REL. 08, CREATED)
01-NOV-1995 (REL. 32, LAST SEQI
15-DEC-1998 (REL. 37, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 22-526 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22-526 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 139-245.
 33.6%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5]
STRUCTURE BY NMR OF 78-138
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 385:602-609(1997).
                                                                                                                                                                                                                                                                                                                                                               (HEMOPOIETIC CELL KINASE)
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97263487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98453315
                                      32;
                                                                                                                                                                                                                                                    HCK_HUMAN
P08631;
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                  MYELOID AND B-LYMPHOLD LINEAGES.
--- ALTERNATIVE PRODUCTS: THE P60-HCK AND P59-HCK ARE PRODUCED BY THE USE OF ALTERNATIVE INITIATION SITES.
--- SIMILARITY: CONTAINS 1 S42 DOMAIN.
--- SIMILARITY: CONTAINS 1 S43 DOMAIN.
--- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
--- DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
         "RT loop flexibility enhances the specificity of Src family SH3
domains for HTV-1 Nef.";
BIOCHEMISTRY 37:14683-14691(1998).

-! FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
DEGRANULATION PROCESS OF NEUTROPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 WFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKIRTL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
S -> C (IN G306833).
F9B6EE42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFERASE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN; ALTERNATIVE INITIATION; 3D-STRUCTURE.
                                                                                                                                           -!- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYROSINE-PROTEIN KINASE P60-HCK.
TYROSINE-PROTEIN KINASE P59-HCK.
MYRISTATE (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 233; DB 1; Le
Pred. No. 1.62e-29;
24; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0107; PROTEIN_KINASE_ATP; PROSITE; PSO0109; PROTEIN_KINASE_IYR; PROSITE; PS50001; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.38;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16591; G306832; -. EMBL; M16592; G306833; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00069; pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 4HCK; 17-JUN-98.
PDB; 5HCK; 17-JUN-98.
PDB; 1AD5; 15-MAY-97.
PDB; 1BU1; 11-NOV-98.
MIM; 142370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
138
241
515
515
276
290
381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2HCK; 20-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A27812; TVHUHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
262
268
290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB;
ö
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                       XIPHOPHORUS HELLERI.
BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ATHERINOMORPHA;
CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECLILIDAE; XIPHOPHORUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 WYFGKLSRKDTERLLLLPGNERGTFLIRESETTKGAYSLSLRDWDETKGDNCKHYKIRKL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA--QAKV--C-HYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
3EEC9C23 CRC32;
                                                                                                                                                                                                                                                                                                                                                        MANNING, JIO113.
AANNING C., OTTLES., SCHARTL M.;
"Conservation of structure and expression of the c-yes and fyn genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES)
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROPEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOWAIN.
-!- SIMILARITY: TO OTHER PROPEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 233; DB 1; Length 544; Pred. No. 1.62e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORILATION;
TRARNSFERASE; ATP-BINDING; MYRISTATIC (BY SIMILARITY).
LIPID
DOMAIN
92 153 SH3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
175 ADGSLYLQKGRLFPGLEELLTYYK-ANWKLIQNPLLQPC 212
                                                                                   544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0109; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; S42; 1.
PROSITE; PS50002; S43; 1.
PRAM; PF00017; S43; 1.
PFAM; PF00018; S43; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 ADGSLYLQKGRLFPGLEELLTYYKAN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 DNGGYYITTRTQFMSLQMLVKHYTEH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61288 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%;
Similarity 39.5%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00069; pkinase; 1.
HSSP; P12931; 1FMK.
PROTO-ONCOGENE; TYROSINE-PI
                                                                                                                                                                                                                                                                                                                                                                                               in lower vertebrates.";
ONCOGENE 6:361-369(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54970; G64484; -.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-RIO LANCETILLA;
MEDLINE; 91187435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                T 14
YES_XIPHE
P27447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                      (C-YES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

ë

204 DNGGFYISPRSTFSTLQELVDHYKKGNDGLCQK-LSVPC 241

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 WYFSGVSRTQAQQLLLSPPNEFGAFLIRPSESSLGGYSLSVRAQAKVCHYRVSMAAADGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 WYFGDVKRAEAEKRLMVRGLPSGTFLIRKAETAVGNFSLSVRDGDSVKHYRVRKLDTGGY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
56885 MW; 2B724CE9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M25245; G159274; -.

R PIR; A34094; TVHAST.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS50001; SH2; 1.

R PROSITE; PS50001; SH2; 1.

R PROSITE; PS50001; SH2; 1.

R PRAM; PF00017; SH2; 1.

R PFAM; PF00016; SH3; 1.

R PFAM; PF00016; SH3; 1.

R PFAM; PF00069; pkinase; 1.

R PFAM; PF00069; pkinase; 1.

H SSP; P0523; 1PRL.

TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; PHOSPHORYLATION;

TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; PHOSPHORYLATION;

TRANSFERASE; ATP-BIDING; MYRISTYLATION; SH3 DOMAIN.

LIPID.

Z MYRISTATË (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDINE, 90066418.

MEDINE, 00066418.

Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOL. CELL. BIOL. 9:4141-4151(1989).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                            HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).
EUKARYOTA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; ANTHOMEDUSAE;
HYDRIDAE; HYDRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 232; DB 1; Length 509;
Pred. No. 2.69e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Mismatches 37; Indels
                                                                                          01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE STK (EC 2.7.1.112) (P57-STK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                  509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 FITTRAPFNSLYELVQHYTKDADGLV-CALTLPC 218
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.2%;
37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 37.2%;
ses 35; Conservative
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 1
126 2
240 4
246 2
268 2
360 3
390 3
                               STK_HYDAT
P17713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
STEPTIFIFIFIFIER PRANCE PRODUCE CONTRACTOR PRANCE PRODUCE CONTRACTOR PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

Search completed: Thu May 20 12:56:17 1999 Job time: 15 secs.

* * * * * *	(TM)

**************************************	(ME) (ME)
***	**************************************

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 13.40 Seconds 378.732 Million cell updates/sec MPsrch_pp

Thu May 20 12:56:35 1999; Tabular output not generated. Run on:

>US-09-099-053-2 (120-212) from US09099053.pep (4 of 6) 699 Description:

1 WYFSGVSRTQAQQLLLSPPN.....LLTYYKANWKLIQNPLLQPC 93 Perfect Score: Seguence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremp19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_lnvertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 39.060; Variance 68.598; scale 0.569

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description ü Query Match Length DB Score Result

Pred. No B-CELL SRC-HOMOLOGY TY B-CELL SRC-HOMOLOGY TY SRC RELATED TYROSINE K DSRC41.

NON-RECEPTOR PROTEIN T SRC-RELATED INTESTINAL P56LCK. TSUP1 SRC (FRAGMENT). (SCHMIDT-RUPPIN D STRA C-SRC. LYMPHOCYTE-SPECIFIC PR TYROSINE KINASE. C-SRC PRODUCING P SRC TYROSINE KINASE. DJ370M22.1 (GROWTH FAC GADS PROTEIN. PROTEIN-TYROSINE KINAS GRB-2-RELATED MONOCYTI PP62V. GENE 061364 061745 062662 093813 064813 064813 013152 013880 013882 013880 013880 013880 013880 013880 013880 013880 098915 092957 043726 075791 064817 089100 086362

3.98e-27	1.67e-26	2.68e-26	6.94e-26	6.94e-26	2.88e-25	4.62e-25	4.62e-25	4.62e-25	1.91e-24	1.91e-24	1.26e-23	2.01e-23	2.01e-23	2.01e-23	3.22e-23	1.31e-22	3.34e-22	3.34e-22	5.33e-22	5.45e-21	8.66e-21	8.66e-21	5.50e-20	8.72e-20
PP62V.	H-19 PROVIRAL SEQUENCE	TYROSINE KINASE.	LYN PROTEIN TYROSINE K	P60 SRC.	SRC-LIKE ADAPTER PROTE	P120 POLYPROTEIN.	P120-GAG-ABL POLYPROTE	PROTO-ONCOGENE TYROSIN	PUTATIVE SRC-LIKE ADAP	GARDNER-RASHEED FELINE	GARDNER-RASHEED FELINE	SH2/SH3 ADAPTOR PROTEI	GAG-ONC FUSION PROTEIN	COMPLETE GENOME.	BLK-PROTEIN TYROSINE K	TYROSINE-PROTEIN KINAS	SH2/SH3 ADAPTOR PROTEI	C-SRC KINASE.	FGR MRNA.	SH2/SH3 ADAPTOR PROTEI	PS9FYN.	PROTO-ONCOGENE FYN,	TYROSINE KINASE RECEPT	PROTEIN TYROSINE PHOSP
086363	060567	064993	013064	092806	060898	092809	039477	013869	013239	039851	061404	P79956	028414	085466	016291	007461	024218	073786	063206	055032	Q16248	062844	063614	Q64509
14	1	14	13	14	11	14	14	4	4	14	11	13	ဖ	14	4	14	Ŋ	13	11	11	4	11	Ξ	11
546	526	526	488	525	281	980	981	1149	276	663	517	377	392	812	505	526	410	450	517	377	534	537	615	597
32.8	•	32.2		31.9	31.5	31.3	31.3	31.3	30.9	30.9	30.3	30.2	30.5	30.5	30.0	29.6	29.3	29.3	29.5	28.5	28.3	28.3	•	27.6
229	226	225	223	223	220	219	219	219	216	216	212	211	211	211	210	207	202	205	204	199	198	198	194	193
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

LT 1

O(01364)
O(01364)
O(01364)
O(01364)
O(1364)
O(1364)
O(1364)
O(1-NOV-1996 (TREMBLREL. 01, CREATED)
O(1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O(1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
O(1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
B-CELL SRC-HOMOLOGY TYROSINE KINASE (PROTEIN TYROSINE KINASE).
B-KEN OR BSK.
MUS WUSCULLG (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; AMEDINE; 95137395.

MEDLINE; 95137395.

MEDLINE; 95137395.

MEDLINE; 95137395.

A OBEGGWELSH C., WELSH M.;

T "Cloning of BSK, amurine FRK homologue with a specific pattern of tissue distribution.";

RT "Cloning of Ty7773.

REPRE, 1236123, 6777773; -...

REPRE, MGD: MGI:103265; FRK.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PFAM; PF00018; SH3; 1.

DR PFAM; PF00018; SH3; 1.

SQ SEQUENCE 512 AA; 58891 MW; DECF53C7 CRC32; 123 WFFGAIKRADAEKQLLYSENQTGAFLIRESESQKGDFSLSVLDEGVVKHYRIRRLDEGGF 182 Query Match 39.5%; Score 276; DB 11; Length 512; Best Local Similarity 37.6%; Pred. No. 4.85e-37; Matches 35; Conservative 26; Mismatches 32; Indels RESULT A PAC

512 AA 183 FLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPC 215 LT 2 PRELIMINARY; PRT; 061745; 01-NOV-1996 (TREMBLREL. 01, CREATED) RESULT ID Q6 AC Q6 DT 01 g

ö

~

```
093411
093411
093411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                094879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laloo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                               ŏ
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATIUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
                                                                                                                                                               the SEQUENCE FROM N.A.

SC STRAIN=BALB/C; TISSUE-MAMMARY GLAND;

RX MEDLINE; 9525166.

RA THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;

RT THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;

RT "iyk, a novel intracellular protein tyrosine kinase differentially

RT expressed in the mouse mammary gland and intestine.";

RD EMBL: Z4877; G736264; ...

DR RGJ: MGI.103265; FRK.

DR RGJ: S00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00101; SH2; 1.

DR PFAM; PF00018; SH3; 1.

DR PFAM; PF000169; PK1328; 1.

SQ SEQUENCE 512 AA; $8928 MW; 808D1612 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 WFFGAIKRADAEKQLLYSENQTGAFLIRESETQKGDFSLSVLDEGVVKHYRIRRLDEGGF 182 | 1:1::: |:: || : || : || : || || || || || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
B-CELL SRC-HOMOLOGY TYROSINE KINASE (INTESTINAL TYROSINE KINASE)
FRK OR IYK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE;
MEDLINE; 96330334.
SUNITHA I., AVIGAN M.I.;
The apical membranes of maturing gut columnar epithelial cells contain the enzymatically active form of a newly identified fyn-related tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY, TISSUE-SMALL INTESTINE;
SUNITHA I., AVIGAN M.I.;
BIOCHIM. BIOPHYS. ACTA, GENE STRUCT. EXPR. 1221:348-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.2%; Score 274; DB 11; Length 51 Best Local Similarity 36.6%; Pred. No. 1.30e-36; Matches 34; Conservative 27; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC RELATED TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8A3172C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVIGAN M.1.;
SUBMITTED (MAY-1994) TO EMBL/GENBANK/DDBJ DAY
EMBL; U09583: G339625;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
R PFAM; PF00017; SH2; 1.
R PFAM; PF00018; SH3; 1.
R PFAM; PF00069; pkinase; 1.
R PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 FLTRRKVFSTLNEFVNYYTTTSDGLCVKLEKPC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 356-416 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONCOGENE 13:547-559(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                     FRK OR IYK.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT 3
062662
062662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                  117 WFFGAIKRADAEKQLLYSENQTGAFLIRESESQKGDFSLSVLDEGVVKHYRIRRLDEGGF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NON-RECEPTOR PROTEIN TYROSINE KINASE LALOO.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOLAS, CHORDATA, VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIĂ; PIPOIDEA; PIPIDAE; KENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 WYFRKIKRIEAEKKLLLPENEHGAFLIRDSESRHNDYSLSVRDGDTVKHYRIRQLDEGGF 189
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAINSCANTON S;

A MEDLINE; 96268448.

TAKAHASHI F., ENDO S., KOJIMA T., SAIGO K.;

TREGULATION of cell-cell contacts in developing Drosophila eyes by Dsrc41, a new, close relative of vertebrate c-src.";

GENES DEV. 10:1645-1656(1996).

R EMBL; D42125; D1008290; -...

R FLXBASE; FBGN0004603; Src41.

R FLXBASE; FBGN0015, SAI.

R PFAM; PF00018; SH3; 1.

OR PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  рy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. WEINSTEIN D.C., MARDEN J., CARNEVALI F., HEMMATI-BRIVANLOU A.; "FGF-mediated mesoderm induction involves the Src-family kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             DROSOPHILA MELANOGASTER (FRUIT FLY).
EURARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTENYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
PROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 496;
Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 264; DB 5; Length 517;
Pred. No. 1.76e-34;
12; Mismatches 31; Indels
                    Pred. No. 3.48e-36;
25; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 AA
                                                                                                                                                                                                       177 FLTRRKTFSTLNEFVNYYTTTSDGLCVKLEKPC 209
  Score 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.2%; Score 260;
                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                               02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.9%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 YLQKGRLFPGLEELLTYY 197
Query Match 38.9%;
Best Local Similarity 37.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 FIARRITFRILQELVEHY 207
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

PRT;

```
PRELIMINARY;
                          01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q12850
Q12850;
                                                              P56LCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
               ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                           SIK.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                    117 WYFKGMSRKEAERQLLSPVNKSGAFMIRDSETMKGCFSLSVRDSGDTVKHYKIRTLDDGG 176
                                                  120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRAQA-KVCHYRVSMAADGS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 WFFGCISRSEAMHRLQAEDNSKGAFLIRVSQKPGADYVLSVRDAQAVRHYRIWKNNEGRL 137
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                           VASIOUKHIN V., SERFAS M.S., SIYANOVA E.Y., POLONSKAIA M., COSTIGAN V.J., LIU B., THOMASON A., TYNER A.L.; "A novel intracellular epithelial cell tyrosine kinase is expressed in the skin and gastrointestinal tract."; oncogene 10:349-357(1995).
                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC-RELATED INTESTINAL KINASE (EC 2.7.1.112)
(PROPERN-TYROSINE KINASE) (TRYROSYLPROPERN KINASE) (PROTEIN KINASE)
(TYROSINE)) (HYDROXYARYL-PROTEIN KINASE):...
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-HSD: ICR; TISSUE-INTESTINE;
MEDLINE: 9426846.
SIYANOVA E.Y., SERFAS M.S., MAZO I.A., TYNER A.L.;
"TYTOSINE kinase gene expression in the mouse small intestine.";
ONCOGENE 9:2053-2057(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIYANOVA E.Y.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
               ٠.
ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
?;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Pred. No. 1.25e-33;
20; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.1%; Score 252; DB 11; L. Best Local Similarity 38.3%; Pred. No. 6.14e-32; Matches 36; Conservative 18; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AA; 51972 MW; 5A749D95 CRC32;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-HSD: ICR AND BALB/C; TISSUE-INTESTINE; STRAINE; 95140424.
                                                                                                                                                              451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 HLNEAVSFSNLSELVDYHKTQ-SLSHGLQLSMPC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 YLQKGRLFFGLEELLTYYKANWKLIQN-PLLQPC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: 016805; G847795; --
EMBL: AF015545; G2738777; --
MGD: MGI: 99683; SIK.
PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.
PROSITE: PS00109; PROTEIN_KINASE_ATP: 1.
                                                                                                                                                             PRT;
                                                                                   177 FFIST-RIPFPSLPELVRHYQGK 198
                                                                                                   179 LYLOKGRL-FPGLEELLTYYKAN 200
  44.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-77 FROM N.A.
             37; Conservative
                                                                                                                                                             PRELIMINARY;
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFERASE. SEQUENCE
                                                                                                                                                                         064434;
                                                                                                                                                T 6
            Matches
                                                                                                                                                RESULT
                                                                                   g
                                                                                                            ó
                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

RESULT

```
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LEGKEMIA;
MEDLINE; 94187714.
MEDLINE; 94187714.
MEDLINE; 94187714.
MISSUE-LEGKEMIA; KAMPS M.P.;
Wincogenic activation of the Lck protein accompanies translocation the LCK gene in the human HSB2 T-cell leukemia.";
MOL. CELL. BIOL. 14:2429-2437(1994).
EMBL; U07236; G460966; ---
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE; 95155308.
WOGEL L.B., FUUTTA D.J.;
PPO phosphorylation and binding to p561ck is an early event in
interleukin-2-induced onset of cell cycle progression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241; DB 4; Length 363;
Pred. No. 1.26e-29;
21; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SEQUENCE FROM N.A. | MEDLINE; 96085119. | WOELL L.B., ARTHUR R., FUJITA D.F.; | WOELL L.B., ARTHUR R., FUJITA D.F.; | BIOCHIM. BIOPHYS. ACTA 1264:168-172(1995). | REMBL; U23852; G775208; -. | PFAM; PF00017; SH2; 1. | R PFAM; PF00018; SH2; 1. | R PFAM; PF00018; SH3; 1. | R PFAM; PF000069; pkinase; 1. | R PFAM; PF00069; pkinase; 1. | SEQUENCE 363 AA; 40866 MW; D2822D6A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOGEL L.B., FUJITA D.J.;
"The SH3 domain of p561ck is involved in binding to phosphatidylinositol 3'-kinase from T lymphocytes.";
MOL. CELL. BIOL. 13:7408-7417(1993).
                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 DNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 AA
    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-lymphocytes.";
J. BIOL. CHEM. 270:2506-2511(1995)
01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 40.4%;
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
    (TREMBLREL.
                                      (TREMBLREL. (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00017; SH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A MEDLINE; 94067101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDA REPRENTED DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DEL PROPERTICA DE LA PROPERTICA DEL PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DEL PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPE
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 5
                                                                                                   LT 10
Q85477
Q85477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CT 11
093080
093080;
                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TESULT ON THE SULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
    g
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEELS. KIM M., LEE K.-H., KANG K.-N., LEE S.-T.;

TEELS. KILOTHER STUTCTURE OF THE human PTK6 gene demonstrates that PTK6 constitutes a distinct family of "non-receptor tyrosine kinase.";

MOL. CELLS 8:401-407(1998).

R EMBL; VASR49; G5155026;

R EMBL; U61412; G3551733; JOINED.

R EMBL; U61408; G3551733; JOINED.

R EMBL; U61408; G3551733; JOINED.

R EMBL; U61409; G3551733; JOINED.

R EMBL; U61409; G3551733; JOINED.

R EMBL; U61410; G3551733; JOINED.

R EMBL; U61410; G3551753; JOINED.

R EMBL; U61410; G3551753; JOINED.

R EMBL; U61410; G3551753; JOINED.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                 127 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 186
                                                                                                                                                                                        78 WFFGCISRSEAVRRLQAEGNATGAFLIRVSEKPSADYVLSVRDTQAVRHYKIWRRAGGRL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94309916.
MITCHELL P.J., BARKER K.T., MARTINDALE J.E.;
"Cloning and characterisation of cDNAs encoding a novel non-receptor tyrosine kinase, brk, expressed in human breast tumours.";
ONCOGENE 9:2383-2390(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE: 97430836.
PARK S.H., LEE K.H., KIM H., LEE S.T.;
"Assignment of the human PTK6 gene encoding a non-receptor protein tyrosine kinase to 20q13.3 by fluorescence in situ hybridization.";
CYTOGENET. CELL GENET. 77:271-272(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                      7;
                                                                                Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                       175 ADGSLYLQKGRL-FPGLEELLTYYKANWKLIQNPLLQPC 212
                                                                                                                                                                                                                                               187 DNGGFYI-SPRITFPGLHELVRHYTNASDGLCTRLSRPC 224
                                                                            34.5%; Score 241; DB 4; I
40.4%; Pred. No. 1.26e-29;
rative 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 240; DB 4; Pred. No. 2.04e-29; 16; Mismatches 39
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 512 Aa; 58412 MW; 12B0BA65 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00069; pkinase; 1.
NCE 451 AA; 51834 MW; 4AC30408 CRC32;
                                                                                                                                                                                                                                                                                                                                                                          451 AA
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%;
larity 39.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDAT!
CATARRHINI; HOMINIDAE; HOMO
                                                                                                   larity 40.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=BREAST CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00017; SH2; 1
PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 98419955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROSINE KINASE.
BRK OR PTK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                   II 9
Q13882
Q13882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                        SOR
                                                                                                                                                                 g
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
```

```
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROUS SARCOMA VIRUS.
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 86062903.
NISHIZAMA M., MAYER B.J., TAKEYA T., YAMAMOTO T., TOYOSHIMA K.,
HANAFUSA H., KAWAI S.;
"Two independent mutations are required for temperature-sensitive
cell transformation by a Rous sarcoma virus temperature-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROUS SARCOMA VIRUS.
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92278773.

MARONEY A.C., QURESHI S.A., FOSTER D.A., BRUGGE J.S.;

MARONEY A.C., CORRESHI S.A., FOSTER D.A., BRUGGE J.S.;

reversible transformation of mammalian cells.";

ONCOGENE 7:1207-1214(1992).

EMBL; S37068: G249851.

NON_TER 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ι,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 235; DB 14; Length 523
Pred. No. 2.25e-28;
26; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235; DB 14;
Pred. No. 2.25e-28;
26; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M1753; G210226; -
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
SFAM; PF00018; SH3; 1.
SEAM; PF00018; SH3; 1.
SEQUENCE 523 AA; 58742 MW; 2C76C501 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 AA; 58970 MW; 08DA9189 CRC32;
                                                                                                                                                                                                                                                                           AA.
138 HINEAVSFLSLPELVNYHRAQ-SLSHGLRLAAPC 170
                                                    180 YLQKGRLFPGLEELLTYYKANWKLIQN-PLLQPC 212
                                                                                                                                                                                                                                                                       523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|: |::|: |::|: |::|::|| | |::|::|| | |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:
                                                                                                                                                                                                                                                                                                                                                                  01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08
08
08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 33.6%;
Local Similarity 38.6%;
nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.6%;
Similarity 38.6%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                  (TREMBLREL. (TREMBLREL. (TREMBLREL. (
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSUP1 SRC (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
01-NOV-1996
01-NOV-1998
```

ä

3,

'n

g G ö

```
MEDLINE; 97008971.

WEIJLAND A., NEUBAUER G., COURTREIDGE S.A., MANN M., WIENERGA R.;

"The purification and characterization of the catalytic domain of Src
expressed in Schizosaccharomyces pombe. Comparison of
unphosphorylated and tyrosine phosphorylated species.";
EUR. J. BIOCHEM. 240:756-764(1996).
                                                                                                                             120 WYFSGVSRTQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 83155664.
TAKEYA T., HANARUSA H.;
"Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus."; CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r,
                               .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity exons and possible mechanism for the genesis of the 3' end of v-src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
2
                                                                                                                                                                                                                                                                                                                                                                                                                           098915; 091343;
01-FEB-1997 (TREMBLEEL. 02, CREATED)
01-FEB-1997 (TREMBLEEL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
GENE C-SRC PRODUCING PROTEIN PP60-C-SRC.
THIS GENE IS HOMOLOGOUS TO THE ROUS SARCOMA VIRUS GENE V-SRC
(PP60C-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-SRC OR C'SCR.
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 235; DB 13; Length 533;
Pred. No. 2.25e-28;
26; Mismatches 20; Indels
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEILAND A.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
Pred. No. 2.25e-28;
26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase: 1.
SEQUENCE 533 AA; 60010 MW; 0D446FF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; V00402; E281134; -...
EMBL; V00402; E1181089; -...
EMBL; S43579; E97011; -...
PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TXR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOL. CELL. BIOL. 11:4165-4176(1991).
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                  208 DSGGFYITSRIQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                        175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 484-533 FROM N.A. MEDLINE; 91304409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.6%;
.larity 38.6%; E
Conservative 2
   Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                      7 14
Q98915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                      RESCIL
PERMENTARY REPRESENTARY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                           용
                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 WYFSGVSRIQAQQLLLSPPNEPGAFLIRPSESSLGGYSLSVRA-Q-AK---VCHYRVSMA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 83155664.

TAKEYA T., HANAFUSA H.;

"Structure and sequence of the cellular gene homologous to the RSV str dene and the mechanism for generating the transforming virus.";

CELL 32:881-890(1983).

EMBL; J00844; G901820;

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; SH2: 1.

PRAM; PF00017; SH2: 1.
                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
(SCHMIDT-RUPPIN D STRAIN).
ROUS SARCOMA VIRUS.
VIRUSES: RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALLUS GALLUS (CHICKEN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 235; DB 14; L. Pred. No. 2.25e-28; 26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pkinase; 1.
AA; 60038 MW; 8E987D6B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 AA
                                                                                                                                                                                   526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 235;
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
208 DSGGFYITSRTQFSSLQQLVAYY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 DSGGFYITSRTQFSSLQQLVAYY 230
                                     175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ADGSLYLQKGRLFPGLEELLTYY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HANAFUSA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                               064994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 13
Q90992
Q90992;
                                                                                                                                                   T 12
Q64994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIRE SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF S
                                                                                                                                                      RESULT
```

유

ద ö

ò

'n

Search completed: Thu May 20 12:59:38 1999 Job time : 183 secs.

****	(TM)	******
******		****
********		****
*****		****
*******		******
***************************************		\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
*******		********
*****		******

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Thu May 20 13:00:28 1999; MasPar time 20.61 Seconds 259:028 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>US-09-099-053-2 (230-480) from US09099053.pep (5 of 6) 1882 Description: Perfect Score:

1 FALGRKLGEGYFGEVWEGLW......ECWRSSPEERPSFATLREKL 251 Sequence:

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

summaries % 6.0 7.0 Minimum Match Listing first Post-processing:

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part8 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part16 17:part16 19:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 33.669; Variance 147.292; scale 0.229 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score_distribution...

SUMMARIES

	Pred. No.	4.02e-168	1.41e-85	3.15e-84	3.15e-84	4.16e-82	1.01e-81	9.78e-79	3.87e-76	3.73e-66	4.31e-63	9.40e-62	3.18e-60	3.18e-60	3.18e-60	3.18e-60	7.66e-60
•	Description	Human SAD.	Breast tumor kinase,	pTK gene LpTK-2 prod.	Protein tyrosine-kina	Chicken pp60 c-src pr	Human pp60 c-src prot	Sequence of pp60(c-sr	(Beta-galactosidase N	Abelson Related Gene,	Drosophila Src28C tyr	Abelson Related Gene,	N-terminal truncated	Megakaryocyte kinase	Cytoplsmic tyrosine k	TEC tyrosine kinase.	ITK tyrosine kinase.
CHINALICO	A	W89248	R63088	R41941	R85929	R39705	R39706	R32299	R14201	R15156	R94538	R15157	R71132	R84181	R71133	R94536	R94535
	DB	39	12	æ	14	ω	ထ	ဖ	m	m	17	ო	13	15	13	17	17
	% Duery Match Length DB	488	451	505	505	533	536	259	417	1146	441	1182	466	507	507	630	620
	% Ouery Match	100.0	54.9	54.1	54.1	53.0	52.8	51.1	49.7	44.2	42.5	41.7	40.9	40.9	40.9	40.9	40.6
	Score	1882	1033	1019	1019	997	866	962	935	831	799	785	769	169	769	169	765
	Result No.	П	7	٣	4	S	છ	7	8	თ	10	11	12	13	14	15	16

4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Tyrosine kinase domai BMX tyrosine kinase. Megakaryocyte kinase BTK tyrosine kinase. BTK tyrosine kinase. Mouse haematopoietic-Rat REXT eph-related Mouse Bsk receptor pro Rat receptor tyrosine Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related PTK Cek7. Eph-related Exceptor pro Eph-related CEK6. Mouse developmental k Eph-related CEK6. Eph-related Exceptor pro Eph-related PTK Cek5. Eph-related PTK Cek8. Eph-rel
R711131 R94533 R8451482 R8451482 R875184 R876168 R876147 R876168 R876168 R84612 R8612
246 13 675 17 675 17 675 17 659 20 659 20 972 819 971 15 7100 135 72 13 72 13 72 13 984 13 998 19 998 11 998 11 998 11 998 11 998 11 998 11 998 11 998 13 998
4 M W W W W W W W W W W W W W W W W W W
757 7449 7449 7447 7335 7335 7330 7330 7330 7031 7031 7033 7033 7033
11110000000000000000000000000000000000

ALIGNMENTS

```
Warely variety.

Were nucleic acid encoding specific protein tyrosine phosphatases -

useful for identifying specific modulators for treatment and

prevention of cancer and neurodegenerative disease

Claim 2: Page 154-155; 193pp; English

The present invention describes isolated, enriched or purified nucleic

acids encoding PrD04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

present sequence represents human SAD. The above proteins, other than

ALK-7, are protein tyrosine phosphatases (PTPS) and are used to identify

substances that modulate their activity (i.e. agonists and antagonists,

including NBP) in vitro. These substances are used to treat

or prevent diseases associated with abnormal signal transduction

pathways that involve the proteins, particularly cancer (e.g. leukaemia

and lymphoma), while modulators of ALK-7 (which is a type I receptor

serine/threonine kinase) are used to promote neuronal survival,

particularly for treating Alzhahamer's, Parkinson's or Huntington's

diseases. Nucleic acid fragments of the polynucleotides encoding the
                                                                                                  PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine Kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Muntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                      m
                                                                                                                                                                                                                                                                                                                                                                                                                  App H, Clary D, Courtneidge SA, Hui TH, Jallal Markby D, Onrust S, Peles E, Plowman GD; N-PSDB; V81743.
                     standard; Protein; 488 AA.
                                                           10-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                 23-OCT-1997; US-063595.
28-APR-1997; US-04428.
20-MAY-1997; US-04922.
11-JUN-1997; US-049477.
11-JUN-1997; US-049916.
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                     27-APR-1998; U08439
                                                                                                                                                                                     Homo sapiens.
WO9849317-A2.
05-NOV-1998.
                                                                                Human SAD
T 1
W89248 S
W89248;
  RESULT
```

```
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                              WO9315201-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                               191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                            RESULT
 88888
                                                                                                                                        염
                                                                                                                                                                                 g
                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                     a
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                   δ
                                                                                                                                                             ò
                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                           ò
                                                                                    ö
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                    349
                                                                                                                                                             290 AVCSGGEPVIIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHR 349
                                                                                                                                                                                                                                    350 dlaarnvlvddglackvadfglarllkddiyspsssskipvkwtapeaanyrvfsgksdv 409
                                                                                                         230 falgrklgegyfgevweglwlgslpvaikviksanmkltdlakeigtlkglrherlirlh 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 29-31; 52pp; English.
A brk (breast tumor kinase) cDNA fragment was used to screen a cDNA library prepared from human breast tumor cell line T-47D. 2 CDNAs were isolated. The slightly longer clone lambda-t2 (Q81189)
                                                                                                                                                  290 avcsggepvyivtelmrkgnlgaflgtpegralrlppllgfacqvaegmsyleegrvvhr
                                                                                                                                                                                                       /note= "potential regulatory tyrosine equivalent to Tyr-527 of c-src"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein tyrosine kinase and its DNA - isolated from human breast tumour, useful for diagnosis and prognosis of cancerous
                                                                                    ö
                                                              Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strong indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "putative autophosphorylation site"
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                 12-AUG-1995 (first entry)
Breast tumor kinase, brk.
Breast tumor kinase; brk; protein-tyrosine-kinase; PTK; breast cancer; metastasis; prognosis; diagnosis; T-47D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "putative ATP binding domain" 312..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to PTK SH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                          "similar to PTK SN3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamalati
                                                             Score 1882; DB 39;
Pred. No. 4.02e-168;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of PTK specificity in subdomain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ^{\mathsf{the}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barker KT, Crompton MR, Gusterson BA, Mitchell PJ, Page MJ, Spence P; WPI; 95-066901/09.
N-PSDB; Q81189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
15..68
/note= "similar to F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "corresponds
                                                                                                                                                                                                                                                                                                                                    T 2
R63088 standard; Protein; 451 AA.
R63088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1995.

08-JUL-1994; G01479.

09-JUL-1994; GB-014233.

11-MAR-1994; GB-004817.

(CANC-) CANCER RES INST.

(WELL ) WELLCOME FOUND ITD.
                                                               Query Match
Best Local Similarity 100.0%;
                                                                                   251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     78..169
/note= "s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198..203
                                                                                                                                                                                                                                                                                             470 RPSFATLREKL 480
                                                                                                                                                                                                                                                                                470 rpsfatlrekl 480
                                          488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9502057-A
                                           Sequence
                                proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                          g
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                               g
 888888
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                              ð
                                                                                                                                                                       ò
```

```
D5-AUG-1993. U00586.

22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R 22-JAN-1993; U00586.

R Avraham H, Cowley S, Groopman J, Scadden D;

WPI; 93-30330/40.

N-PSDB; Q4976.

New protein tyrosine kinase genes and proteins encoded by genes rare of human mega-karyocytic origin

Tare of human mega-karyocytic origin

Tare of human mega-karyocytic origin

ST Glaim 3; Fig 5; 60pp; English.

TR genes were identified using two sets of degenerative

TR genes were identified using two sets of degenerative

ST Glaim 3; Fig 5; 60pp; English.

TR genes were identified using two sets of degenerative

ST Glaim 3; Fig 5; 60pp; English.

TR genes were identified using two sets of degenerative

SEGMENTS of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers of primers: a first set which amplifies highly

CONSERVED of primers of primers: a first set which amplifies highly

CONSERVED of primers: a first set which amplifies highly

CONSERVED of primers of primers: a first set which amplifies highly

CONSERVED of pr
                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 FALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTD-LAKEIQTLKGLRHERLIRL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 ctledpjyiitelmrhgslgeylgndtgskihltgqvdmaaqvasgmaylesrnyihrdl 355
                                                                                                                                                                                                                                                                                                                                                                               ftlcrklgsgyfgevfeglwkdrvgvaikvisrdnllhggmlgseigamkklrhkhilal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pTK gene LpTk-2 prod.
pTK; protein tyrosine kinase; catalytic domain; c-kit; megakaryocyte;
lymphocyte; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 llkrlgsgqfgevweglwnnttpvavktlkpgsmdpndflreaqimknlrhpkliqlyav 295
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 HAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 rdlaarnilvgentlckvgdfglarlikedvy-lshdhnipykwtapealsrghystksd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 vwsfgillhemfsrgqvpypgmsnheaflrvdagyrmpcplecppsvhklmltcwcrdpe
encoded brk (R63088), which was identified as a novel putative non-receptor kinase of use as a prognostic/diagnostic of breast
                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
m
                                                                                                                                                                                                             Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1019; DB 8; Length 505; Pred. No. 3.15e-84;
                                                                                                                                                                                                         Score 1033; DB 12; Length 4
Pred. No. 1.41e-85;
42; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R41941 standard; Protein; 505
R41941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 54.1%;
Local Similarity 53.6%;
hes 135; Conservative
                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 grpcfkalrerl 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 AA;
                                                                                   tumor metastasis.
Sequence 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the publication
```

SS.

476

g

ö

ò

g

g

ò

```
Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced monouclear cell adhesion and fibronectin prodn bisclosure; Page 64-66; 31pp; English.

C. The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in Q46687) is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and than non-transformed counterparties. They migrate at faster rates than non-transformed counterpartis; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced monouclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  levklgggcfgevwmgtwngttrvaiktlkpgnmspeaflgeagvmkklrheklvglyav 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 CSGGEPVIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVUHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fgilltelttkgrvpypgmvnrevldqvergyrmpcppecpeslhdlmcqcwrrdpeerp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 vse-epiyivteymskgslldflkgemgkylrlpglvdmaaqiasgmayvermnyvhrdl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 raanilvgenlvckvadfglarliedneytarggakfpikwtapeaalygrftiksdvws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced monounclear cell adhesion and fibronectin prodn Disclosure; Page 75-77, 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 997; DB 8; Length 533;
Pred. No. 4.16e-82;
40; Mismatches 71; Indels
23-DEC-1993 (first entry)
Chicken pp60 c-src protein.
Endothelial; tyrosine kinase protein; pp60 c-src;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pp60 c-src protein.
Endothelial; tyrosine kinase protein; pp60 c-src;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bell L, Luthringer DJ, Madri JA, Warren SL;
WPI: 93-243209/30.
                                                                                                                                                                              22-JUL-1993.
05-JAN-1993, US00445.
06-JAN-1992; US-820011.
(UYYA) UNIV YALE.
Bell L, Luthringer DJ, Madri JA, Wi
WFI; 93-243209/30.
P-PSDB; R39705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R39706 standard; Protein; 536
R39706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 53.0%;
Local Similarity 54.5%;
les 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1993.
05-JAN-1993; US00445.
06-JAN-1992; US-820011.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 tfeylq 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 SFATLR 477
                                                                                                                gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R39705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapien.
                                                                                                                                                   WO9314193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DDT AC DD
   ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National States of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
                                                                                                                                                                                                                    416 vwsfgillyeiitygkmpysgmtgagvigmlagnyrlpgpsncpggfynimlecwnaepk 475
                                                                                                                                                                                                                                                               236 llkrlgsgqfgevweglwnnttpvavktikpgsmdpndflreaqimknlrhpkliqlyav 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctledpiyiitelmrhgslqeylqndtgskihltqqvdmaaqvasgmaylesrnyihrdl 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 aarnvlvgehniykvadfglarvfkvdnediyesrheiklpvkwtapeairsnkfsiksd 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                     356 aarnvlvgehniykvadfglarvfkvdnediyesrheiklpvkwtapeairsnkfsiksd
                                                                                                                                               352 AARNVLVDDGLACKVADFGLARLLK-D--DIYSPSSSSKIPVKWTAPEAANYRVFSQKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 AARNVLVDDGLACKVADFGLARLLK-D--DIYSPSSSSKIPVKWTAPEAANYRVFSQKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           э;
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1019; DB 14; Length 505;
Pred. No. 3.15e-84;
43; Mismatches 71; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein tyrosine-kinase LpTK2.
Protein tyrosine-kinase; pTK; LpTK2; agonist; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee JM, Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IT 5
R39705 standard; Protein; 533 AA.
R39705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.6%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1995.
04-APR-1995; U04228.
04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D, 1
                                                                                                                                                                                                                                                                                                                                                                                                                          469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                           erptfetlrwkl 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erptfetlrwkl 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 95-366160/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9527061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R85929
```

NAME OF THE SECOND OF THE SECO

296

셤

ò

ద à

ò

ద

476

g

ò

ò

S C

RESULT ID R3 AC R3

Ä

Gaps

<u>.</u>;

Length 533;

387

351

447

```
While 94-03804/0.7 Computer modelling design of specific affectors - using three-dimensional conformation of enzyme affector complex three-dimensional conformation of enzyme affector complex Example; Pages 51-52; 115pp; English.

The inventors provide a crystal structure of CAMP-dependent protein kinase (CAMP, with its catalytic subunit intact. The crystals contain a bound inhibitor peptide (PKI(5-24)) which comprises a fragment of the heat stable protein kinase inhibitor (PKT). PKT, PKT, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP, CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 vse-epiyivteymskgslldflkgetgkylrlpqlvdmaaqiasgmayvermnyvhrdl 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
cesse polypeptide (Given in Q46688) is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced monounclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 levklgggcfgevwmgtwngttrvaiktlkpgtmspeaflgeagvmkklrheklvglyav 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Residues 14,22,117,119,126,140 and 235 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEGRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 raanilvgenlvckvadfglarliedneytarggakfpikwtapeaalygrftiksdvws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 fgilltelttkgrvpypgmvnrevldqvergyrmpcppecpeslhdlmcqcwrkepeerp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1993 (first entry)
Sequence of pp60(c-src) which is the proto-oncogene homologue of the src protein kinase from Rous Sarcoma Virus.
Inhibitor peptide; cellular protein kinase; proto-oncogene; src protein kinase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 993; DB 8; Length 536; Pred. No. 1.01e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Invariant residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sowadski JM, Taylor SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R32299 standard; peptide; 259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also invariant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.8%; :
larity 54.1%; ]
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1991; US-735614.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-1993.
22-JUL-1992; U06137.
                                                                                                                                                                                                                                                                                                                                                                                        536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knighton DR, SOW
WPI; 93-058804/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 tfeylg 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                 implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9302209-A
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALL STATES OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE SOLIT OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
        8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
kinase corresp. to points of contact for cAPK and prints.

Kinase corresp. to points of contact for cAPK and PKK(5-24), and designing an inhibitor of the first protein kinase allowing ionic and hydrophobol: interactions with these residues, thus producing an inhibitor of the first protein kinase. In the example, the inventors use this methodology to design an inhibitor for pp6(c-src) which is the proto-oncogene homologue of the src protein kinase from Rous Sarcoma Virus. The invariant residues in pp60(c-src) are given in FT above. These residues are incorporated into the appropriate position using a coordinate set of the invariant residues present in most protein kinases. Once the template is in place and the catalytic site from pp60(c-src) has been superimposed onto the emplate, it is possible to visualise the catalytic site. The site can additionally be refined using the complementary target phosphorylation site for pp60(c-src) (se R32300). Residues are altered using computer modelling until a fit is achieved for Sequence 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fgilltelttkgrvpypgmvnrevldqvergyrmpcppecpeslhdlhcqcwrkepeerp 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              5 levklgggcfgevwmgtwngttrvalktlkpgtmspeaflgeagvmkklrheklvglyav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 4.2; 15pp; Japanese.

The sequence consists of the N-terminal amino acids of the betagalactosidase gene fused with the lck gene. It is produced by E.coli transformed with a recombinant vector (see 013983). It is useful for producing an antibody specifically immunoreactive with only a lck gene-derived polypeptide in T cells. The antibody may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 vse-epiyivteymskgslldflkgetgkylrlpqlvdmaaqlasgmaybermnyvhrdl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               raanilvgenlvckvadfglarliedneytarqgakfpikwtapeaalygrftiksdvws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fused polypeptide - has amino acid sequence of beta-galactosidase with a LCK gene conjugated to the N-terminal via DNA having multi-cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSKIPVKWTAPEAANYRVFSQKSDVWS
contact with PKI(5-24) in a complex, generating a model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1991 (first entry) (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                         Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "beta-galactosidase fragment" 27..417
                                                                                                                                                                                                                                                                                                                                                                     Score 962; DB 6; 1
Pred. No. 9.78e-79;
40; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "lck gene polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 8
R14201 standard; Protein; 417 AA.
R14201;
                                                                                                                                                                                                                                                                                                                                                                     51.1%;
larity 53.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1989; 338268.
28-DEC-1989; JP-338268.
(TOKU) TOKUYANA SODA KK.
WPI; 91-300980/41.
N-PSDB; Q14201.
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
ses 131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multi-cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tfeylg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J03201994-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                         Query Match
points
of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
8888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

S

ò g ò g ò g ò g à

```
Location/Qualiflers
                                                                                                                                                                                                         1.55
/label- SH3_domain
                                                                                                                                                                                                                               65...155
/label= SH2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 10
R94538 standard; Protein; 441 AA.
R94538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.3%;
Matches 109; Conservative
                                                                                                                                                                                                                                                       ..425
                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 vlmdql 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLREKL 480
                                          drpsfa 497
                                                               ERPSFA 474
                                                                                                                                                                                                                                                                                                   modified_site
                                                                                                                                                                                                                                                                            binding_site
                                                                                                                                                                                                                                                                                                                         WO9611275-A1
                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                       domain
                                                               469
                                          492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                    ò
                                         g
                                                                ò
                                                                                                          요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                ω
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5B; 40pp; English.

The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes....Arg.is-expressed as two-transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A and B (Q14937) and it is assumed that they are joined
                                                                                  155 lverlgaggfgrcgw-gtttgttkvavkslkggsmsagrlpaeanlmkglghgrlvrlya 213
                                                                                                 252 itmkhklggggygevyvgvwkkysltvavktlkedtmeveeflkeaavmkeikhpnlvgl 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 lgvctleppfyivteympygnlldylrecnreevtavvllymatqissameylekknfih 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vwafgvllweiatygmspypgidlsgvydllekgyrmegpegcppkvyelmracwkwspa 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        he amino acid sequence is represented as found in the specification.
                                                                Gaps
                                                                                                                                                                                                                   sfgillteivthgripypgmtnpevignlergyrmvrpdncpeelyglmrlcwkerpedr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rdlaarnclvgenhvvkvadfglsrlmtgdtytahagakfpikwtapeslayntfsiksd
                                                                                                                                                                         273 Iraanilvsdtlsckiadfglarliedneytaregakfpikwtapeainygtftiksdvw
                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human gene related to abl proto-oncogene - designated "Abelson Related Gene", arg, useful for tumour diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1146;
                                          Length 417;
                              Score 935; DB 3; Length 41, Pred. No. 3.87e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 831; DB 3; Length 114
Pred. No. 3.73e-66;
49; Mismatches 85; Indels
lck gene-derived polypepti<u>des.</u>in human cells.
417 AA;
                                                                                                                                                                                                                                                                                                                                                                               proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                       12-FEB-1992 (first entry)
Abelson Related Gene, A transcript.
Arg; diagnosis; therapy; tumour; abl
Homo saplens.
                                                                                                                                                                                                                                                                                                                                  R15156 standard; Protein; 1146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1991, 559029.
22-OCT-1991; 559029.
30-JUL-1990; US-559029.
(USSH ) NAT INST OF HEALTH.
KTUH G, ALTONSON SA, KING CR;
WPI: 91.353425/48.
N-PSDB; Q14936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; :
ilarity 45.1%; I
Conservative 4
                                         49.78;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the arg second exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 111; Conserv
                                                  Local Similarity
es 127; Conser
                                                                                                                                                                                                                                                                 ptfdylrsvl 402
                                                                                                                                                                                                                                                                                      471 PSFATLREKL 480
         recognise lck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                    Sequence
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                               351
                                                                                                                                                                                                                     333
                                                                                                                                                                                                                                                                 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                        RESULT
         ပ္ပင္တ
                                                                                                                                                                                                                                                                                                                                   g
```

ö αq ò d ò

```
187 lgsgqfgvvrrgkwrgsidtavkmmkegtmseddfieeakvmtklqhpnlvqlygvctkh 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 LGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAVCSGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 rpiyivteymkhgsllnylrrhektlignmgllldmciqvskgmtylerhnyihrdlaar 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nclvgsenvvkvadfglaryvlddgytssggtkfpikwappevlnytrfssksdvwaygv 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulate haematopoietic cell growth.

Disclosure: Page 28-29; 40pp; English.

The amino acid sequence (R94538) of Drosophila Src28C tyrosine heavy-identified non-receptor tyrosine kinase family, BTK (R94534), TTK (R94535) and TEC (R94536), and with novel human cytoplasmic styrosine kinase BMX (see also R94533). Close homology was found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 NVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWSFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 799; DB 17; Length 441;
Pred. No. 4.31e-63;
50; Mismatches 86; Indels 1;
10-JUL-1996 (first entry)
Drosophila Src28C tyrosine kinase.
Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
cell growth; cell proliferation; tumour; diagnosis; therapy;
Src28C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 96-209856/21.
Cytoplasmic tyrosine kinase BMX and related DNA - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                   'label- Tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                       87..209 1
Tabel ATP-binding_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-1996.
09-CCT-1995; F10555.
07-CCT-1994; US-320432.
(UYHE-) UNIV HELSINKI LICENSING LTD OY.
Alitalo R;
```

ä

o

```
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9529185-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1995
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R84181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                                                                                                                                   Matches
    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5D; 40pp; English.
The human gene encoding this protein is closely related to but distinct from the abl proto-oncogene and is a member of the tyrosine kinase encoding family of genes. Arg is expressed as two transcripts. By analogy with c-abl, the alternative 5' arg sequences have been designated A (014936) and B and it is assumed that they are joined to the arg second exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 itmkhklrgghyrevyvgvwkkysltvavktlkedtmeveeflkeaavmkeikhpnlvgl 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::::|| |::| |:| |:| |:| |:| |:| |:| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 lalctleppfyivteympyrnlldylrgcnrekvtavvllymatgissameylekknfih 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 vwafgvllweiatygmspypgidlsqvydllekgyrmegpegcppkvyelmracwkwspa 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid sequence is represented as found in the specification. Sequence 1182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rdlaapnclvgenhvvkvadfglsrlmtadtytahagakfpikwtapeslayntfsiksd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                               22-OCT-1991.
22-OCT-1991; 559029.
30-JUL-1990, INST 559029.
30-JUL-1990, INST 559029.
Kruh G, Arronson SA, King CR;
WPI; 91-53425/48.
NOVEL Numan gene related to abl proto-oncogene - designated
"Abelson Related Gene", arg, useful for tumour diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.7%; Score 785; DB 3; Length 1182; Best Local Similarity 43.5%; Pred. No. 9.40e-62; Matches 107; Conservative 49; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytoplasmic; tyrosine kinase; blood; cell differentiation; screening; anticancer agent; SH3; src homology domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                   Abelson Related Gene, B transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1995 (first entry)
N-terminal truncated cytoplsmic tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "tyrosine kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "SH3 domain"
81..155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "SH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R71132 standard; Protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1995.
25-AUG-1994; J01411.
25-AUG-1993, JP-210403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakano S;
WPI; 95-106842/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drpsfa 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||||
469 ERPSFA 474
                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                            US7559029-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9506113-A.
                                                                                                                                                                                                                                                                                      therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
```

```
9
Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy claim 1; Page 40-42; 58pp; English.

A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. This sequence comprises an N-terminal truncated fragment of the enzyme (residues 42-507 of R71133). The DNA screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 gvilh-gglyivmehvskgnlvnflrtr-gralvntagllgfslhvaegmeyleskklvh 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 rdlaarnilvsedlvakvsdfglakaerkgl----dssrlpvkwtapealkhgkftsksd 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vwsfgvllwevfsygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaepa 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 VWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYVLMLECWRSSPE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 ltlgaqigegefgavlqgeylgq-kvavknikc-dvtaqafldetavmtkmqhenlvrll 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New POLY: nucleotide(s) encoding megakaryocyte tyrosine kinase(s) - used to develop prods. for the treatment and diagnosis of kinase related signal transduction abnormalities.

Claim 15: Fig 18-C: 82pp: English.

Human megakaryocyte kinase MKK1 (R84181) is a 58 kDa cytosolic tyrosine kinase showing 54% homology with csk. It appears to play a regulatory role in the growth and differentiation of megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be produced in host cells by expression of encoding cDNA (T00616), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 769; DB 13; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Megakaryocyte kinase MKKI.
Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
cellular signal transduction; leukaemia; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1995; U05008.
22-APR-1995; UG-232545.
21-APR-1994; US-232545.
21-APR-1995; US-426509.
(PLAC.) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(SUGE.) SUGEN INC.
Gishizky M, Sures I, Ullrich A;
WPI: 95-382959/49.
N-PSDB; T00616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.18e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Catalytic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48..111
/label- SH3_domain
122..196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SH2_domain
233..478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R84181 standard; Protein; 507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
Local Similarity 47.6%;
les 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 rrppfrklaekl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 ERPSFATLREKL 480
```

^

```
Cytoplasmic tyrosine kinase; BMX; cell growth; cell proliferation; Mus musculus.
                                                                                                                                                                       .r 15
R94536 standard; Protein; 630 AA.
R94536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 40.9%;
Local Similarity 47.5%;
les 116; Conservative
                                                                                                                                                                                                                10-JUL-1996 (first entry) TEC tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                246..344
/label= Si
374..611
                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                         467 rrppfrklaekl 478
                                                                                                                                               469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 96-209856/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_site
                                                                                                                                                                                                                                                                                                                                                                                                              binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                            domain
                                                      349
          290
                                351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                            407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
                                                                                                                       g
                                                                                                                                                                                            qq
                                                       ò
                                                                            g
                                                                                                  δ
                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activative for use as cancer therapy
Claim 1: Page 42-44; 58pp; English.
A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are usful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. Sequence 507 AA:
                                                                   .
6
                                                                                                                                 gvilh-gglyivmehvskgnlvnflrtr-gralvntagllgfslhvaegmeyleskklvh 350
                                                                                    235 ltlgaqiqeqefgavlggeylgg-kvavknikc-dvtaqafldetavmtkmghenlvrll 292
                                                                                                    390 AVCSGGEPVIVITELMRKGNLQAFLGTPEGRAL-RLPPLLGFACQVAEGMSYLEEDRVVH 348
                                                                                                                                                                             351 rdlaarnilvsedlvakvsdfglakaerkgl----dssrlpvkwtapealkhgkftsksd 406
                                                                                                                                                                                           407 vwsfgvllwevfsygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaepa 466
                                                                                                                                                                                                                                       235 ltlgaqigegefgavlqgeylgq-kvavknikc-dvtaqafldetavmtkmqhenlvrll 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 gvilh-gglyivmehvskgnlvnflrtr-gralvntaqllqfslhvaegmeyleskklvh 350
                                                                   Gaps
                                                                  ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 9;
                                           507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 769, DB 13; Length 507;
Pred. No. 3.18e-60;
42; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                     cytoplasmic, tyrosine kinase, blood, cell differentiation, screening, anticancer agent; SH3; src homology domain.
                                                                 81; Indels
                                            Length
 e.g. leukaemia
                                         Score 769; DB 15;
Pred. No. 3.18e-60;
42; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "SH2 domain"
233..478
/note= "tyrosine kinase domain"
 treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "SH3 domain"
122..196
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         R71133 standard; Protein; 507 AA.
R71133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1995.
25-AUG-1994; J01411.
25-AUG-1993; JP-210403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.98;
                                        40.9%;
Local Similarity 47.6%;
les 120; Conservative
                                                                                                                                                                                                                                                                                                                                                              27-OCT-1995 (first entry)
Cytoplsmic tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                       467 rrppfrklaekl 478
                                                                                                                                                                                                                                                                                             469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 120; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-106842/14.
                    507 AA;
         thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; 084888.
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens,
used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9506113-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakano S;
                      Sequence
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                    349
                                                                                                                                  293
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                RESULT
ပ္ပပ္ပင္တ
                                                                                                                                 8
                                                                                                                                                                             g
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                        ò
                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                            à
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348
                                                                                                                                                                                                 Cytoplasmic tyrosine kinase BMX and related DNA - useful to stimulate haematopoietic cell growth.

Disclosure; Page 25-27; 40pp; English.

Cytoplasmic tyrosine kinase TEC (R94536) is expressed in murine haematopoietic cells. The sequences of TEC and 2 other members of a newly-identified non-receptor tyrosine kinase family, ITK (R94538) and BTK (R94534), and of the Drosophila Src28C tyrosine kinase (R94538), were compared with that of novel cytoplasmic tyrosine kinase BMX (see also R94533). Close homology was found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 relgsglfgvvrlgkwragykvaikairegamceedfieeakvmmklthpklvglygvct 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qqkpiyivtefmergcllnflrqrqghfsr-dmllsm-cqdvcegmeylernsfihrdla 490
                                                                                                                                                                   vwsfgvllwevfsygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaepa
rdlaarnilvsedlvakvsdfglakaerkgl----dssrlpvkwtapealkhgkftsksd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQ-VAEGMSYLEEQRVVHRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMX; haematopoietic cell;
lon; tumour; diagnosis; therapy; TEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "the N-terminal region contains
pleckstrin homology region consisting
a 7-strand antiparallel beta-sheet"
184..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 769; DB 17; Le
Pred. No. 3.18e-60;
40; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375..398 1
| Sapel = ATP-binding_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- N-terminal_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-00T-1995; F10555, 07-0CT-1994; US-320432. (UXHE-) UNIV HELSINKI LICENSING LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH2_domain
```

```
qq
```

Dp Qy

οy

⁶¹¹ fedl 614 | 1

^{| 1} 473 FATL 476

Search completed: Thu May 20 13:03:22 1999 Job time: 174 secs.

			(TM)
	ı		
	ı	_	
	<u></u>	- -	
	<u> </u>		<u> </u>
	 	- }	

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 13:04:25 1999; MasPar time 17.36 Seconds 541.572 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (230-480) from US09099053.pep (5 of 6) 1882 1 FALGRKLGEGYFGEVWEGLW......ECWRSSPEBRPSFATLREKL 251 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 46.462; Variance 96.799; scale 0.480 pir60 1:pirl 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred.	1				Н	7.26e-	7.26e-1	1.13e-1	7.03e-1	4.41e-1	1.10e-16	2.74e-1	2.74e-16	1.73e-1	6.86e-1	1.72e-	4.30e-1	4.30e-1	4.30e-	1.70e-1	1.07e-1	1.07e-1	1.07e-1	1.69e-
Description		protein-tyrosine -x.ma.		protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina		protein-tyrosine kina	protein-tyrosine kina	p59(Xfyn) - Xiphophor	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina		protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina	protein-tyrosine kina
QI QI		A30040	156322	S24553	S24552	S24551	S24550	S49016	I38396	151592	TVHUFR	A34104	B34104	A44991	A43806	I49552	TVHUSY	A49114	TVFVS1	TVCHS	S20808	S33568	TVHUSC	A39939
DB	10	۷ (7	~	7	~	7	7	~	7	~	7	7	7	7	~	Н	~	Н	H	~	~	Н	7
Length		4 -	496	206	334	362	505	451	505	537	529	532	532	534	537	512	537	542	268	533	526	534	542	507
% Query Match	;		7.88	58.3	57.0	55.7	55.7	54.9	54.1		53.6	53.5	53.5	53.5	53.3	53.5	53.1	53.1	53.1	53.0	'n	52.8	ς.	52.7
Score		100	1670	1097	1072	1049	1049	1033	1019	1015	1008	1006	1006	1007	1004	1002	1000	1000	1000	266	993	993	993	992
Result No.	-	٦ ،	7	m	4	S	ဖ	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

.67e	-16	6-1	.69e-16	e-16	.68e-1	e-16	.64e-1	2.64e-164	2.64e-164	e-16	1.65e-163	.61e-16	91-8	.58e-	.58e-16	.63	.09e-16	.09e-16	-16	-5	
	tyrosine kina tyrosine kina			sine kina	tyrosine kina	tyrosine kina	sine kina					tyrosine kina		nse	sine kina						
	protein-tyro protein-tyro		protein-tyro		protein-tyro		protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyro	- 1	protein-tyro	protein-tyro	p56-tck - mouse	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	protein-tyrosine	
TVFVMT	A43610	TVFVS2	TVFVPR	TVHAST	TVCHYS	OKFVYR	S15582	TVFVR	S26420	TVFVG9	I51593	TVFV60	137206	I48845	S31645	TVHUYS	TVHUHC	A23639	A45501	833569	
Н С	v ~	٦	-	-	П	ч	N	ч	7	Н	~	٦	7	~	~	H	П	~	7	7	
523	541	557	587	509	541	526	526	526	526	528	544	526	505	509	541	543	505	209	537	536	
	52.7			52.6	52.6	52.4	52.4	52.4		52.2	•				•	51.9					
991	0 0 0 0 0 0	992	992	686	686	987	986	986	986	983	982	981	979	976	916	977	975	975	974	973	
24	7 7 7 8	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1	
ENTRY	A56040 #type complete
TITLE	Y
	esnow -
ORGANISM	#Iormal_name Mus musculus #common_name house mouse
DATE	<pre>01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 12-Jun-1998</pre>
ACCESSIONS	35 50 40
ひていないといい	0.400000 0.400000
# # P P P P P P P P P P P P P P P P P P	, N
	R - Takeda N - Chiba T - Ikawa V - Aizawa S
# tournal	Mol. Cell. Biol. (1994) 14:6915-6925
#title	A novel nonreceptor tyrosine kinase. Srm: cloning and
#accession	A56040
##status	preliminary
##molecule	##molecule_type mRNA
##residues	
##Cross-re	##cross-references GB:D26186; NID:9529072; PID:d1005873; PID:9529073
GENETICS	
#map_position	
CLASSIFICATION	
	se homology; SH3 homology
KEYWORDS	ATP; phosphotransferase
FEATURE	
62-111	SH3 homology #label SH3\
232-491	
240-248	_
SUMMARY	
Query Match	89.8%; Score 1690; DB 2; Length 496;
Matches 215;	
Db 234 FVFGRK	LGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTKEIEALKSLRHERLIRLH 293
QY 230 FALGRK	FALGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLH 289
Db 294 AICSLG	AICSLGEPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHR 353
Qy 290 AVCSGG	AVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHR 349
NG AG TO 354 HO	A 12 TO A DANT WORLD TO A TOTAL A DESCRIPTION OF A SECURITION AND ASSOCIATION AND ASSOCIATION AND ASSOCIATIONA ASSOCIATION ASSOCIATION ASSOCIATION ASSOCIATION ASSOCIATION ASS
7	
Oy 350 DLAARN	DLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSOKSDV 409

414 WSFGILLYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEE 473

~

```
##cross-references EMBL:X61604; NID:g10155; PID:g10156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
CLASSIFICATION
                                #gene
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                  122-214
238-496
246-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64-323
72-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                        FEATURE
61-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
               GENETICS
                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTRY
TITLE
                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 FVLRKKLGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTKENEALKSLRHERLIRLH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AICSLGEPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469
                                                                                                                                                             #formal_name Mus musculus #common_name house mouse
26.Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                          ##cross-references GB:D49427; NID:g684971; PID:g684972
CLASSIFICATION #superfamily unassigned Ser/Thr or Tyr-specific protein
kinases; protein kinase homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      src-type tyrosine kinase 4
#formal_name Spongilla lacustris
07-May-1993 #sequence_revision 07-May-1993 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 WSFGVLLHEVFTYGQCPYEGMINHETLQQIMRGYRLPRPAACPAEVYVLMLECWRSSPEE
                                                                                                                                                                                                                                                      J. Invest. Dermatol. (1995) 21:533-538
Identification of a novel cDNA clone encoding protein tyrosine kinase in murine skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 DLAARNVLVGDDLTCKVADFGLARLLKDDVYSPSSGSKIPVKWTAPEAANYRVFSQKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 WSFGILLYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEE

    freshwater

                                                                                                                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN\
"region protein kinase ATP-binding motif--------
#length 496 #molecular-weight 55731 #checksum 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, September 1991
S24553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 496;
                                                                                                                                                                                                                                                                                                                 preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1670; DB 2; Length 49
Pred. No. 5.06e-302;
24; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S24553 #type complete
protein-tyrosine kinase (EC 2.7.1.112) 4
(Spongilla lacustris)
                                                                                                                                                                                                                                         Kawachi, Y.; Nakauchi, H.; Otsuka, F.
                                                                                                                                     #type complete
                                                                                                                                                                                                                                                                                                                                            1-496 ##label RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
##residues 1-506 ##label RAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%;
84.9%;
                                                                                                                                                                                            12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213; Conservative
                                                                                                                                                   srm - mouse
                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                          ||:|| |||||
470 RPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|| |||||
|RPSFATLREKL 480
                                           474 RPTFAILREKL 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 RPTFAILREKL 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                 156322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $24550
                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
#submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                      #journal
#title
                                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                         fauthors #
                                                                                                                                                                                                                                                                                                                                                                                                                     62-111
232-491
240-248
                                                                                                                                                                                                          ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                               ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                     RESULT
                                                                                                                                   ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
               ð
                                           g
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $24552 #type fragment
protein-tyrosine kinase (EC 2.7.1.112) 3 - freshwater sponge (Spongilla lacustris) (fragment)
src-type tyrosine kinase (FC 2.7.1.112) 4 #formal_name Spongilla lacustris
07-May-1993 #sequence_revision 07-May-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
*superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                                                                                                                                           411
                                                                                                                                                                                                                                                                                                                                                                                                               LLRGLGAGQFGEVWEGLWNGTTSVAVKTLKPGTMSIEEFLEEASIMKQLRHPKLIQLYAV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQRKLGQGNFGEVWAGVWNGTTAVAVKTLKPDTMEVKDFVQEAQVMKKIHHPNLLQLYAV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 CIKEEPIYIVTELMKHGSLLEYL-RGDGRSLKLPDLVDMCSQVASGMSYLEQQNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AARNILVGEHKICKVADFGLARVIDEEIYEAKLGAKFPIKWTAPEAAMYSRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGIVLYEVITYGRFPYPGMTNAQVLEQIQQSYRMPRPMGCPEKLYAIMMDCWREDPASRP
                                                                                                          #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif\
#active_site Lys #status predicted
#length 506 #molecular-weight 57561 #checksum 9002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain SH2 homology (fragment) #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1072; DB 2; Length 334;
Pred. No. 1.85e-181;
58; Mismatches 63; Indels C
                                                                                                                                                                                                                                                                                                          Length 506;
                                                                                                                                                                                                                                                                                                                                                            60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:X61603; NID:g10153; PID:g10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #active_site Lys #status predicted
#length 334 #checksum 6597
                                                                                                                                                                                                                                                                                                       Score 1097; DB 2; Pred. No. 1.85e-186;
                                                                                                                                                                                                                                                                                                                                                            50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-334 ##label RAU
                                                                                                                                                                                                                                                                                                    Query Match 58.3%;
Best Local Similarity 54.7%;
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.0%;
Best Local Similarity 51.4%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raulf, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 TFETL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 SFATL 476
```

128 292 188 352 248 412 308 472

엄

à 셤 à g ò 셤 à

```
##molecule_type mRNA
##residne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
larity 53.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-Sep-1998
                                                                                                                            S24550
Raulf, F.
submitted t
S24550
                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              849016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 TFETLQ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132;
                                             ALTERNATE_NAMES
                                                                                                                                                          #submission
                                                                                                                                                                                                                                                           #gene
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                             #accession
                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                     122-214
238-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
                                                                                                            ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                    246-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472
                                                                                                                                                                                                                                                                                                                      FEATURE
61-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                              ORGANISM
                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                          GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä

    freshwater sponge

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                                                                            AVCTQGEPVYIITELMSKGSLLDYLQGEAG-ALKLPQLIDMAAQVAAGMAYLELHNYIHR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSFGILITELVTYGRIPYPGMSNAEVLQNLDKGYRMPCPVTTPESLYQIMLDCWKRNPAD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                          307
                                                                                                                                                                            95 ITLIRKLGAGQFGEVYQGLWNNSTPVAVKTLKAGTMQPAAFLAEAQIMKKLRHPKLIQLY 154
LGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAV 291
                                                                                                                                                                                                                                                                                                     protein tyrosine kinase (EC 2.7.1.112) 2 - freshwater s (Spongilla lacustris) (fragment) src-type tyrosine kinase 2 #formal_name Spongilla lacustris 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                           AARNILVGEGNVCKVADFGLARVIKEDIYNPREGTKFPIKWTAPEAALYNRFTIKSDVWS
                                                                                                                                                        FGVLISEIVTHGRMPYPGMTNRQVLEAVDRGYRMPCPEGCPDPLYKIMLSCWKHEPDDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLAARNILVGDNNICKVADFGLARLIVSDDYNATEGAKFPIKWTAPEAALFNRFSIKSDV
                             CTIGEPIYIVTELMKYGSMLEYLKHGEGKNITLHQMVDMSAQIASGMTYLEAHSYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels ---1;-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain SH2 homology (fragment) #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 362 #checksum 2776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1.362 ##label RAU
##cross-references EMBL:X61602; NID:g10151; PID:g10152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1049; DB 2; 1 Pred. No. 7.26e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raulf, F. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|:|:|
RPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPTFEALOWRL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 135; Conserv
                                                                                                                                                                                                                                          :| :|:: |
SFATLREKL 480
                                                                                                                                                                                                                      TFESLKNLL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S24551
                                                                                                                                                                                                                                                                                                                                                                  ALTERNATE_NAMES
```

CLASSIFICATION

#dene

KEYWORDS

FEATURE

GENETICS

Query Match

SUMMARY

Matches

셤 ò

230 155 290 214 350 274 410 334

g

g

ò

d ð

ò

RESULT

g

ö

93-351 101-109

#submission #accession

#authors

ACCESSIONS REFERENCE

ORGANISM

TITLE

```
..
E-
                                                      2.7.1.112) 1 - freshwater sponge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGVVLYEIITYGRFPYPGMTNPEVLEKIQQNYRMPCPANCPKQFHDIMLDCWREDPASRP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 CTKEEPIYIVTELMKYGSLLEYLRGEDG-VLKIEQLVDVAAQVASGMSYLEQQNYIHRDL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, Lowe, P.N.; Page, M.J.; Gusterson, B.A.; Crompton, M.R. Oncogene (1904) 9:2383-2390 Cloning and characterisation of cDNAs encoding a novel cloning and characterisation of christ expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIRRLGAGQFGEVWEGLWNGTTSVAVKTLKPGTMSVEEFLQEASIMKRLRHPKLIQLYAV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S24550 #type complete
protein-tyrosine kinase (EC 2.7.1.112) 1 - freshwater s;
(Spongilla lacustris)
src-type tyrosine kinase 1
#formal_name Spongilla lacustris
07 May-1993 #sequence_revision 07-May-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 AARNILVGEHGICKVADFGLARVIDEEIYEAHTGAKFPIKWTAPEAAMYNRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849016 #type complete
protein-tyrosine kinase (EC 2.7.1.112) brk - human
protein-man Homo sapiens #common_name man
07-May-1995 #sequence_revision 21-Jul-1995 #text_c)
                                                                                                                                                                                                                                                                                                        September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 505 #molecular-weight 57693 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-451 ##label MIT ##cross-references EMBL:X78549; NID:9515025; PID:9515026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels
                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-505 ##label RAU
##cross-references EMBL:X61601; NID:q10149; PID:q10150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1049; DB 2; L
Pred. No. 7.26e-177;
49; Mismatches 64;
                                                                                                                                                                                                                                                                                                     to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
```

US-09-099-053-2-05.rpr

```
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                  *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILCRKLGSGYFGEVFEGLWKDRVQVAIKVISRDNLLHQQMLQSEIQAMKKLRHKHILAL 250
                                                                                                                                                                                                                                                                                                                          251 YAVVSVGDPVYIITELMAKGSLLELLRDSDEKVLPVSELLDIAWQVAEGMCYLESQNYIH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDLAARNILVGENTLCKVGDFGLARLIKEDVY-LSHDHNIPYKWTAPEALSRGHYSTKSD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWSFGILLHEMFSRGOVPYPGMSNHEAFLRVDAGYRMPCPLECPPSVHKLMLTCWCRDPE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references GDB:355675
#map_position 4435-4435
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology APP: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Lee, J.; Wang, 2.; Luoh, S.M.; Wood, W.I.; Scadden, D.T. #journal Gene (1994) 138:247-251
#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.
#cross-references WUID:94171047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Homo sapiens #common_name man
15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
09-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase AIP-binding motif
#length 451 #molecular-weight 51834 #checksum 5817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain SH3 homology #label SH3\
#domain protein Kinase homology #label KIN\,
#region protein Kinase AP-binding motif
#length 505 #molecular-weight 58254 #checksum 9379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138396 #type complete
protein-tyrosine kinase (EC 2.7.1.112) FRK - human
FYN-related kinase (FRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ώ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.1%; Score 1019; DB 2; Length 505; larity 53.6%; Pred. No. 7.03e-171; Conservative 43; Mismatches 71; Indels
                                                                                                                                                                                                                           Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
##cross-references EMBL:U00803; NID:q392887; PID:g392888
                                                                                                                                                                                                                         Score 1033; DB 2; I
Pred. No. 1.13e-173;
42; Mismatches 68;
                   ##cross-references GDB:378058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary-
                                                                                                                                                                                                                           54.9%;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| | :|||:|
ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORPCFKALRERL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDB: FRK
GDB: BRK
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 140; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 135; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138396<sup>°</sup>
138396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I38396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATE_NAMES
                                    CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSIONS
REFERENCE
#authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                            78-170
189-448
197-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232-494
240-248
                                                                                                                                                                                                                                                                                                  191
                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469
                                                                                                                                                                                                                                                                                                                                                                                                                                                      311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
49-105
                                                                                           FEATURE
15-67
                                                                         KEYWORDS
 #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENETICS
                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ά
```

```
the c-yes and fyn
                                                             355
              356 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSD 415
                                                                                                                                            416 VWSFGILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQQFYNIMLECWNAEPK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 LIKRLGNGQFGEVWMGTWNGTTKVAVKTLKPGTMSPESFLEEAQIMKKLRHDKLVQLYAV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                     151592 #type complete
p59(Xfyn) - Xiphophorus helleri
#formal_name Xiphophorus helleri
04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAV
                                                           296 CTLEDPIYIITELMRHGSLQEYLQNDTGSKIHLTQQVDMAAQVASGMAYLESRNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 RSANILVGDNLVCKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPASLHELMLQCWKKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain SH3 homology #label SH3\
#domain protein kinase homology #label KIN
#length 537 #molecular-weight 60447 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status
##nolecule_type mRND
##residues
##cross-references EMBL:X54971; NID:g64481; PID:g64482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hannig, G.; Ottilie, S.; Schartl, M.
Oncogene (1991) 6:361-369
Conservation of structure and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1015; DB 2;
Pred. No. 4.41e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes in lower vertebrates #cross-references MUID:91187435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 53.9%;
1 Similarity 53.7%;
132; Conservative
                                                                                                                                                                                                                                                                                     469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                      476 ERPTFETLRWKL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| |:
472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFEYLQ 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89-138
269-527
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512
                                                                                                                                                                                                                                                                                                                                                                   TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                    DATE
                                                                                                                          g
                                                                                                                                                                                         a
                            δ
                                                         g
                                                                                          à
                                                                                                                                                                                                                        δά
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Op
                                                                                                                                                         à
                                                                                                                                                                                                                                                                                     δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
#authors
                84-133
144-241
261-519
269-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETICS
     FEATURE
                                                                                                                             3,6
                                                                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTRY
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE
                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ă
                                                                                                                                                         Katamine, S.; Notario, V.; Rao, C.D.; Miki, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins, K.C.
Mol. Cell. Biol. (1988) 8:259-266
Primary structure of the human fgr proto-oncogene product p55
                                                                                                                                                                                                                                                                                                                                                                 .,
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalyzes the phosphorylation of a peptidyl tyrosine residue
                                                                                                                                                                                                                                                                                                                                                                                                                     the
IM-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphoprotein; phosphotransferase; prote-oncogene; thiolester bond; transforming protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inoue, K.; Ikawa, S.; Semba; K:: Sukegawa, J.; Yamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brickell, P.M.; Patel, M.
Br. J. Cancer (1988) 58:704-709
Structure and expression of c-fgr protooncogene mRNA in
Epstein-Barr virus converted cell lines.
A45930
                                                                 #formal_name Homo sapiens #common_name man
31-Dec-1988 #sequence_revision 30-Sep-1989 #text_change
22-May-1998
                                                                                                                                                                                                                                                                                                         ##residues 1-529 ##label REA
##cross-references GB:M19722; GB:J03429; NID:g182573; PID:g182574
NCE A28353
                                                                                                                                                                                                                                                                                                                                                                        #journal Oncogene (1987) 1:301-304
#title Isolation and sequencing of cDNA clones homologous to
v-fgr oncogene from a human B lymphocyte cell line,
         TVHUFR #type complete protein-tyrosine kinase (EC 2.7.1.112) fgr - human kinase-related transforming protein (fgr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A24842
Nishizawa, M.; Semba, K.; Yoshida, M.C.; Yamamoto, Sasaki, M.; Toyoshima, K.
Mol. Cell. Biol. (1986) 6:511-517
Structure, expression, and chromosomal location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references GB:M12724; NID:9182581; PID:9553286
NCE A45930
                                                                                                                         A27676; A28353; A24842; A45930; S24306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:120615; OMIM:164940 #map_position 1p36.2-1p36.1 FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-177;524-529 ##label BRI
##cross-references GB:M27454
NCE S24306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #crocs
#accession Actor
##molecule_type DNA
##molecule_type III-416 ##label REB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #accession Akoooo
##molecule_type mRNA
##molecule_type 1-143 ##label INO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-142 ##label PAT ##cross-references EMBL:X52207
                                                                                                                                                                                                                                    (c-fgr).
#cross-references MUID:88094395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c-fgr gene.*
#cross-references MUID:87064334
                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB: FGR
                                                                                                                                            A27676
                                                                                                                                                                                                                                                                       A2767
                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #description
                                                    ALTERNATE_NAMES ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
#journal
                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal
                                                                                                                                                                                                #journal
                                                                                                                         ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #title
                                                                                                                                                                                                               #title
                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
RESULT
```

```
A34104 #type complete
protein-tyrosine kinase (EC 2.7.1.112) src 1 - African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transforming protein (src) 1
#formal_name Xenopus laevis #common_name African clawed frog 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                     Ĥ
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif\
#modified_site myristylated amino end (Gly) (in mature form) #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steele, R.E.; Chosn, R.; Ral, B.B.A.; Winokur, S.T.; Unger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
preliminary; not compared with conceptual translation
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal Oncogene (1992) 7:2345-2350
#title Structural organization of a src gene from xenopus laevis.
#cross-references MUID:93064714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 FALGRKIGEGYFGEVWEGIWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLH 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 AVVSE-EPIXIVTEFMCHGSLLDFLKNPEGQDLRLPQLVDMAAQVAEGMAYMERMNYIHR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 AVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHR 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 WSFGILLTELITKGRIPYPGMNKREVLEQVEQGYHMPCPPGCPASLYEAMEQTWRLDPEE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase-related transforming protein (src); kinase-related
                                                                                                                                                                                                                                                                                                                                                                                                                                        263 ITLERRIGIGCFGDVWLGTWNGSTKVAVKTLKPGTMSPKAFLEEAQVMKLLRHDKLVQLY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:M24704; GB:J04822; NID:g214804; PID:g214805
NCE I51564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
#journal J. Biol. Chem. (1989) 264:10649-10653
#title The two Xenopus laevis SRC genes are co-expressed and produces functional pp(60src).
#cross-references MUID:89278134
                                                                                                                                                                             #binding_site palmitate (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 DLRAANILVGERLACKIADFGLARLIKDDEYNPCQGSKFPIKWTAPEAALFGRFTIKSDV
                                                                                                                                                                                                                                      #active_site Lys #status predicted
#length 529 #molecular-weight 59478 #checksum 2467
                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                            Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status preliminary; translated from GB/EMBL/DDBJ#molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                  49; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-113 ##label ST2
##cross-references GB:M33646; NID:g214808; PID:g214810
                                                                                                                                                                                                                                                                                                                         Score 1008; DB 1; I
Pred. No. 1.10e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-532 ##label STE
                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                                                                                                                      Query Match 53.6%;
Best Local Similarity 53.6%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 RPTFEYLQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 RPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
```

ဖ

```
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B34104  #type complete
protein-tyrosine kinase (EC 2.7.1.112) src 2 - African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP: autophosphorylation: phosphoprotein; phosphotransferase; tyrosine-specific protein kinase
ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                 386
                                                                                                                                                                                                                                                                                                                                                                                          446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase-related transforming protein (src); kinase-related transforming protein (src) 2 #formal_name Xenopus laevis #common_name African clawed f: 30-Mar-1990_*sequence_revision 30-Mar-1990 #text_change
                                                                                                                                                                                                                                                                                                                                    292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. (1985) 13:1747-1761
Two divergent cellular src genes are expressed in Xenopus
                                                                                                                                                                                                                                       268 LELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 327
                                                                                                                                                                                                                                                                           232 LGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAV 291
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 FGILLTELTIKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. (1989) 264:10649-10653
The two Xenopus laevis SRC genes are co-expressed and
produces functional pp(60src).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:9214797
                                                                                                                                                                                                                                                                                                                 VSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMNYVHRDL
                                                                                                                                                                                                                                                                                                                                                                                        RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                    #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 532 #molecular-weight 59856 #checksum 7110
                                                                                                                                                                                                      1;
                                                                                                                                                                Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                              Score 1006; DB 2; Length 532
Pred. No. 2.74e-168;
40; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #residues 1-532 ##label STE
##cross-references GB:M23422; GB:J04822; NID:g214796;
GCE 151563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:M30858; NID:g214799; PID:g555569
                                                     #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439-492 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #cross-references MUID:89278134
#accession B34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #cross-references MUID:85215578
#accession I51563
                                                                                                                                                              tch 53.5%;
al Similarity 54.5%;
134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B34104; I51563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steele, R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A34104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    src
464/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 TEEYLQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #introns
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fauthors
                                                                                     264-522
272-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
                                                                  147-244
                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                      387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #title
                                                     87-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
KEYWORDS
                                                                                                                              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                           446
                                                                                                                                                                                                                                                                   328 VSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMNYVHRDL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 388
                                                                                                                                                                                            268 LELKLGGGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 LEKKLGQGCFAEVWLGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 329
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A44991 *type complete protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse kinase-related transforming protein (fyn) kinase-related transforming protein (fyn) #formal_name Mus musculus #common_name house mouse 03.Jun-1993 *sequence_revision 30-Sep-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cooke, M.P.; Perlmutter, R.M. New Biol. (1989) 1:66-74 Expression of a novel form of the fyn proto-oncogene in hematopoietic cells.
                                                                                                                                                                                                                                                                                       387 RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                 232 LGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANMKLTDLAKEIQTLKGLRHERLIRLHAV
                                                                                                                                                                                                                                                                                                                                                                                                                     FGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRKDPEERP
#domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN\
#region protein Kinase ATP-binding motif
#length 532 #molecular-weight 59736 #checksum 7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 534 #molecular-weight 60057 #checksum 2574
                                                                                                                                                       Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 534;
                                                                                                                                                       71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain SH3 homology #label SH3/
#domain SH2 homology #label SH2/
                                                                                                                                 Pred. No. 2.74e-168;
40; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1007; DB 2; I
Pred. No. 1.73e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches
                                                                                                                  Score 1006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     =
=
=
=
=
=
=
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary
                                                                                                                ch 53.5%;
1 Similarity 54.5%;
134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 53.5%;
Local Similarity 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A44991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A44991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A44991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 TFEYLQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149-246
266-524
274-282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
                   147-244
264-522
272-280
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                             SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
```

```
intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||:| ||: ||
ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 QRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                 I48608
                                                                                                                                                                                                                                                                                                                                                                                                                  148608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                                                                          ##status
                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                         REFERENCE
#authors
#journal
                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                    #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123-215
239-501
247-255
                                      ACCESSIONS
                                                                                                                #title
                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-537 ##label STE ##cross-references GB:X52188; GB:X52189; NID:g64701; PID:g64702 ##cross-references GB:X52188; GB:X52189; NID:g64701; PID:g64702 FICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; autophosphorylation; phosphorrotein; phosphotransferase; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                               #formal_name Xenopus laevis #common_name African clawed frog 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 31-Oct-1997 A43806
                                                                                                                                                                                                                                                                                             A43806 #type complete protein-tyrosine kinase (EC 2.7.1.112) fyn - African clawed
                                    RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS 448
                                                       352 AARNVLVDDGLACKVADFGLARLIKDDIYSPSSSSKIPVKWTAPEAANIKVFSQKSDVWS 411
                                                                                                          FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWKKDPEERP 508
                                                                                                                               273 LIKRLGNGQFGEVWMGIWNGNTKVAIKTLKPGTMSPESFLEERQIMKKLKHDKLVQLYAV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS 451
292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVARGMAYIERMNYIHRDL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                              Steele, R.E.; Deng, J.C.; Ghosn, C.R.; Fero, J.B. Oncogene (1990) 5:369-376
Structure and expression of fyn genes in Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149552 #type complete
protein-tyrosine kinase (EC 2.7.1.112) bsk/iyk - mouse
intestinal tyrosine kinase
#formal_name Mus musculus #common_name house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMLNCWKKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 537 #molecular-weight 60846 #checksum 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.86e-168;
46; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.3%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A43806
                                                                                                                                                                                                                   472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 TFEYLQ 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 SFATLR 477
                                                                                                                                                                                 509 TEEYLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#title
                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149-246
269-527
277-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
                                    389
                                                                                                          449
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTRY
                                  음
                                                                      à
                                                                                                      g
                                                                                                                                              õ
                                                                                                                                                                               셤
                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKSLRHPKLIQLYAV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology ATP; intestine; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                 Oberg-Welsh, C.; Welsh, M.
Gene (1995) 152:239-242
Cloning of BSK, a murine FRK homologue with a specific
pattern of tissue distribution.
                                                                                                                                                                                                                                                                                                                                                                                   Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemiecki, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. (1995) 209:582-589 iyk, a novel intracellular protein tyrosine kinase differentially expressed in the mouse mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 CTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFIQQVDMAAQVASGMAYLESQNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESKHEIKLPVKWTAPEAIRTNKFSIKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 VWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQNYRLPQPSNCPQQFYSIMLECWNVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain SH3 homology #label SH3\
#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif
#length 512 #molecular-weight 58891 #checksum 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1002; DB 2; Length 51:
Pred. No. 1.72e-167;
45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-153,'T',155-236,'H',238-512 ##label RE ##cross-references EMBL:248757; NID:9736263; PID:9736264
                                                                                                                                                                                                                                                                                                                                      NID:q556287; PID:q77773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                             translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Thu May 20 13:07:19 1999 Job time: 174 secs.
                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
##residues 1-512 ##label
##cross-references GB:L36132;
                                                                                                                                                                                                       #cross-references MUID:95137395
#accession I49552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tross-references MUID:95251656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.2%;
                     09-Apr-1998
I49552; I48608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
```

****	(TM)

*****	'' '/

****	<u>'</u> ']

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 13:07:36 1999; MasPar time 12.30 Seconds 576.996 Million cell updates/sec Tabular output not generated.

>US-09-099-053-2 (230-480) from US09099053.pep (5 of 6) 1882

1 FALGRKLGEGYFGEVWEGLW......ECWRSSPEERPSFATLREKL 251 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Searched:

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 47.757; Variance 83.764; scale 0.570 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	0.00e+00	4.93e-221	4.18e-215	1.17e-209	1.17e-209	1.47e-202	1.30e-201	5.86e-200	1.74e-199	1.74e-199	1.01e-199	5.17e-199	4.55e-198	4.55e-198	2.33e-197	2.05e-196	3.53e-196	6.08e-196	3.53e-196	6.08e-196	3.53e-196	3.53e-196	1.80e-195
	Description	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	NEURONAL PROTO-ONCOGEN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS
	QI .	SRM_MOUSE	SRK4_SPOLA	SRK3_SPOLA.	SRK2_SPOLA	SRK1_SPOLA	FRK_HUMAN	FYN_XIPHE	FGR_HUMAN	SRC2_XENLA	SRC1_XENLA	FYN_MOUSE	FYN_XENLA	FYN_HUMAN	SRC_AVISS	SRC_CHICK	SRC_HUMAN	LCK_CHICK	SRC_RSVPA	FYN_CHICK	SRCN_MOUSE	SRC_AVIST	SRC_AVIS2	STK_HYDAT
	DB 	7	-	٦	П	П	٦	Н	~	П	٦	П	-	П	П	Н	Н	٦	Н	H	7	Н	٦	П
	Length	496	206	334	362	505	505	536	529	531	531	533	536	536	568	532	535	507	523	533	540	557	587	509
% Query	Match	88.7	58.3	57.0	55.7	55.7	54.1	53.9	53.6	53.5	53.5	53.5	53.3	53.1	53.1	53.0	52.8	52.7	52.7	52.7	52.7	52.7	52.7	52.6
	Score	1670	1097	1072	1049	1049	1019	1015	1008	1006	1006	1007	1004	1000	1000	266	866	992	991	992	991	992	992	686
Result	S .	н	7	m	4	S	φ	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.80e-195	5.35e-195	9.22e-195	9.22e-195	4.71e-194	8.11e-194	4.14e-193	7.13e-193	2.11e-192	1.23e-192	3.64e-192	3.64e-192	6.26e-192	1.08e-191	9.47e-191	2.81e-190	4.83e-190	2.16e-188	1.25e-188	6.40e-188	3.26e-187	1.66e-186
PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	PROTO-ONCOGENE TYROSIN	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS
YES_CHICK	SRC_RSVH1	SRC_AVISR	SRC_RSVP	YES_AVISY	YES_XIPHE	BLK_HUMAN	SRC_RSVSR	YES_MOUSE	YES_HUMAN	LCK_MOUSE	HCK_HUMAN	YES_XENLA	YRK_CHICK	YES_CANFA	FGR_FSVGR	LCK_HUMAN	HCK_RAT	HCK_MOUSE	FGR_MOUSE	LYN_RAT	LYN_MOUSE
П	Н	1	Н	Н	Н	Н	Н	Н	-	-	-	٦	Н	Н	Н	Н	Н	Н	Н	-	ч
541	526	526	526	528	544	504	526	541	543	208	526	537	535	539	545	508	503	524	517	511	511
52.6	52.4	52.4	52.4	52.2	52.2	52.0	52.0	51.9	51.9	51.8	51.8	51.8	51.7	51.5	51.4	51.3	51.0	51.0	50.9	50.7	50.5
989	687	986	986	983	982	979	8.46	916	977	975	975	974	973	696	296	996	959	960	957	954	951
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 α

```
SIMILARITY: CONTAINS 1 SH3 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRK3_SPOLA
P42689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                        16 SH2.

495 PROTEIN KINASE.

248 ATP (BY SIMILARITY).

262 ATP (BY SIMILARITY).

354 BY SIMILARITY.

384 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

78 R -> G (IN REF. 2).

278 LRK -> FGR (IN REF. 2).

278 LRK -> FOATURE (IN REF. 2).

278 N -> I (IN REF. 2).

278 N -> I (IN REF. 2).

278 N -> I (IN REF. 2).

278 N -> I (IN REF. 2).

278 N -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 92334872.
OTTILIE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
Multiple src-related kinase genes, srkl-4, in the fresh water sponge spongilla lacustris..;
ONCOGENE 7:1625-1630(1992).
-! CAPALYIT ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 FVLRKKLGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTKENEALKSLRHERLIRLH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AICSLGEPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGFACQVAEGMSYLEERRVVHR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLAARNVLVGDDLTCKVADFGLARLLKDDVYSPSSGSKIPVKWTAPEAANYRVFSOKSDV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSFGILLYEVFTYGQCPYEGMTNHETLQQISRGYRLPRPAVCPAEVYVLMVECWKGSPEE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- ALTERNATIVE PRODUCTS: STRI AND SRK4 MAY ARISE BY ALTERNATIVE
                                                                                                                                                      TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1670; DB 1; Length 496; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE-PROTEIN KINASE SRK4 (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 AA
   ٠<del>٠</del>:٠٠
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     88.78;
84.98;
                                                                                                                                                                         SH3 DOMAIN; PHOSPHORYLATION
                                                                        PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPTFAILREKL 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPSFATLREKL 480
                                                                                                                                                                                                                                                                                                      384
78
236
278
496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
                                                                                                                                                    TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRK4_SPOLA
P42690;
                                     PROSITE;
PROSITE;
                                                                                                                                                                                                                              DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                     PROSITE;
 PROSITE;
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
 DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DORK KAN DOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92334872.
OTILLE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
"Multiple src-related kinase genes, srkl-4, in the fresh water sponge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LLRGLGAGQFGEVWEGLWNGTTSVAVKTLKPGTMSIEEFLEEASIMKQLRHPKLIQLYAV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 CTKEEPIYIVTELMKHGSLLEYL-RGDGRSLKLPPDLVDMCSQVASGMSYLEQQNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AARNILVGEHKICKVADFGLARVIDEEIYEAKLGAKFPIKWTAPEAAMYSRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 FGIVLYEVITYGRFPYPGMTNAQVLEQIQQSYRMPRPMGCPEKLYAIMMDCWREDPASRP
                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.

SH3.

SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPONGILLA LACUSTRIS (FRESHWATER SPONGE).
EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRK3 (EC 27.1.112) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1097; DB 1;
Pred. No. 4.93e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
807A71D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AA
                                                                                                                                                                                EMBL; X61604; G10156; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PRAM; PF00017; SH3; 1.
PFAM; PF00017; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00013; ZPTK.
                                                                                                                                                                                                              . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 SF
493 PF
254 A1
268 A1
359 BX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%;
54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spongila lacustris.";
ONCOGENE 7:1625-1630(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
240
246
246
368
359
359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 92334872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ||
472 SFATL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 TFETL 485
```

SCHARTL M.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                       in the fresh water sponge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 ITLIRKLGAGQFGEVYQGLWNNSTPVAVKTLKAGTMQPAAFLAEAQIMKKLRHPKLIQLY 154
                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AVCTQGEPVYIITELMSKGSLLDYLQGEAG-ALKLPQLIDMAAQVAAGMAYLELHNYIHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 DLAARNILVGDNNICKVADFGLARLIVSDDYNATEGAKFPIKWTAPEAALFNRFSIKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 WSFGILITELVTYGRIPYPGMSNAEVLQNLDKGYRMPCPVTTPESLYQIMLDCWKRNPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFERAGE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.

1 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Mismatches 65; Indels
                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1049; DB 1; 1
Pred. No. 1.17e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E00C78BE CRC32;
                              ີ.
ບ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRKI (EC 2.7.1.112).
SRK1.
MEDLINE; 92334872.
OTTLILE S., RAULF F., BARNEKOW A., HANNIG G.
"Multiple src-related kinase genes, srkl-4,
Spongilla lacustris.";
ONCOGENE 7:1625-1630(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X61602; G10152; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; PARTIAL.
PFAM; PF00107; SH2; 1.
PFAM; PF00107; SH2; 1.
PFAM; PF00523; 2PTK.
                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 53.8%;
les 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
348
109
123
214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 RPTFEALQWRL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
101
123
123
214
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 5
SRK1_SPOLA
P42686;
                                                                                                                                                                                                                                          DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
ID SR
AC P4
DT 01
DT 01
DT 01
DT SR
GN SR
     STATE THE TERM TO BE A STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE OF THE TERM TO STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@licenseries.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 CTIGEPIYIVTELMKYGSMLEYLKHGEGKNITLHQMVDMSAQIASGMTYLEAHSYIHRDL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LQRKLGQGNFGEVWAGVWNGTTAVAVKTLKPDTMEVKDFVQEAQVMKKIHHPNLLQLYAV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 FGVLISEIVTHGRMPYPGMTNRQVLEAVDRGYRMPCPEGCPDPLYKIMLSCWKHEPDDRP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                   PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AARNILVGEGNVCKVADFGLARVIKEDIYNPREGTKFPIKWTAPEAALYNRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00107; PROTEIN KINASE_ATP: 1.
PROSITE: PS00109; PROTEIN_KINASE_TR: 1.
PROSITE: PS50011; SH2: 1.
PROSITE: PS50011; SH2: 1.
PROSITE: PS50002; SH3: PARTIAL.
PRAM: PF000017; SH2: 1.
PFAM: PF00069; pkinase: 1.
PFAM: PF00069; pkinase: 1.
HSSP: P12931: 1FMK.
TRANSFERASE: TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRK2_SPOLA STANDARD; PRT; 362 AA.
P42688;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRK2 (EC 2.7.1.112) (FRAGMENT).
ATP + A PROTEIN TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1072; DB 1; I Pred. No. 4.18e-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
7B64FB9B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPONGILLA LACUSTRIS (FRESHWATER SPONGE)
                                                                                                                              -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37880 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%;
51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 51.4%;
es 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
321
80
94
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 TFESLKNLL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 SFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                        DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
```

셤

g

ò

g

à

g

ò

엄

ö

ò

ä

Gaps

Length 362;

213

```
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
   RESULT
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                        MEDLINE; 92334872.
OTTILE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
OTTILLE S., RAULF F., BARNEKOW A., HANNIG G., SCHARTL M.;
Multiple src-related kinase genes, srkl-4, in the fresh water sponge spongilla lacustris.",
ONCOGENE 7:1625-1630(1992).
-I-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN: PROTEIN: ATP - A PROTEIN TYROSINE - ADP +
PROTEIN: AND A PROTEIN FROSHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pest Local Similarity 53.7%; Pred. No. 1.1/e 202,
Matches 132; Conservative 49; Mismatches 64; Indels 11, Gaps
                                                                                                                                                                                                                             -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLRRLGAGQFGEVWEGLWNGTTSVAVKTLKPGTMSVEEFLQEASIMKRLRHPKLIQLYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CIKEEPIYIVTELMKYGSLLEYLRGEDG-VLKIEQLVDVAAQVASGMSYLEQQNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGVVLYEIITYGRFPYPGMTNPEVLEKIQQNYRMPCPANCPKQFHDIMLDCWREDPASRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARNILVGEHGICKVADFGLARVIDEE1YEAHTGAKFPIKWTAPEAAMYNRFTIKSDVWS
                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- ALTERNATIVE PRODUCTS: SRK1 AND SRK4 MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
              EUKARYOTA; METAZOA; PORIFERA; DEMOSPONĞIAE; CERACTINOMORPHA;
HAPLOSCLERIDA; SPONGILLIDAE; SPONGILLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3.
SH2.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1049; DB 1;
Pred. No. 1.17e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_AIP; 1. PROSITE; PS00107; PROTEIN_KINASE_AIP; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. PROSITE; PS50001; SH2; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1049;
 SPONGILLA LACUSTRIS (FRESHWATER SPONGE)
                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 SH2 DOMAIN. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 PI
254 A:
268 A:
359 Bi
57693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFERASE; TYROSINE-PROTEI
SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%;
53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359
505 AA;
                                                           SEQUENCE FROM N.A. MEDLINE; 92334872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFETLQ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| ||:
SFATLR 477
                                                                                                                                                                                                                SPLICING
                                                                                                                                                                                                                                              DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            CANCE W.G., CRAVEN R.J., BERGMAN M., XU L.H., ALITALO K., LIU E.T.; "Rak, a novel nuclear tyrosine kinase expressed in epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DERIVED FROM TISSUES
                              01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE FRK (EC 2.7.1.112) (NUCLEAR TYROSINE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE.

-! SUBCELLULAR LOCATION: CYTOPLASMIC (PROBBLE).

-! TISSUE SPECIFICITY: RESTRICTED TO CELLS LINES DERIVED FROM TISSOF LYMPHOLD, BRAIN: BREAST, COLON AND BLADDER ORIGIN.

-! SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN BELOGGS TO THE RESTRAILLY.

-! SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                   LEE J., WANG Z., LUOH S.-M., WOOD W.I., SCADDEN D.T.; "Cloning of FRK, a novel human intracellular SRC-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93293373.

CANCE W.G., CRAVEN R.J., WEINER T.M., LIU E.T.;

Novel protein kinases expressed in human breast cancer.";

INT. J. CANCER 54:571-577(1993).

-! - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> A (IN REF. 2)
C4226A83 CRC32;
   505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U00803; G392888; -.
EMBL; U2212; G732528; -.
PROSITE; P800107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PRAM; PF00017; SH3; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                            CELL GROWTH DIFFER. 5:1347-1355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> R
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110
208
208
268
262
354
387
115
58254 ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
TRANSFERASE; TYROSINE-PROTI
                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE FROM N.A.
   STANDARD;
                                                                                                                                                                                                                                                                  kinase-encoding gene.";
GENE 138:247-251(1994).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
505 AA;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      TISSUE=LYMPHOID;
MEDLINE; 94171047.
FRK_HUMAN
P42685; Q13128;
O1-NOV-1995 (REI
O1-NOV-1995 (REI
                                                                                              KINASE RAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
NP_BIND
BINDING
```

```
SEQUENCE OF 1-143 FROM N.A.
                                                                                                                                                                                         Query Match
                                                                                                DOMAIN
MOD_RES
NP_BIND
BINDING
                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (C-FGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                         LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.'
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
В
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          XIPHOPHORUS HELLERI, CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; EUKARYOA; METAZOA; CARATHOPTERYGII; ATHERINOMORPHA; EUTELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ATHERINOMORPHA; CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECILLIDAE; XIPHOPHORUS.
                                               236 LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAV 295
                                                           296 CTLEDPIYIITELMRHGSLQEYLQNDTGSKIHLTQQVDMAAQVASGMAYLESRNYIHRDL 355
                                                                                                  356 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSD 415
                                                                                                                                          416 VMSFGILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQQFYNIMLECWNAEPK 475
                                                                                                                                                                               QF.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-RIO LANCETILLA;
MEDLINE; 91187435.
HANNIG G., OTTILIE S., SCHARIL M.;
"Conservation of structure and expression of the c-yes and fyn genes
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (REL. 23, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN)
                             'n
        Length 505;
                            71; Indels
     Score 1019; DB 1; I
Pred. No. 1.47e-202;
43; Mismatches 71;
                                                                                                                                                                                                                                                                       536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54971; G64482; -.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                        PRT;
                  53.6%;
       Query Match 54.1%;
Best Local Similarity 53.6%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00018; SH3; 1.
PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                        |||:| ||| ||
469 ERPSFATLREKL 480
                                                                                                                                                                                                           476 ERPTFETLRWKL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00017; SH2;
                                                                                                                                                                                                                                                                      FYN_XIPHE P27446;
                                                                                                                                                                                                                                                            g
                                                                                                                                                                   셤
                                                                                                                                                                                                          원
                                                                                                                                                                                      ò
                                                                                                         ò
                                                                                                                                                 ö
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 88094395.
RATAMINE S., VOTARIO V., RAO C.D., MIKI T., CHEAH M.S.C.,
TRONICK S.R., ROBBINS K.C.;
"Primary structure of the human fgr proto-oncogene product p55c-fgr.";
                                                                                                                                                             SH3.
SH2.
SH2.
PHOTEIN KINASE.
PHOSPHORLATION (BY PKC) (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                    PHOSPHORY LATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                                                                                                                                                                                                                BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
BA03DB12 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 LIKRLGNGQFGEVWMGTWNGTTKVAVKTLKPGTMSPESFLEEAQIMKKLRHDKLVQLYAV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (REL. 10, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Structure, expression, and chromosomal location of the human c-fgr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 RSANILVGDNLVCKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPASLHELMLQCWKKDPEERP
HSSP; P06241; 1AOT.
PROTO-ONCOGENE; TRANSFERASE; TYROSINE-PROTEIN KINASE; PHOSPHOR
ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 87064334.
NISHIZAWA M., SEMBA K., YOSHIDA M.C., YAWAMOTO T., SASAKI M.,
                                                                                                                                                                                                                                                                                                                                                                                 Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                          BY SIMILARITY.
MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                 Score 1015; DB 1; 1
Pred. No. 1.30e-201;
                                                                                                                                                                                                                                                                                                                                                                                                                           45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. CELL. BIOL. 8:259-266(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL. BIOL. 6:511-517(1986)
                                                                                                                                                                                                                                                                                                                                              MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 111-416 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               53.9%;
larity 53.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                            60316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                        11
284
298
389
419
530
                                                                                                                                                                                                                        11
276
298
389
419
530
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 132; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 TFEYLQ 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOYOSHIMA K.;
                                                        LIPOPROTEIN.
INIT_MET
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGR OR SRC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGR_HUMAN
P09769;
                                                                                                                                                                                                                                                                              ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
```

ဖ

```
SRC2_XENLA
P13116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                       셤
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           INOUE K., IKAWA S., SEMBA K., SUKEGAWA J., YAMAMOTO T., TOYOSHIMA K.; "Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from a human B lymphocyte cell line, IM-9."; ONCOGENE 1:301-304(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 ITLERRLGTGCFGDVWLGTWNGSTKVAVKTLKPGTMSPKAFLEEAQVMKLLRHDKLVQLY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLRAANILVGERLACKIADFGLARLIKDDEYNPCQGSKFPIKWTAPEAALFGRFTIKSDV 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSFGILLTELITKGRIPYPGMNKREVLEQVEQGYHMPCPPGCPASLYEAMEQTWRLDPEE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
B2B2227E CRC32;
                                                                                    -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE-PROTEIN KINASE; PROTO-ONCOGENE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVVSE-EPIYIVTEFMCHGSLLDFLKNPEGQDLRLPQLVDMAAQVAEGMAYMERMNYIHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY'SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1008; DB 1; I
Pred. No. 5.86e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION; SH2 DOMAIN; SH3 DOMAIN.

77 138 SH3.

DOMAIN 144 241 SH2.
                                                                                                                                                                                                                                                                                                                                                                      EMBL, M19722; G182574; -.
EMBL, M12724; G553286; -.
EMBL, M12719; G553286; JOINED.
EMBL, M12720; G553286; JOINED.
EMBL, M12721; G553286; JOINED.
EMBL, M12721; G553286; JOINED.
EMBL, M12721; G553286; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 PI
59478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.6%;
53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00069; pkinase; 1. HSSP; P06241; 1SHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.6%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291
382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A27676; TVHUFR.
PIR; A28353; A28353.
MIM; 164940; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00017; SH2;
PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
269
291
382
412
529 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPIFEYLQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:| |:
RPSFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470
RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA RRARA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                       XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA: BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

CGABE595 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 LELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two divergent cellular src genes are expressed in Xenopus laevis.";
NUCLEIC ACIDS RES. 13:1747-1761(1985).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89278134.
STEELE R.E., UNGER T.F., MARDIS M.J., FERO J.B.;
"The two Xenopus laevis SRC genes are co-expressed and each produces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFERASE; ATP-BINDING; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Mismatches 71; Indels
                                                    01-0AN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-2 (EC 2.7.1.112) (P60-SRC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
MYRISTATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1006; DB 1; 1
Pred. No. 1.74e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN. BELONGS TO THE SRC SUBFAMILY.
531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M23422; G214797; -...
EMBL; M30858; G555569; -...
EMBL; M30857; G555569; JOINED.
PIR; B34104; B34104.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1...
PROSITE; PS50011; PROTEIN_KINASE_ATP; 1...
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1...
PROSITE; PS50001; SH2; 1...
PROSITE; PS50002; SH3; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3 DOMAIN; SH2 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  functional pp60src.";
J. BIOL. CHEM. 264:10649-10653(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59605 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 438-491 FROM N.A. TISSUE=ERYTHROCYTE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.5%;
Best Local Similarity 54.5%;
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518
279
293
384
414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 85215578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEELE R.E.;
```

```
506 TFEYLQ 511
                                                                                                                                                                                                                                                                                               472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                T 11
FYN_MOUSE
P39688;
  ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminal
                                              Query Match
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         MUS
                                                                                                                                                                                                                                                                                                                                 RESULT
    SFF
                                                                                                                                     g
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                         g
                                                                                                                                                            ŏ
                                                                                                                                                                                 g
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              445
                                                                                          ARRIVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWS 411
                                                                                                                        FGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRKDPEERP 505
                                                                                                                                     CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                   produces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00069; pkinase; 1.
HSSP; P00523; 22PK.
TRANSFERASE; ATP-BINDIG; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION;
MYRIGTYLATION; SH3 DOMAIN; SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        functional pp6 src.";
J. BIOL. CHEM. 264.10649-10653(1989).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN. TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
327 VSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMNYVHRDL
                                                                            RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                   each
                                                                                                                                                                                                                                                           01-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-1 (EC 2.7.1.112) (P60-SRC-1).
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89278134.
STEELE R.E., UNGER T.F., MARDIS M.J., FERO J.B.;
"The two Xenopus laevis SRC genes are co-expressed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY). SIMILARITY).
                                                                                                                                                                                                                                       531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY. MYRISTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M24704; G214805; -.
PIR: A34104; A34104.
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SATP (BY
                                                                                                                                                                                                                                                                                                                   XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
243
518
279
293
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                      TFEYLQ 511
                                                                                                                                                                                         SFATLR 477
                                                                                                                                                                                                                                      SRC1_XENLA P13115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                              412
                                                                                                                                                                                         472
                                                      292
                                                                             386
                                                                                                  352
                                                                                                                        446
                                                                                                                                                                    206
                               9
                                                      8
                                                                          g
                                                                                                  ò
                                                                                                                       <del>Q</del>
                                                                                                                                             ö
                                                                                                                                                                   g
                                                                                                                                                                                           ö
```

```
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 LELKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 326
                                                                                                                                                                                                                                     327 VSE-EPIYIVTEYMSKGSLLDFLKGEMGRYLRLPQLVDMAAQIASGMAYVERMNYVHRDL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 BY SIMILARITY.
414 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
59725 MW; AB0705D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN).
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94019312.
SHENY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LUBLIN D.M.;
"Palmitylation of an amino-terminal cysteine motif of protein
tyrosine kinases p561ck and p59fyn mediates interaction with
g1lycosyl-phosphatidylinositol-anchored proteins.";
MOL. CELL. BIOL. 13:6385-6392(1993).
                                                                                                                                                                                                                                                                                                                                              292 CSGGEPVXIVTELMRGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                  386 RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 FGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPDCPESLHDLMFQCWRKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97345356.
WOLVEN A., OKAMURA H., ROSENBLATT Y., RESH M.D.;
"Palmitoylation of p59fyn is reversible and sufficient for plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOEGL M., ZLATKINE P., LEY S.C., COURTNEIDGE S.A., MAGEE A.I.; "Palmitoylation of multiple Src-family kinases at a homologous terminal motif".
                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В.Н.
                                                                                                      Length 531;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91175680.
COOKE M.P., PERLANUTER R.M.;
"Expression of a novel form of the fyn proto-oncogene in hematopoietic cells.";
NEW BIOL. 1:66-74(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEE C., KIM M.G., JEON S.H., PARK D.E., PARK S.D., SE
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                      Score 1006; DB 1; I
Pred. No. 1.74e-199;
                                                                                                                                                         40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane association.";
MOL. BIOL. CELL 8:1159-1173(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOCHEM. J. 303:749-753(1994).
                                                                                                   53.5%;
54.5%;
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCULUS (MOUSE).
384 3
414 4
531 AA;
                                                                                                                              Local Similarity
nes 134; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 91175680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95071286.
```

```
412 FGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYVLMLECWRSSPEERP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A43806; A43806.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN. BELONGS TO THE SRC SUBFAMILY
                                                                                                                                                                                     XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P06241; 1FYN.
PROTO-ONCOGENE; TRANSFERASE; TY
LIPOPROTEIN.
INIT MET 0 0 BY
LIPID 1 1 M
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 2 2 PN
LIPID 3 SI
DOMAIN 148 245 SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52188; G64702; -.
EMBL; M27502; G214163; -.
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
1
2
1
2
4
5
2
3
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
284
298
389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00017; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 AA;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
270
270
11
276
2298
389
                        508 TFEYLQ 513
                                       :| |:
472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00069;
                                                                                               FYN_XENLA
P13406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
MOD_RES
NP_BIND
BINDING
                                                                                   a
                                                ŏ
 à
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   MEDLINE; 96551668.

A GAUEN L.K.T., LINDER M.E., SHAW A.S.;
GAUEN L.K.T., LINDER M.E., SHAW A.S.;
GAUEN L.K.T., LINDER M.E., SHAW A.S.;
Multiple features of the p59fyn src homology 4 domain define a motif
"Multiple features of the p59fyn src homology 4 domain define a motif
"for immune receptor tyrosine-based activation motif (ITAM) binding
"T for immune receptor tyrosine-based activation motif (ITAM) binding
"T for immune receptor tyrosine-based activation motif (ITAM) binding
"T for immune receptor tyrosine-based activation";
"I GEL BIOL 133:1007-1015(1996).
"I CELL BIOL 133:1007-1015(1996).
"I CHALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PROSPHATE.
"I CHALYTIC CONTAINS 1 SH3 DOMAIN,
"I SHALLARITY: CONTAINS 1 SH3 DOMAIN.
"I SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 LEKKLGQGCFAEVWLGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWKKDPEERP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY) B235E6FA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1007; DB 1; 1
Pred. No. 1.01e-199;
46; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; S42; 1.
PROSITE; PS50017; S43; 1.
PF00017; S42; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILAR!
MYRISTATE.
PALMITATE.
PALMITATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P06244; 1FYN.
PROTO-ONCOGENE; TRANSFERASE; TY
ATP-BINDING; MYRISTYLATION; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59926 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 53.5%;
Local Similarity 52.8%;
nes 130; Conservative
                                                                                                                                                                                                                                                                                                                      EMBL; M27266; G309241; -.
EMBL; U70324; G1575677; -.
PIR; A44991; A44991.
MGD; MGI:95602; FYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
245
520
520
281
295
386
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 AA;
            MYRISTOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPOPROTEIN.
INIT_MET
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPID
LIPID
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                                          01-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NUV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1004; DB 1; Length 536;
Pred. No. 5.17e-199;
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 90191723.

STEBLE R. E., DENG J.C., GHOSN C.R., FERO J.B.;
"Structure and expression of fyn genes in Xenopus laevis."
ONCOGENE 5:369-376(1990).
-!- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
-!- CATALYTICA: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
MYRISTATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87236822 CRC32
536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE
```

```
ij
                                                                                                      450
                    272 LIKRLGNGQFGEVWMGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 331
                                332 VSE-EPIYIVTEYMSKGSLLDFLKDGEGRALKLPNLVDMAAQVARGMAYIERMNYIHRDL 390
                                                                        292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 87089775.
KAWARAMI T., PENNINGTON C.Y., ROBBINS K.C.;
"Isolation and oncogenic potential of a novel human src-like gene.";
MOL. CELL. BIOL. 6:4195-4201(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Crystal structure of the SH3 domain in human Fyn; comparison of the three-dimensional structures of SH3 domains in tyrosine kinases and
                                                                                                                                                                                                                                                                      01-JAN-1988 (REL. 06, CREATED)
01-FEB-1994 (REL. 38, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PETERS D.J., MCGREW B.R., PERRON D.C., LIPTAK L.M., LAUDANO A.P.; "In vivo phosphorylation and membrane association of the fyn proto-oncogene product in IM-9 human lymphoblasts."; ONCOGENE 5:1313-1319(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSACCHIO A., SARASTE M., WILMANNS M.; High-resolution crystal structures of tyrosine kinase SH3 domains complexed with proline-rich peptides."; NAT. STRUCT. BIOL. 1:546-551(1994).
                                                                                                                 391 RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                               FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMLNCWKKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                SEMBA K., NISHIZAWA M., MIYAJIMA N., YOSHIDA M.C., SUKEGAWA J., YAMANASHI Y., SASKI M., YAMANOTO T., TOYOSHIMA K.; "Yes-related protoconcogene, syn, belongs to the protein-tyrosine kinase family.";
                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOBLE M.E.M., MUSACCHIO A., SARASTE M., COURTNEIDGE S.A.,
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SH3 DOMAIN.
  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROC. NATL. ACAD. SCI. U.S.A. 83:5459-5463(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
MYRISTOYLATION, AND PHOSPHORYLATION.AT.TYR-530..
MEDLINE; 91016431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 80-141.
 Mismatches
                                                                                                                                                                                                                                                    536 AA.
  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 12:2617-2624(1993).
 Conservative
                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93327750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95393198
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 86287278
                                                                                                                                                                                     511 TFEYLQ 516
                                                                                                                                                                                                          472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIERENGA R.K.;
131;
                                                                                                                                                                                                                                                                                                                 SYN) (SLK).
                                                                                                                                                                                                                                         JT 13
FYN_HUMAN
P06241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spectrin
 Matches
                                                                                                                                              451
                                                                                                                                                                                    Dp
                                                           g
                                                                                                    g
                                                                                                                         ò
                                                                                                                                             g
                                                                                                                                                                                                          ò
                                        ò
                                                                                 ò
                                                                                                                                                                  ò
```

```
REPORTED HEAD CONTINUENT NOT CONTINUENT NOT THE PROPERTY NEED OF 84-140 IN COMPLEX WITH NEE.

RED. C.H. SARKERA K. MIRA O. N. CHARLE B.T. WINTENN J. T. C.P. SARKERA K. MIRA O. N. CHARLE B.T. SARKERA K. WINTEN D. S. C. SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES SALLES S
```

```
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                        LIPID
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                 388
                                                                                                                                                                                                                                                                                                                                                          448
                                                                                                                                                                                                                                                                                                                                                                                                472
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
ID SP
AC PC
DT 21
DT 01
DT 11:
DE PI
GN SI
 d
                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                       ij
                 PROTEIN KINASE.
PHOSPHORYATION (BY PKC) (BY SIMILARITY)
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                       BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION.
A -> S (IN REF. 2).
A -> R (IN REF. 2).
                                                                                                                                                                                                                                                                         332 VSE-EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 390
                                                                                                                                                                                                                                                                                                       351
                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                          352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPPAANYRVFSQKSDVWS 411
                                                                                                                                                                                                                                                                                                                                              510
                                                                                                                                                                                                                                                                  272 LIKRLGNGQFGEVWMGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 331
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                  292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALMIRLPPLIGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                    RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                             FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWKKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVIAN SARCOMA VIRUS (STRAIN S1).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES
                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                         Length 536;
                                                                                                                                                                                                                                                      Indels
                                                                      PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC
                                                                                                                                                                                                                                        Score 1000; DB 1; L
Pred. No. 4.55e-198;
46; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SRC
                                                                                                                                                                                                                             01B18DD0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            568 AA
PS50011; PROTEIN_KINASE_DOM; 1. PS50001; SH2; 1. ... PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                        Query Match 53.1%;
Best Local Similarity 52.8%;
Matches 130; Conservative
                                                                                                                                                                                                                             60630
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                    298
389
530
530
183
836
836
82
107
110
118
113
113
134
                                                                                                                                                                                                                                                                                                                                                                       TFEYLQ 516
                                                                                                                                                                                                                                                                                                                                                                              :| |:
SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                      T 14
SRC_AVISS
P14084;
      PROSITE;
PROSITE;
                                                                                                                        ACT_SITE
MOD_RES
MOD_RES
CONFLICT
                                                                     LIPID
LIPID
DOMAIN
DOMAIN
DOMAIN
MOD_RES
NP_BIND
BINDING
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                          STRAND
                                                                                                                                                       STRAND
                                                                                                                                                             STRAND
                                                                                                                                                                    STRAND
                                                                                                                                                                                       STRAND
                                                                                                                                                                                              STRAND
                                                                                                                                                                                                           STRAND
                                                                                                                                                                                                                      STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRC).
V-SRC.
                                                                                                                                                                                 TURN
                                                                                                                                                                                                    TURN
                                                                                                                                                                                                                                                                                                                    391
                                                                                                                                                                                                                                                                                                                                             451
                                                                                                                                                                                                                                                                                                                                                                      511
                                                                                                                                                                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
269 LEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVRLYAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESQUENCE FROM N.A.
MEDLINE; 87064539
MEDLINE; 87064539
IKAWA S., HAGINO-YAMAGISHI K., KAWAI S., YAMAMOTO T., TOYOSHINA K.;
"Activation of the cellular src gene by transducing retrovirus.";
MOL. CELL. BROL. 6:2420-2428(1986)
-!-FUCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
KIRASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
... PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 7F080D52 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRC_CHICK STANDARD; PRT; 532 AA.
SRC_CHICK G92013;
21-JUL-1986 (REL. 01, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                          KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 VSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 568;
                                                                                                                                                                                                                                       1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

1 O TITEO.

2 ONTAINS 1 SH3 DOMAIN.

1 O SIMILARITY: CONTAINS 1 SH3 DOMAIN.

1 O SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE C.

2 DOMAIN. BELONGS TO THE SRC SUBFAMILY.

3 PROSITE: PSOOLOGY: PROTEIN. KINASE_ATP; 1.

3 PROSITE: PSOOLOGY: PROTEIN. KINASE_DOM; 1.

4 PROSITE: PSSOOLO; SH3; 1.

5 PROSITE: PSSOOLO; SH3; 1.

5 PROSITE: PSSOOLO; SH3; 1.

5 PROSITE: PSSOOLO; SH3; 1.

6 PROSITE: PSSOOLO; SH3; 1.

7 PROSITE: PSSOOLO; SH3; 1.

8 PROSITE: PSSOOLO; SH3; 1.

8 PROSITE: PSSOOLO; SH3; 1.

8 PRAM: PFOOLOGY: SH3; 1.

8 PFAM: PFOOLOGY: SH3; 1.

8 PFAM: PFOOLOGY: SH3; 1.

8 PFAM: PFOOLOGY: SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFERASE; PHOSPHORYLATION; ATP-BINDING; MYRISTYLATION; SH3 DOMAIN; SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE-PROTEIN KINASE; TRANSFORMING PROTEIN; ONCOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1000; DB 1;
Pred. No. 4.55e-198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARI
ATP (BY SIMILARI
BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYRISTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 53.1%;
Local Similarity 54.5%;
les 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRC.
GALLUS GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
245
520
281
295
386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
295
386
316
416
568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 TFEYLQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| |:
SFATLR 477
```

```
10WE;
10WF;
1PRL;
1PRM;
1RLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1NLO;
PDB; 1NLP;
                                                                                                                                                                                                                                                                                                                                                                                                                          1RLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; F
PROSITE; F
PROSITE; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                   PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                         PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                               PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                      PDB;
                                                                                                                                                                                                                                                                                                                                                PDB;
                                                                                                                                                                                                                                                                                                                                                          PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 86151652.
COOPER J.A., GOULD K.L., CARTWRIGHT C.A., HUNTER T.;
"Tyr527 is phosphorylated in pp60c-src: implications for regulation.";
SCIENCE 231:1431-1434(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
MEDLINE, 98070614.
WILLIAMS J.C., WEITLAND A., GONFLONI S., THOMPSON A.,
COURTINEIGE S.A., SUPERTI-FURGA G., WIERENGA R.K.;
The 2.35 A crystal structure of the inactivated form of chicken Src:
a dynamic molecule with multiple regulatory interactions.";
J. MOL. BIOL. 274:757-775(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                               the
its normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95063992.
FENG S., CHEN J.K., YU H., SIMON J.A., SCHREIBER S.L.;
"Two binding orientations for peptides to the Src SH3 domain:
development of a general model for SH3-ligand interactions.";
SCIENCE 266:124-1247(1994).
-!- FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED
                             SEQUENCE FROM N.A.
MEDLINE: 83155664.
TAKENA T., HANAFUSA H.;
Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";
CELL 32:881-890(1983).
                                                                                                                                                                                       in 5'
                                                                                                                                                                                                                                                                  KAMPS M.P., TAYLOR S.S., SEFTON B.M.; "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites."; NATURE 310:589-592(1984).
                                                                                                                                                                                                                                                                                                                                                ο.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YU H., ROSEN M.K., SCHREIBER S.L.; "1H and 15N assignments and secondary structure of the Src SH3
                                                                                                                                                                          DORAI T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity exons and possible mechanism for the genesis of the 3' end of v-src.";
                                                                                                                                                                                                                                                                                                                       PHÓSPHORYLATION.
MEDLINE: 86028181.
GOULD K.L., WOODGETT J.R., COOPER J.A., BUSS J.E., SHALLOWAY
EUKARYOTA; METAZOA; CHORDATA; VERTEBRAȚA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                   "Protein kinase C phosphorylates pp60src at a novel site."; CELL 42:849-857(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                       SMART J.E., OPPERMANN H., CZERNILOFSKY A.P., PURCHIO A.F., ERIKSON R.L., BISHOP J.M.;
"Characterization of sites for tyrosine phosphorylation in transforming protein of Rous sarcoma virus (pp60v-src) and cellular homologue (pp60c-src).";
PROC. NATL. ACAD. SCI. U.S.A. 78:6013-6017(1981).
                                                                                                                                                                                                                       MOL. CELL. BIOL. 11:4165-4176(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 80-139.
MEDLINE; 93279385.
YU H., ROSEN M.K., SCHREIBER S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 76-139.
                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION AT TYR-415. MEDLINE; 82082387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS LETT. 324:87-92(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION AT TYR-526.
                                                                                                                                                     SEQUENCE OF 1-18 FROM N.A. MEDLINE; 91304409.
                                                                                                        REVISION TO 525.
TAKEYA T., HANAFUSA H.;
                                                                                                                              CELL 34:319-319(1983).
                                                                                                                                                                                                                                            ATP-BINDING SITE.
MEDLINE; 84270751
                                                                                                                                                                                                                                                                                                                                                          HUNTER T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 LEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGNMSPEAFLQEAQVMKKLRHEKLVQLYAV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                      AMU MACKOLHADELS.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
BUXDME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE
PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE
ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE
C-TERMINAL END OR BY OTHER MUTATIONS.
POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.
SIMILARITY: CONTAINS I SH2 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN
CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION;
SH3 DOMAIN; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 997; DB 1; Length 532; Pred. No. 2.33e-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY PKC) ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION.
65406BF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00069; pkinase; 1.
IYROSINE-PROTEIN KINASE; PROTO-ONCOGENE;
TRANSFERASE; ATP-BINDING; MYRISTYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILP; 27-JAN-97.

PS00107; PROTEIN KINASE_ATP; 1

PS00109; PROTEIN_KINASE_TYR; 1

PS500011; SH2; 1.

PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΜW.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00402; G63354; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S43604; E75862; -
S43616; E75867; -
S43587; E75861; -
S43614; E75866; -
S43614; E75866; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
280
294
385
415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-95.
27-JAN-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-95.
07-FEB-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1SRL; 31-MAY-94
1SRM; 31-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-DEC-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-96
                                        AND MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
385
415
526
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
147
266
11
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A00630;
```

ä

```
507 TFEYLO 512
:| |:
472 SFATLR 477
       Ob
            οy
                pp
                    QY
                         QQ
    ò
```

Search completed: Thu May 20 13:08:17 1999 Job time: 41 secs.

...<u>.</u>

*****	(TM)	******
******	' <u></u>	***
***************************************	'' 	
*****		*******

******		***
******		****
*****		*****

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein • protein database search, using Smith-Waterman algorithm

Run on: Thu May 20 13:08:37 1999; MasPar time 28.94 Seconds 473.314 Million cell updates/sec

Tabular output not generated.

Title: >US-09-099-053-2
Description: (230-480) from USO9099053.pep (5 of 6)
Perfect Score: 1882
Sequence: 1 FALGRKLGEGYFGEVWEGLW......ECWRSSPEERPSFAILREKL 251

Scoring table: PAM 150 Gap 11 Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl9

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 45.968; Variance 92.064; scale 0.499

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ae 2			:	1	
Watch	'	Watch Length DB	DB	ΩI	Description	Pred. No.
57.2		517	l lo	094879	DSRC41.	4.84e-190
54.9		451	4	013882	TYROSINE KINASE.	6.75e-181
54.5		517	ഗ	077050	SRC-TYPE PROTEIN TYROS	3.09e-179
54.3		451	11	064434	SRC-RELATED INTESTINAL	2.09e-178
53.8		206	11	062662	SRC RELATED TYROSINE K	1.54e-176
53.5		496	Ŋ	045539	F49B2.5 PROTEIN.	1.68e-175
53.3		527	13	091952	C-SRC TYROSINE KINASE.	1.13e-174
53.2		512	11	061745	B-CELL SRC-HOMOLOGY IY	1.83e-174
53.2		512	11	Q61364	B-CELL SRC-HOMOLOGY IY.	1.83e-174
53.1		534	4	016248	P59FYN.	4.74e-174
53.1		537	11	062844	PROTO-ONCOGENE FYN.	4.74e-174
52.8		496	13	093411	NON-RECEPTOR PROTEIN T	1.34e-172
52.8		526	11	060567	H-19 PROVIRAL SEQUENCE	1.34e-172
52.7		533	13	098915	GENE C-SRC PRODUCING P	2.16e-172
52.7		533	13	090992	C-SRC.	2.16e-172
52.7		587	14	064817	PROTEIN-TYROSINE KINAS	3.48e-172
52.4		525	14	092806	P60 SRC.	3.78e-171
52.4		526	14	007461	TYROSINE-PROTEIN KINAS	3.78e-171
52.2		812	14	085466	COMPLETE GENOME.	1.58e-170
51.9		505	4	016291	BLK-PROTEIN TYROSINE K	4.46e-169

1.86e-168 1.86e-168 3.00e-168	26e-16	19e-1	e-16	a-16	e-16	1.60e-164	91e-1	.14e-1	6-1	.16e-14	a-1	16e-14	8-1	9-1	5.22e-133	5.22e-133	5.22e-133	e-13	13	4.53e-127	1.16e-126
LYN PROTEIN TYROSINE K PP62V.	GARDNER-RASHEED FELINE		Н	GAG-ONC FUSION PROTEIN	GARDNER-RASHEED FELINE	SRC.	TYROSINE KINASE.	FGR MRNA.	SRC TYROSINE KINASE.	P120 POLYPROTEIN.	P120-GAG-ABL POLYPROTE		TYROSINE KINASE.	TEC29.	TYPE 1	DSRC29A TYPE 2 PROTEIN	FPS/FES-RELATED TYROSI	FER (FMS/FPS RELATED)	PROTEIN TYROSINE KINAS	ABELSON RELATED GENE (NON-RECEPTOR PROTEIN-T
013064 Q86363 Q86363	039851	083080	012850	028414	061404	085477	064993	063206	092957	092809	039477	013869	076978	045032	076132	076133	P70451	061561	042455		v
	44	74	4	9	11	14	14	11	14		14	4	Ŋ	Ŋ	Ŋ	s	11	11	13	11	വ
488 546 545	663	526	512	392	517	523	526	517	535	980	981	1149	879	588	603	786	823	453	627	376	298
51.7	4.	51.2	급	Ö	50.9	。	。	ö	48.2	44.6	4	44.6	43.3	42.6	42.6	42.6	42.6	42.2	41.9	41.0	40.9
973 973	967	963	959	957	957	954	955	952	907	840	840	840	814	801	801	801	801	794	788	772	770
22	22.	26	27	28	50	30	31	32	33	34	35	. 36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

432 FGILLTELVTYGRIPYPGMTNAEVLTQVEHGYRMPQPPNCEPRLYEIMLECWHKDPMRRP 491

qq

a

Mon May 24 07:23:58 1999

```
409 VWSFGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYVLMLECWRSSPE 468
                                                                                                                                                                                              08,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                            (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                      (TREMBLREL.
                                                              :|| | :|||:|
469 ERPSFATLREKL 480
                                        430 QRPCFKALRERL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 PTFEFLQ 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471 PSFATLR 477
                                                                                                                                     LT 3
077050
077050;
01-NOV-1998 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q64434
Q64434;
                                                                                                                                                                                                                                                                             ACSRC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                   Best
                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 FTLCRKLGSGYFGEVFEGLWKDRVQVAIKVISRDNLLHQQMLQSEIQAMKKLRHKHILAL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 YAVVSVGDPVYIITELMAKGSLLELLRDSDEKVLPVSELLDIAWQVAEGMCYLESQNYIH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWSFGILLHEMFSRGQVPYPGMSNHEAFLRVDAGYRMPCPLECPPSVHKLMLTCWCRDPE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDLAARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSD 408
412 FGVLLHEVFTYGQCPYEGMTNHETLQQIMRGYRLPRPAACPAEVYVLMLECWRSSPEERP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE; 98419955.
LEE H., KIM M., LEE K.-H., KANG K.-N., LEE S.-T.;
Excor-intron structure of the human PTK6 gene demonstrates that PTK6 constitutes a distinct family of non-receptor tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=RREAG CARCINOMA;
MEDILINE; 94309916.
MITCHELL P.J., BARKER K.T., MARTINDALE J.E.;
MITCHELL P.J., BARKER K.T., MARTINDALE J.E.;
"Cloning and characterisation of cDNAs encoding a novel non-receptor tyrosine kinase, brk, expressed in human breast tumours.";
ONCOGENE 9:2383-2390(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 97430836.
PARK S.H., LEE K.H., KIM H., LEE S.T.;
"Assignment of the human PTK6 gene encoding a non-receptor protein tyrosine kinase to 20q13.3 by fluorescence in situ hybridization.";
CYTOGENET. CELL GENET. 77:271-272(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDLAARNILVGENTLCKVGDFGLARLIKEDVY-LSHDHNIPYKWTAPEALSRGHYSTKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.9%; Score 1033; DB 4; 55.6%; Pred. No. 6.75e-181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase; 1.
AA; 51834 MW; 4AC30408 CRC32;
                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                         451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U61408; G3551753; JOINED.
EMBL; U61409; G3551753; JOINED.
EMBL; U61410; G3551753; JOINED.
EMBL; U61411; G3551753; JOINED.
PROSITE; PS00107; PROTEIN_KINĀSE_ĀĀPF;".].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U61412; G3551753; -
U61406; G3551753; JOINED.
U61407; G3551753; JOINED.
                                                                                                                                                                                            01,
01,
08,
                                                                                                                                                                                                                                                                                                                                   CATARRINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELLS 8:401-407(1998). x78549; G515026; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
TYROSINE KINASE.
                                                                                                                                                                                            01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00017; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 140; Conser
                                      TFETLOWKL 500
                                                                        472 SFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00018;
PF00069;
                                                                                                                                                                                                                                                                         BRK OR PTK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                     T 2
Q13882
                                                                                                                                                                          013882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                      492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                 AND PRESENTED TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO THE SULP TO T
                                      g
                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                      ECHINOIDEA; EUECHINOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 LDTKLGSGQFGEVWKGLWNGNTEVAVKTLRPKTMTPAAFLAEANIMKTCRHENLVQLYAV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 CSDMEPIYIVTELMKHGSLLDFLKDGDGRHLKLPQLVDMGAQVANGMAYLERKNYVHRDL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 AARNVLVNTGNICKVADFGLARMIQDDEYMARQGAKFPIKWTSPEAALYGRFTIKSDVWS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 FGILLTELIHYGRIPYPGMMNMEVLEQVERGYRMPRMNNCPDSLYDMCMMKCWHKDPQQR 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASIOUKHIN V., SERFAS M.S., SIYANOVA E.Y., POLONSKAIA M., COSTIGAN V.J., LIU B., THOMASON A., TYNER A.L.; An novel intracellular epithelial cell tyrosine kinase is expressed in the skin and gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                 ř.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC-RELATED INTESTINE, KINASE (EC 2.7.1.112)
(PROTEIN-TYROSINE KINASE) (TYROSYLPROTEIN KINASE) (PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWS
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

ONODERA H., KOBARI K., SAKUMA M., SATO M., SUYEMITSU T., YAMASU "Expression of a src-type protein tyrosine kinase gene, AcSrcl, the sea urchin embryo.";

The sea urchin embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                    ANTHOCIDARIS CRASSISPINA (SEA URCHIN).
EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHIN
ECHINACEA; ECHINOIDA; ECHINOMETRIDAE; ANTHOCIDARIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%; Score 1025; DB 5; 53.0%; Pred. No. 3.09e-179;
                                                                                                                                                                                                                                                                                                                                                                                                       DEV. GROWTH DIFFER. 0:0-0(1999).
EMBL; AB016815; D1034710; -.
SEQUENCE 517 AA; 58568 MW; 5A7285C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HSD: ICR AND BALB/C; TISSUE=INTESTINE; MEDLINE; 95140424.
  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥Ÿ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches
517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TYROSINE)) (HYDROXYARYL-PROTEIN KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEI
SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PRT;
                                                                                                                                 SRC-TYPE PROTEIN TYROSINE KINASE
```

 \sim

```
SECUENCE FROM N.A.
MEDLINE: 94150718.
MILSONGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMONRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WAISON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
J. 2. M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KERSHAW J.;
SUBMITIED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z81543; E1346996; -.
SEQUENCE 496 AA; 56307 MW; C766F63E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
F49B2.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1LT 6
045539
045539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT ON THE SOLL ON THE SOLL ON THE SOLL ON THE SOLL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL ON THE SOL
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SRC RELATED TROSINE KINASE.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MARINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 HAVCSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEDRVVH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 FILCKKLGAGYFGEVFEALWKGQVHVAVKVISRDNLLHQHTFQAEIQAMKKLRHKHILSL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 YAVATAGDPVYIITELMPKGNLLQLLRDSDEKALPILELVDFASQVAEGMCYLESQNYIH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 RDLAARNVLVTENNLCKVGDFGLARLVKEDIY-LSHEHNVPYKWTAPEALSRGHYSIKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 VWSFGVLLHEIFSRGQMPYPGMSNHETFLRVDAGYRMPCPLECPPNIHKLMLSCWSRDPK
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-HSD: ICR; TISSUB-INTESTINE;
SIZANOVA E.Y., SEFFAS M.S., MAZO I.A., TYNER A.L.;
"Tyrosine kinase gene expression in the mouse small intestine.";
ONCOGENE 9:2053-2057(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE DAWLEY, TISSUE-SMALL INTESTINE;
SUNITHA I., AVIGAN M.I.;
BIOCHIM. BIOPHYS. ACTA, GENE STRUCT. EXPR. 1221:348-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUNITARY I., AVIGAN M.I.; The apical membranes of maturing gut columnar epithelial or contain the enzymatically active form of a newly identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1021; DB 11;
Pred. No. 2.09e-178;
42; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA; 51972 MW; 5A749D95 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE;
MEDLINE; 96330334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE OF 356-416 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 54.3%;
al Similarity 55.2%;
139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                      SEQUENCE OF 1-77 FROM N.A.
ONCOGENE 10:349-357(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| | | ||||
469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 ORPCFKDLCEKL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 139; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      062662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPRESENT SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
3
                                                                                                                                                                                                                                                                                                                                                                       356
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                237 LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKSLRHPKLIQLYAV
                                                                                                                                                                                                                                                                                                                                                                                                                        297 CTLEDPIYIITELMRHGSLQEYLQNDGGSKIRLTQQVDMAAQVASGMAYLESQNYIHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESKHEIKLPVKWTAPEAIRTNKFSIKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 VWSFGILLYEIITYGKMPYSGMTGAQVIHMLGQNYRLPQPSNCPEQFYSIMMECWNVEPK
                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                            Length 506;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                       SUBMITTED (MAY-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U09583; G939625; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                        Score 1012; DB 11;
Pred. No. 1.54e-176;
45; Mismatches 71;
                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE; AVIGAN M.I.;
                                                                                                                                                                             PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 506 AA; 58166 MW; 8A3172C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
fyn-related tyrosine kinase.";
ONCOGENE 13:547-559(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06,
09,
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.8%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 QRPTFETLHWKL 488
                                                      SEQUENCE FROM N.A.
```

```
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ATHERINOMORPHA;
CYPRINODONTIFORMES; CYPRINODONTOIDEI; POECILLIDAE; XIPHOPHORUS.
                                                                                                                                                                                                                 468
                                                      231 LIRQIGAGQFGEVWEGRWNVNVPVAVKKLKAGTADPTDFLAEAQIMKKLRHPKLLSLYAV 290
                                                                     CTRDEPILIVTELMQE-NLLTFLQRR-GRQCQMPQLVEISAQVAAGMAYLEEMNFIHRDL 348
                                                                                                                                                            349 AARNILINNSLSVKIADFGLARILMKENEYEARTGARFPIKWTAPEAANYNRFTTKSDVW 408
                                                                                                                                                                         501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEVKMGQGCFGEVWRGTWNGTTQVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 VSE-EPIYIVTEFMDQGSLLEFLKGQYSTMLRLPQLVDFASQIASGMAYVERMNYVHRDL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAANILVGDNLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS 441
                               Gaps
                                                                                                                        SFGILLTEIVTFGRLPYPGMTNAEVLQQVDAGYRMPCPAGCPVTLYDIMQQCWRSDPDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGILLVELATKGRVPYPGMVNREVLDQVERGYRMPCPSECPASLHELMLNCWRKEAEERP
                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 527;
    Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SSP.F1, RIO SOTO LA MARINA, MEXICO;
RAULF F., SAM S., ROBERTSON S.M., MAEUELER W., SCHARTL M.;
SUBMITTED (FEB-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X64658; 665305; TO
Score 1007; DB 5; Length 49
Pred. No. 1.68e-175;
53; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1003; DB 13; Length 5
Pred. No. 1.13e-174;
42; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 527 AA; 59078 WW; 40D366Al CRC32;
                                                                                                                                                                                                                                                                                                                                               527 AA.
                                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                         01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.3%;
larity 54.1%;
Conservative
  Query Match 53.5%;
Best Local Similarity 53.2%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                           Q91952,
Q91952,
Q01052,
Q1-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                               C-SRC TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                         XIPHOPHORUS XIPHIDIUM
                                                                                                                                                                                                                                                                                  |:| ||: ||
471 PSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 133; Conserv
                                                                                                                                                                                                                                                                   PTFETLOWKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFEYLQ 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412
                                                                                                                                                                                                               409
                                                                                                                                                                                                                                                                   469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472
                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                  ò
                                                                                                                                                        g
                                                                                                                                                                                     ö
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                ğ
```

```
'n
                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRK OR BSK.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESKHEIKLPVKWTAPEAIRTNKFSIKSD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 VWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQNYRLPQPSNCPQQFYSIMLECWNVEPK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKSLRHPKLIQLYAV 302
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 95251656.
THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
THUVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
THOVESON M., ALBRECHT D., ZUERCHER G., ANDRES A., ZIEMIECKI A.;
The mouse mammary gland and intestine.";
BIOCHEM. BIOPHYS. RES. COMMUN. 209:582-589(1995).
EMBL; 248757, G736544, -
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFIQQVDMAAQVASGMAYLESQNYIHRDL
061745 PRELIMINARY; PRT; 512 AA.
061745 (01745)
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
05-CELL SRC-HOMOLOGY TYROSINE KINASE (INTESTINAL TYROSINE KINASE).
FRK OR IYK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRK homologue with a specific pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
B-CELL SRC-HOMOLOGY TYROSINE KINASE (PROTEIN TYROSINE KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1002; DB 11;
Pred. No. 1.83e-174;
45; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00069; pkinase; 1.
NCE 512 AA; 58928 MW; 808D1612 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
MFDLINE; 95251656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%;
llarity 52.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDERG'WELSH C., WELSH M.;
"Cloning of BSK, a murine Fitissue distribution.";
GENE 152:339-242(1995).
EMBL; L36132; G777773; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00017; SH2; 1
PFAM; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:| ||: ||
469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 QRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 95137395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 9
Q61364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                        FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCORDANCE
ACCO
        RESULT
                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

S

g

g

ò

g

ò

g

à

ö

g ö g

ò

```
352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSKIPVKWTAPEAANYRVFSQKSDVWS 411
                                                                                          449 FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWKKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                               01,
08,
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL. (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL.
                                                                                                                                                                                                                                                                                                                        11 PRELIMIN 062844 062844 01-NOV-1996 (TREMBLE 01-NOV-1998 (TREMBLE D1-NOV-1998 (TREMBLE PROTO-ONCOGENE FYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| |:
472 SFATLR 477
                                                                                                                                                                         509 TFEYLQ 514
                                                                                                                                                                                                                 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512 TEEYLQ 517
                                                                                                                                                                                                                                472
                                             d
                                                                                                                ò
                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95123064.

MEDLINE; 95123064.

REGURENCE FROM N.A.

RELEY K., SLOCKOMBE P., PROUDFOOT K., WAHID S., MANDAIR K.,

REBBINGTON C.;

"Human p59fyn(T) regulates OKT3-induced calcium influx by a mechanism of stinct from PIP2 hydrolysis in Jurkat T cells.";

J. IMMUNOL. 154:1136-1145(1995).

REMBL; S74774; G802051.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PRAM; PF00017; SH2; 1.

DR PFAM; PF00018; SH3; 1.

SR PFAM; PF00069; pkinase; 1.

SR SEQUENCE 534 AA; 60226 MW; D3941652 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                243 LLKRLGSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKSLRHPKLIQLYAV 302
                                                                                                                                                                                                                                                                                                                                                                                 303 CTLEDPIYIITELMRHGSLQEYLQNDGGSKIHFIQQVDMAAQVASGMAYLESQNYIHRDL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 AARNVLVGEHNIYKVADFGLARVFKVDNEDIYESKHEIKLPVKWTAPEAIRTNKFSIKSD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 VWSFGILLYEIITYGKMPYSGMTGAQVIQMLSQNYRLPQPSNCPQQFYSIMLECWNVEPK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 LEKKLGGGCFAEVWLGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 VSE-EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 CSGGEPVXIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEGRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPERALYGRFTIKSDVWS 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.1%; Score 1000; DB 4; Length 534; Best Local Similarity 52.4%; Pred. No. 4.74e-174; Matches 129; Conservative 46; Mismatches 70; Indels' 1; Gaps
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            ÷,
                                                                                                                                                                                                                                   Length 512;
                                                                                                                                                                                                                             Score 1002; DB 11; Length 5 Pred. No. 1.83e-174; 45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                           PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; Pkinase; 1.
SEQUENCE 512 AA; 58891 WW; DECF53C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 AA.
                  निन
                     PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
01,
08,
                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.8%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLT 10

016248

016248;

01 NOV-1996 (TREMBLREL. 01

01 NOV-1996 (TREMBLREL. 01

01 NOV-1998 (TREMBLREL. 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 ERPSFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 QRPTFETLHWKL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT

SOLT
```

```
ï
                                                                                                                                                                                               RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUT 12
093411
093411
091411
093411
093411
093411
091412
093411
0918
01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
NON-RECEPTOR PROTEIN TYROSINE KINASE LALOO.
XENOPUS LAEVIS (ARRICAN CLAWED FROG).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, AMPHIBIA, BATRACHIA, ANURA,
MESOBATRACHIA, PIPOIDEA, PIPIDAE, XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 FGILLTELVTKGRVPYPGMNNREVLEQVERGYRMPCPQDCPISLHELMIHCWKKDPEERP 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 LIKRLGNGQFGEVWMGTWNGNTKVAIKTLKPGTMSPESFLEEAQIMKKLKHDKLVQLYAV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 VSE-EPIYIVTEYMNKGSLLDFLKDGEGRALKLPNLVDMAAQVAAGMAYIERMNYIHRDL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEGRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 RSANILVGNGLICKIADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN-SHRSP STROKE-PRONE SPONTANEOUSLY HYPERTENSIVE;

C TISSUE-MULLE BRAIN;

A UEYAMA T., SENBA E., TOMITA I.;

L SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

REMBL: U35365; G1101768; -

DR PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.

DR PRAM: PF00017; S12; 1.

DR PFAM: PF00018; S13; 1.

DR PFAM: PF00018; S13; 1.

DR PFAM: PF00069; pkinase; 1.

SEQUENCE 537 Aa; 60701 MW; DOAIDD46 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.1%; Score 1000; DB 11; Best Local Similarity 52.8%; Pred. No. 4.74e-174; Matches 130; Conservative 46; Mismatches 69;
     AA.
  537
                                                           CREATED)
PRT;
```

9

```
(PP60C-SRC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                        T 14
Q98915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V-Src.
                                                                                                                          472
  448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                      RESOLATION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
  ద
                                          ö
                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA; RODENTIA;
SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                                                                                                           231 LSLQKKLGAGQFGDVWLAMYNGHTKVAVKTMKPGSMSPGAFLEEANLMKSLQHDRLVRLH 290
                                                                                                                                                                                                                                                                                                                                    291 AVVTQGEPIYIITEYMQKGSLLDFLKSEEGSDQPLIQLIDFSAQIAEGMWFIEQRNYIHR 350
                                                                                                                                                                                                                                                                                                                                                                                                                     351 DLRAANCLVSETLLCKIADFGLARVIEDSEYTAREGTKFPIKWTSLEAANYGSFTIKSDV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 LEAKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 CSGGEPVIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEGRVVHRDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                              329 VSE-EPIYIVIEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS
SEQUENCE FROM N.A. WEINSTEIN D.C., MARDEN J., CARNEVALI F.", HEMMATI-BRIVANLOU A.; "FGF-mediated mesoderm induction involves the Src-family kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                              ö
                                                                                                                                                                   Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 526;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-MESENCHYMAL;
BODOR J., ROZKOT F., SVOBODA J.;
SUBMITTED (MAY-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
BMBL; X52822; G49657; --
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                 Match 52.8%; Score 993; DB 13; Le Local Similarity 49.0%; Pred. No. 1.34e-172; Les 123; Conservative 59; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 993; DB 11; L. Pred. No. 1.34e-172; 40; Mismatches 75;
                                                                                                       EMBL; AF081803; G3411274; -.
SEQUENCE 496 AA; 56275 WW; BC2C7DA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00017; SH2; 1.
PF00018; SH3; 1.
PF00069; pkinase; 1.
VCE 526 AA; 59061 MW; 0E2418FA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         060567 PRELIMINARX; PRT; 526 ... 060567 Octobro (TREMELREL. 01, CREATED) 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION OF PROVIRAL SEQUENCE (LTR.V-3SCRI,LTR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MESOCRICETUS AURATUS (GOLDEN HAMSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.8%;
Local Similarity 53.4%;
Local Similarity 53.4%;
Local 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 RPTFEYLOSIL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 RPSFATLREKL 480
                                                            laloo.";
NATURE 0:0-0(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V-3SRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA RT RT ODE SO SO
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 RAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWS 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 LGRKLGEGYFGEVWEGLWLGSLPVAIKVIKSANWKLTDLAKEIQTLKGLRHERLIRLHAV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
                             269 LEVKLGOGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 VSE-EPIYIVTEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE: 83155664.
TAKEYA T., HANAFUSA H.;
"Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DORAL T., LEVY J.B., KANG L., BRUGGE J.S., WANG L.H.; Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.
FGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKDPEERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEIJLAND A., NEUBAUER G., COURTREIDGE S.A., MANN M., WIENERGA R "The purification and characterization of the catalytic domain expressed in Schizosaccharomyces pombe. Comparison of unphosphorylated and tyrosine phosphorylated species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                          GENE C-SRC PRODUCING PROTEIN PP60-C-SRC.
THIS GENE IS HOMOLOGGUS TO THE ROUS SARCOMA VIRUS GENE V-SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; ARCHOSAURIA; AVI
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                     02, CREATED)
02, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.7%; Score 992; DB 13; 1 54.1%; Pred. No. 2.16e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMIT PERMITS SH2; 1.
PEAM; PF00017; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 533 AA; 60010 MW; 0D446FF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOL. CELL. BIOL. 11:4165-4176(1991).
EMBL; V00402; E281134; -..
EMBL; V00402; E181088; -..
EMBL; S43579; E97011; -..
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 484-533 FROM N.A. MEDLINE; 91304409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                           Q98915; Q91343;
01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL 32:881-890(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                            508 TFKYLQAQL 516
                                                                                                                                                                       SFATLREKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 97008971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-SRC OR C-SCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEILAND A.;
```

```
MEDLINE; 8315564.

A TAKEYA T., HANAFUSA H.;

MEDLINE; 8315564.

A TAKEYA T., HANAFUSA H.;

Structure and sequence of the cellular gene homologous to the RSV sr of gene and the mechanism for generating the transforming virus.";

ELL 32:881-890(1983).

EMBL; J00844; G901820;

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PRAM; PF000118; SH3; 1.

PRAM; PF00018; SH3; 1.

PRAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 LEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 VSE-EPIXIVTEYMSKGSLLDFLKGEMGKXLRLPQLVDMAAQIASGMAYVERMNYVHRDL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 CSGGEPVYIVTELMRKGNLQAFLGTPEGRALRLPPLLGFACQVAEGMSYLEEQRVVHRDL 351
352 AARNVLVDDGLACKVADFGLARLLKDDIYSPSSSSKIPVKWTAPEAANYRVFSQKSDVWS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 52.7%; Score 992; DB 13; Length 533; Local Similarity 54.1%; Pred. No. 2.16e-172; Local 133; Conservative 40; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
HANAFUSA H.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                           533 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Thu May 20 13:12:45 1999 Job time : 248 secs.
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
C-SRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 TFEYLQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 SFATLR 477
                                                                                                                                                                                  508 TFEYLQ 513
                                                                                                                                                                                                                            :| |:
472 SFATLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                          LT 15
Q90992
Q90992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Loca
Matches
                                                                                                                                                                                                                                                                                                                                          THE SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SULT OF SU
                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                          g
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            õ
```

****	(TM)	*****
*****	<u>-</u>	*****
****	''	****
****		****
*****		******
******		*****
******		******
******		******
***************************************		***************************************

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein '- protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 13:15:14 1999; MasPar time 4.53 Seconds 37:554 Million cell-updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (481-488) from US09099053.pep (6 68 Description: Perfect Score:

9 oţ

> 1 HAIHRCHP 8 Sequence:

Scoring table:

PAM 150 Gap 11

Searched:

170751 seqs, 21266608 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

Mean 15.050; Variance 43.650; scale 0.345 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.....

SUMMARIES

	Pred. No.	2.32e-01	9.75e+01	9.75e+01	9.75e+01	9.75e+01	9.75e+01	9.75e+01	9.75e+01	9.75e+01	1.26e+02	1.26e+02	1.63e + 02	1.63e+02	2.11e+02	2.11e+02	2.11e+02
	Description	lan SAD.	nan kidney calcium	nan placental calci	nan calcium sensor			nan parathyroid cal	nan placental calci	Human parathyroid cal	Secreted protein enco	Human secreted protei	Alpha 2-Macroqlobulin	Human alpha-2-MR.	Antiphospholipid anal	Antibody ACA-6501 epi	Serine protease PfSP2
	Des	Нишап	Human	Human	Human	Human	Human	Human	Human	Hum	Sec	Hum	Alp	Hum	Ant	Ant	Ser
SOLMERALES	QI QI	W89248	W43313	W43312	W43311	R97210	R97208	R97211	R97209	W43314	W88724	W74745	R47861	R60517	W10404	W67128	W01200
	DB	39	29	29	53	17	17	17	17	53	38	37	σ	1	22	36	20
	Query Match Length DB	488	4655	4655	4655	4655	4655	4655	4655	4655	69	84	4544	4544	o,	σ	255
æ	Query	100.0	67.6	67.6	67.6	67.E	67.6	67.6	67.6	67.6	66.2	66.2	64.7	64.7	63.2	63.2	63.2
	Score	68	46	46	46	46	46	46	46	46	45	45	44	44	43	43	43
	Result No	Н	7	m	4	ស	9	7	ω	თ	10	11	12	13	14	15	16

22 111e+02 111e+02 111e+02 111e+02 111e+02 111e+02 112	.50e+0 .50e+0 .50e+0 .50e+0
OCI protein. RII-7 nerve protein uman secreted prote uman secreted prote SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con SV-2 strain SB5 Con Ebbiella pheumonia uman secreted protein pylori ORF 14910 equence of Core alphane equence of the alph uman calcium channe equence of the alph uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe uman calcium channe	Human neuronal calciu Sequence of the alpha Human calcium channel Intracellular protein Human protein tyrosin Human thrombomodulin
W01561 R34674 W726006 W72012 W72012 W72012 W72012 W72012 W72012 W72012 W72012 W72012 W7202 W7532 W7532 W7532 W7532 W7532 W7532 W7532 W7532 W7532 W7673 W7673 W7673 W7673 W7673 W7673 W7673 W7674 W7675 W7675 W7675 W7675 W7675 W7764 W7764 W7764 W7764 W7764 W7767	0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
22 23 25 25 25 25 25 25 25 25 25 25 25 25 25	
343 510 610 910 910 910 910 910 910 910 9	144333
44444444444444444444444444444444444444	
L1112222222222222222222222222222222222	24444 2000 2000 2000 2000 2000 2000 200

ALIGNMENTS

```
A QPGE-) SUGGET INC.

A APP H. Clary D. Courtneidge SA, Hui TH, Jallal B,

App H. Clary D. Courtneidge SA, Hui TH, Jallal B,

B APP H. Clary D. Courtneidge SA, Hui TH, Jallal B,

WPT: 99-0004344/01.

B N-PSDB; V81743.

BT N-PSDB; V81743.

PT New nucleic acid encoding specific modulators for treatment and cancer and neurodegenerative disease

Talma 2; Page 154-155; 193pp; English.

Caids encoding PPPO4, SAD, PTPO5, PTP10, ALP and ALK-7 proteins. The present sequence represents human SAD. The above proteins, other than CALK-7, are protein tyrosine phosphatases (PPPS) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, or brevent diseases associated with abnormal signal transduction

C pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, serine/threonine kinase) are used to promote neuronal survival, cancer cating and Alakhamer's, Parkinson's or Huntington's colliseases. Nucleic acid fragments of the polynucleotides encoding the
                                                                                                PTP04: PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

W type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

W type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

W noudegenerative disease; neuronal survival; Alzheimer's disease;

Homo sapiens.

W W0984331-A2.

N W0984331-A2.

N W098439; US-044428.

R 23-APR-1997; US-044428.

R 20-MAY-1997; US-049756.

R 11-UNN-1997; US-049756.

R 18-JUN-1997; US-0499756.

R 18-JUN-1997; US-0499756.
.T 1
W89248 standard; Protein; 488 AA.
                                                               (first entry)
                                         W89248;
10-MAR-1999
                                                                                     Human SAD
  RESULT
```

```
g
                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Pougs, Volygo,

New Pougs, Volygo,

New Pougs, Volygo,

New Pougs (Volygo)

New Data and Central nervous system disorders

The membraneous glomerulonephritis and central nervous system disorders

Claim 7; Page 145-163; 240pp; English.

Chicsp), deduced from the nucleotide-sequence (see V05996) of a

clone obtained by PCR amplification. Full-length sequences for

thuman placenta (see W43312) and parathyroid (see W43314) are also

claimed. hCSP is considered to be the human homologue of rat

thymann nephritis antigen gp330 on the basis of sequence

similarity. It is proposed that the calcium sensor is a

universal sensor for recognition of variation in extracellular

calcium, and plays a key role in calcium regulation via different

corgan systems. hCSP belongs to the low density lipoprotein

superfamily of glycoproteins. It can be expressed in a claimed

host cell using a vector comprising hCSP cDNA. Also claimed are a

method of using hCSP to treat human membraneous glomerulonephritis,

cut at the use of hCSP to screen for agonists and antagonists of hCSP.

Such (antyagonists are useful in the treatment of conditions
                                                                                                                                            ö
proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoblast
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                   Calcium sensor; human; glycoprotein 330; gp330; kidney; low density lipoprotein; LDL; membraneous glomerulonephritis; osteoporosis; hyperthyroidism; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vitamin D3 production, oestrogen levels, osteoclast or osteob activity, calcium secretion and calcium ion homeostasis, e.g. hyperthyroidism and osteoporosis. Sequence 4655 AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Such (ant)agonists are useful in the treatment of conditions associated with perturbations in parathroid hormone levels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 29; Length 4655;
                                                                                                          Length 488;
                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RHON ) RHONE-POULENC RORER PHARM INC.
Akerstrom G, Crumley GR, Hjalm G, Juhlin C, Morse CC,
                                                                                                          68; DB 39; 1
No. 2.32e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4423..4445
/note= "transmembrane domain"
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal domain' 4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by MIC"
                                                                                                                                                                                                                                                                                                                                      Human kidney calcium sensor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sig_peptide
                                                                                                            Score (Pred. 1
                                                                                                                                                                                                                                                                                    W43313 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%;
larity 50.0%;
Conservative
                                                                                                          Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..4655
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26..4422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1997.
20-MAY-1997; UO8682.
23-MAY-1996; US-652877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98-018219/02.
                                                                      488 AA;
                                                                                                                                                                              haihrchp 488
                                                                                                                                                                                                               481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murray EM, Rask
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; V05996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09744050-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                    W43313;
08-JUN-1998
                                                                         Sequence
                                                         proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                              481
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                888888
                                                                                                                                                                                                               ò
```

```
This sequence comprises a human placental calcium sensor protein (hCSP), deduced from the nucleotide sequence (see V0595) of a cone obtained by PCR amplification. Full-length sequences for clone obtained by PCR amplification. Full-length sequences for claimed. hCSP is considered to be the human homologue of rat claimed. hCSP is considered to be the human homologue of rat similarity. It is proposed that the calcium sensor is a universal sensor for recognition of variation in extracellular calcium, and plays a key role in calcium regulation via different corgan systems. hCSP belongs to the low density lipoprotein superfamily of glycoproteins. It can be expressed in a claimed are a nethod of using hCSP to treat human membraneous glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding inhibitor of gp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human calcium sensor protein and vector encoding inhibitor of gr 330 mediated transport of amyloid beta protein - useful to treat membraneous glomerulonephritis and central nervous system disorders Claim 7; Page 112-130; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and the use of hCSP to screen for agonists and antagonists of hCSP. Such (ant)agonists are useful in the treatment of conditions associated with perturbations in parathroid hormone levels, vitamin D3 production, osetrogen levels, osteoclast or osteoclast activity, calcium secretion and calcium ion homeostasis, e.g.
                                                                Human placental calcium sensor protein. calcium sensor; human; glycoprotein 330; gp330; placenta; low density lipoprotein; LDL: membraneous glomerulonephritis; osteoporosis; hyperthyroidism; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crumley GR, Hjalm G, Juhlin C, Morse CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 29;
Pred. No. 9.75e+01;
                                                                                                                                                                                              26..4422
/note= "extracellular domain"
4423..4445
                                                                                                                                                                                                                                              /note= "transmembrane domain"
4446..4655
                                                                                                                                                                                                                                                                              'note= "C-terminal domain"
                                                                                                                                                                                                                                                                                                                note= "encoded by GAY"
                                                                                                                                                                                                                                                                                                                                               'note= "encoded by GTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "encoded by MTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by ATY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHON ) RHONE-POULENC RORER PHARM INC
                                                                                                                                                                1..25
/label=_Sig_peptide
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                "encoded by
                                                                                                                                                                                                                                                                                                                                                                               ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                note= "encoded by
RESULT 3
ID W43312 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperthyroidism and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                               'note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%;
50.0%;
                                                 08-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1997; U08682.
23-MAY-1996; US-652877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 4210
                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 4094
                                                                                                                                                                                                                                                                                                 Misc_difference 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murray EM, Rask L;
WPI; 98-018219/02.
                                                                                                                                                                                                                                                                                                                              Misc_difference
                                                                                                                                                                                                                                                                                                                                                              Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V05995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9744050-A1.
                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akerstrom G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                 Peptide
                                  W43312;
                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                  Domain
```

ö

Gaps

ö

2; Indels

Pred. No. 9.75e+01;

Mismatches

Morse CC;

Peptide Domain Domain Domain

Matches

පු

δ

```
Isolated human calcium sensor protein - useful develop prods. for diagnosis and treatment of conditions, such as membranous diagnosis and treatment of conditions, such as membranous glomerulonephritis.

Claim 7: Page 143-161; 236pp; English.

500 kDa human calcium sensor proteins (CSP) (R97209-11) were identified as the products of CDNA clones (T28774-76) respectively obtd. from human placental, kidney and parathyroid cDNA libraries.

The CSPs show homology to LDL receptor proteins. CSP can be isolated from parathyroid, placental or kidney tubule cells or obtd. by expression of the encoding sequences in transformed host cells. It is useful for identifying potential (ant)agonists and in the diagnosis and treatment of e.g. membranous glomerulonephritis, and also in the treatment of wounds and ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaim 7: Page 78-96: 236pp: English.

Claim 7: Page 78-96: 236pp: English.

A 500 kba human calcium sensor protein (CSP) (R97208) was identified as the product of cDNA clone (T28773) obtd. from human kidney and placental cDNA libraries. Full-length sequences of placental, kidney and parathyroid CSP (see also R97209-11) were also obtd. They show homology to LDL receptor proteins. CSP can be isolated from parathyroid, placental or kidney tubule cells or obtd. by expression of encoding sequences in transformed host cells. It is useful for identifying potential (ant)agonists and in the diagnosis and treatment of e.g. membranous glomerulonephritis, and also in the treatment of wounds and ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human calcium sensor protein - useful develop prods. for diagnosis and treatment of conditions, such as membranous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1996 (first entry)
Human calcium sensor protein.
Calcium sensor protein; CSP; hyperthyroidism; osteoporosis;
membranous glomerulonephritis; therapy; ulcer; wound; kidney.
  Calcium sensor protein; CSP; hyperthyroidism; osteoporosis; membranous glomerulonephritis; therapy; ulcer; wound; kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 17; Length 4655; Pred. No. 9.75e+01; 2; Mismatches 2; Indels (
                                                                                                                   /note= "unidentified amino acid"
                                                                                                                                                                 30-MAY-1996.
22-NOV-1995; U15203.
23-NOV-1994; US-344836.
(RHON ) RHONE POULENC RORER PHARM INC.
AMERSTROM G Crumley GR, HJalm G, Juhlin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RHON ) RHONE POULENC RORER PHARM INC.
Amerstrom G, Crumley GR, Hjalm G, Juhlin C,
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T
R97208 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-1996.
22-NOV-1995; U15203.
23-NOV-1994; US-344836.
07-JUN-1995; US-487314.
                                                                                                                                                                                                                                                                                                           Rask L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4655 AA;
                                                                                                                                                                                                                                                                                                                                   WPI; 96-268334/27.
N-PSDB; T28775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray EM, Rask L
WPI; 96-268334/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 HAIHRCHP 488
                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T28773.
                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9615801-A1.
                                                                                                                                           WO9615801-A1.
                                                                                                                                                                                                                                                                                                                  Murray EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human calcium sensor protein and vector encoding inhibitor of grown was defined transport of amyloid beta protein - useful to treat membraneous glomentulonephritis and central nervous system disorders of claim 7: Page 80-98; 240pp; Equalish.

This sequence comprises a human calcium sensor protein (hCSP), deduced from the nucleotide sequence (see V0594) of clones of the nucleotide sequence (see V0594) of clones of sequences (see W43312-14) for human kidney, placenta and parathyroid are also claimed. hCSP is considered to be the human parathyroid are also claimed. hCSP is considered to be the human calcium, and plays a key role in calcium sensor is a universal sensor for recognition of variation in extracellular calcium, and plays a key role in calcium regulation via different calcium, and plays a key role in calcium regulation via different calcium, and plays a key role in calcium regulation via different calcium, and plays a key role in calcium regulation via different calcium, and plays a key role in calcium regulation via different calcium, and plays a vector comprising hCSP bonk. Also claimed are a nethod of using hCSP to screen for agonists and antagonists of hCSP. Such (arthygonists are useful in the treatment of conditions associated with perturbations in parathroid hormone levels, vitamin D3 production, osstrogen levels, osteoclast or osteoblast activity, calcium and calcium ion homeostasis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
    Gaps
                                                                                                                                                                                                                                                          Human calcium sensor protein.
Calcium sensor; human; glycoprotein 330; gp330; placenta; kidney;
low density lipoprotein: LDL; membraneous glomerulonephritis;
osteoporosis; hyperthyroidism; therapy.
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 29; Length 4655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 9.75e+01;
2; Mismatches 2; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DNY-1997; UO8682.
23-MAY-1996; US-652877.
(RHON ) RHONE-POULENC RORER PHARM INC.
AMERICAN G, CLUMIEY GR, HJalm G, Juhlin C, Morse CC, Murray EM, Rask L,
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "extracellular domain"
4423..4445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "transmembrane domain"
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R97210;
31-JUL-1996 (first entry)
Human kidney calcium sensor protein.
                                                                                                                                                                                                                                                                                                                                                                                                        1..25
/label= Sig_peptide
26..4422
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                     W43311 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T
R97210 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperthyroidism and osteoporosis. Sequence 4655 AA;
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..4655
                                                                                                                                                                                                                               08-JUN-1998 (first entry)
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray EM, Rask L;
WPI; 98-018219/02.
                                              261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|:| |
481 HAIHRCHP 488
                                                                         | :|:| |
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V05994.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9744050-A1.
```

ô

Gaps

.; 0

Morse CC;

RESULT

g δŏ ပ္ပ

Juhlin C,

ဗ်

Hjalm

GR,

Crumley

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assoluted human calcium sensor protein - useful develop prods. for diagnosis and treatment of conditions, such as membranous glomerulonephritis.

Claim 7: Page 175-193: 236pp; English.
500 kDa human calcium sensor proteins (CSP) (R97209-11) were identified as the products of CDNA clones (T2874-76) respectively obtd. from human placental, kidney and parathyroid cDNA libraries. The CSPs show homology to LDL receptor proteins. CSP can be isolated from parathyroid, placental or kidney tubule cells or obtd. by expression of the encoding sequences in transformed host cells. It is useful for identifying potential (ant)agonists and in the diagnosis and treatment of e.g. membranous glomerulonephritis, and also in the treatment of wounds and ulcers.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                              31-JUL-1996 (first entry)
Human parathyroid calcium sensor protein.
Calcium sensor protein; CSP; hyperthyroidism; osteoporosis;
membranous glomerulonephritis; therapy; ulcer; wound; parathyroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human placental calcium sensor protein.
Calcium sensor protein; CSP; hyperthyroidism; osteoporosis;
membranous glomerulonephritis; therapy; ulcer; wound; placenta.
                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
          Score 46; DB 17; Length 4655;
Pred. No. 9.75e+01;
2; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 17; Length 4655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morse CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.75e+01;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RHON ) RHONE POULENC RORER PHARM INC.
Amerstrom G, Crumley GR, Hjalm G, Juhlin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RHON ) RHONE POULENC RORER PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                    T
R97211 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T
R97209 standard; Protein; 4655 AA.
                 67.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1996.
22-NOV-1995; U15203.
23-NOV-1994; US-344836.
07-JUN-1995; US-487314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1996.
22-NOV-1995; U15203.
23-NOV-1994; US-344836.
07-JUN-1995; US-487314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference 4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference 4094
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4655 AA
                                                                                                                       | :|:| |
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murray EM, Rask I
WPI; 96-268334/27.
N-PSDB; T28776.
                                                                                             261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9615801-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9615801-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amerstrom G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R97209;
31-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                  RACE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE SOLVE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
New human calcium sensor protein and vector encoding inhibitor of gp 330 mediated transport of amyloid beta protein - useful to treat membraneous glomerulonephritis and central nervous system disorders Claim 7; Page 177-195; 240pp; English.

This sequence comprises a human parathyroid calcium sensor protein (hCSP), deduced from the nucleotide sequence (see V05996) of a clone obtained by PCR amplification. Full-length sequences for human placenta (see W43312) and kidney (see W43313) are also claimed. hCSP is considered to be the human homoloque of rat Heymann nephritis antigen gp330 on the basis of sequence similarity. It is proposed that the calcium sensor is a cultivariant seal sensor for recognition of variation in extracellular calcium, and plays a key role in calcium regulation via different cagan systems. hCSP belongs to the low density lipoprotein
                                                                                                                                                                                                            Claim 7: Page 110-128; 236pp; English.
500 kDa human calcium sensor proteins (CSP) (R97209-11) were
identified as the products of CDNA clones (T28774-76) respectively
obtd. from human placental, kidney and parathyroid cDNA libraries.
The CSPs show homology to LDL receptor proteins. CSP can be isolated
from parathyroid, placental or kidney tubule cells or obtd. by
expression of the encoding sequences in transformed host cells. It is
useful for identifying potential (ant)agonists and in the diagnosis and
treatment of e.g. membranous glomerulonephritis, and also in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W43314;
W6-JUN-1998 (first entry)
Human parathyroid calcium sensor protein.
Calcium sensor; human; glycoprotein 330; gp330; parathyroid;
low density lipoprotein; LDL; membraneous glomerulonephritis;
osteoporosis; hyperthyroidism; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 17; Length 4655;
Pred. No. 9.75e+01;
2; Mismatches 2; Indels (
                                                                                                                Tisolated human calcium sensor protein - useful develop prodiagnosis and treatment of conditions, such as membranous glomerulonephritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RHON ) RHONE-POULENC RORER PHARM INC.
Akerstrom G, Crumley GR, Hjalm G, Juhlin C, Morse CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4423..4445
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4446..4655
/note= "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by GTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by ACM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide 26..4422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W43314 standard; Protein; 4655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997.
20-MAY-1997; U08682.
23-MAY-1996; US-652877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4655 AA;
Amerstrom G, Crum]
Murray EM, Rask L;
WPI; 96-268334/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murray EM, Rask L;
WPI; 98-018219/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 hdvhkcsp 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|:| |
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_difference
                                                                                            N-PSDB; T28774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V05997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9744050-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
```

ö

```
Ol-MAR-1999 (first entry)
Secreted protein encoded by gene 191 clone HJAB265.
Secreted protein, fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foctal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; isofaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder: schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                     ö
                                                                                                                                                                                     Gaps
superfamily of glycoproteins. It can be expressed in a claimed host cell using a vector comprising hCSP DNA. Also claimed are a method of using hCSP to treat human membraneous glomerulonephitis, and the use of hCSP to screen for agonists and antagonists of hCSP. Such (antiagonists are useful in the treatment of conditions associated with perturbations in parathroid hormone levels, vitamin D3 production, oestrogen levels, osteoclast or osteoblast activity, calcium secretion and calcium ion homeostasis, e.g. Sequence 4655 AA;
                                                                                                                                                                                   ;
0
                                                                                                                                                         Length 4655;
                                                                                                                                                      Score 46; DB 29; Length 465
Pred. No. 9.75e+01;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               W88724 standard; Protein; 69 AA.
                                                                                                                                                        67.6%;
50.0%;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-057650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-057761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-057764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-057770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-048875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-048899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-048949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-048972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-057667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-048882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-048877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-048964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-04937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1998;
04-JUN-1998; U11422.
18-DEC-1997; US-0709
06-JUN-1997; US-0488
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                             261 hdvhkcsp 268
                                                                                                                                                                                                                                         481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-19
                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                   RESULT
    888888888888
                                                                                                                                                                                                                                          ô
```

```
Claim II; Pages 5/8; //2pp; English.

Criam II; Pages 5/8; //2pp; English.

Criam II; Pages 5/8; //2pp; English.

Criam II; Pages 5/8; //2pp; English.

Criam II; Pages are deposited with the ATCC under deposit numbers ATCC gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97977, 209081, 209089, 209010, 209010, 209010, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 20908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode useful for diagnosts and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders claim 11; Page 578; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress G Fan P, Feng P, Ferrie AM, Fischer CL, Florence C, Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z; WPI; 99-059865/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1997; US-057649.

05-SEP-1997; US-057654.

05-SEP-1997; US-057760.

05-SEP-1997; US-057763.

05-SEP-1997; US-057763.

05-SEP-1997; US-057763.

05-SEP-1997; US-05774.
                                                                             US-057648
US-057648
US-057662
US-057662
US-057768
US-057771
US-057771
US-057776
US-057776
US-057776
US-057776
US-058880
US-048880
US-048880
US-048880
US-048880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V84601
                                                                        05-SEP-1997; C
05-SEP-1997; C
05-SEP-1997; U
05-SEP-1997; U
05-SEP-1997; U
05-SEP-1997; U
                                                                                                                                                                                                                          05-SEP-1997; 05-SEP-1997; 06-JUN-1997; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1997; t
05-SEP-1997; t
05-SEP-1997; t
                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1997;
06-JUN-1997;
                                                                                                                                                                                                                                                                                                            06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                     06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 36-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1997;
```

```
23-MAY-1997; US-MAY-1997; US-MAY-1997; US-UN-1997; US-UN-1997; US-UN-1997; US-UN-1997; US-ANG-1997; US-ANG-19
                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1997;
                                                                                                                                                                                                                                                                                                              22-AUG-1997;
22-AUG-1997;
 ö
                                                                      Gaps
                                                                                                                                                                                                                          Human secreted protein encoded by gene 15 clone HE6DB26. Human secreted protein; testls; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
                                                                      ö
                                       Score 45; DB 38; Length 69;
Pred. No. 1.26e+02;
3; Mismatches 0; Indels
line for gene number and clone identification).
Sequence 69 AA;
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                   /T 11
W74745 standard; Protein; 84 AA.
W74745;
                                                                                                                                                                                                                                                                                                                           /label= unknown
                                        66.2%;
57.1%;
                                                                                                                                                                                                         25-JAN-1999 (first entry)
                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 US-061060.
US-038621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-040336.
US-040626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-043311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-043568.
US-043569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-043669.
US-043670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-047492
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-040333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-043672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-047503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-047581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-043313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-043314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-043578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-043671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-043674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-04357
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                            Misc-difference 84
                                                                                                              :::[|||
481 HAIHRCH 487
                                                                                                34 rplhrch 40
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               02-0CT-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                      11-SEP-1998.
06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                        WO9839448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1997;
                                          Query Match
                                                                    Matches
                                                                                                                                                                 ပ္သင္တ
                                                                                                                          δy
```

```
PR 22-WM-1997 US-047611.

PR 22-WM-1997 US-047611.

PR 22-WM-1997 US-047612.

PR 22-WM-1997 US-047614.

PR 22-WM-1997 US-047614.

PR 22-WM-1997 US-046619.

PR 22-WM-1997 US-0
```

```
(DENZ-) DENZYME APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                  Etzerodt M, Holte
WPI; 94-279681/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1764 htinrcn 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:||:
481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
WO9640197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 haahrc 9
                           Homo sapiens
                                                                      18-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    loss or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   되었다
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Processor of the alpha-2 members of the minorinal Receptor Receptor group are claimed. The alpha-2 mederating and preferred parent receptor Treating and preventing from the are captor for the alpha-2 mederating and prevent receptor. The alpha-2 mederating and members of the minorinal Receptor group are claimed. The alpha-2 macroglobulin/Lbr-receptor receptor for members of the Minorinal Receptor group are claimed. The alpha-2 macroglobulin/Lbr-receptor receptor for members of the minorinal Receptor group are claimed. The alpha-2 macroglobulin/Lbr-receptor related parent receptor. The derive, which are preferred parent receptor. The derive, which are preferred parent receptor. The derive, which are preferrably is a preferred parent forms of the native receptors, are useful for treating and preventing virial (esp. rininoviral) infections.

N.B. the SEQ.ID. listing includes a sequence (no.4) which differs from the alpha-2 mR/LRP sequence as indicated in the Features Table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha 2-Macroglobulin/LDL-receptor related protein.
alpha-2 macroglobulin, Low Density Lipoprotein, LDL; receptor family, LDL receptor related protein, LRP; small rhinovirus receptor; deriv, minor Rhinovirus; alpha2MR/LNP.
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference 211..260 /note= "50 residues not shown in SEQ.ID.No.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Residue not shown in SEQ.ID.No.4" 3050
                                                                                                                                                                           Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Residue not shown in SEQ.ID.No.4"
                                                                                                                                                                                                Pred. No. 1.26e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease, Factor-Xa; recognition site; fusion protein cleavage; protein folding; alpha-2-MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 9; Le
Pred. No. 1.63e+02;
3; Mismatches 0;
                                                                                                                                                                              DB 37;
                                                                                                                                                                                Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                R47861 standard; protein; 4544 AA. R47861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 13
R60517 standard; Protein; 4544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.7%;
57.1%;
                                                                                                                                                                           66.2%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R60517;
22-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference 1990
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1764 htinrcn 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha-2-MR.
                                                                                                                                   84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                            481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                   32 htvhtch 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9401553-A
                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                   uses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
ID R6
AC R6
DT 22
DE HU
KW Se
                                                                                                                                                                                                                                                                                                                                                                           RANGE SULTANGE STATE STATE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SULTANGE SUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                   g
    88888888
                                                                                                                                                                                                                                                                                                              ò
```

```
systemic lupus erythematosus measures parameter parameters and as systemic lupus erythematosus.

Disclosure; Page 27; 118pp; English.

The present sequence is an antiphospholipid (apt) analogue clone 2G12 screened from ACA-6501 phage library. Peptides are derived from screening random peptide phage libraries to identify the sequences which best minic the epitopes recognised by apt antibodies. A method has been produced for identifying analogues of key epitopes recognised by apt antibodies in patients suffering from PAPS, APS and other apt antibody-mediated diseases. The products and methods can be used for the diagnosis and treatment of apt antibody-mediated pathologies such as systemic lupus erythematosus, antibody-mediated pathologies such as systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-50-1996.

06-JUN-1995; U09976.

07-JUN-1995; US-482651.

(LJOL-) LA JOLLA PHARM CO.

Jones DS. Marquis DM, Victoria EJ, Yu L;

WPI; 97-051886/05.

We anti-phospholipid analogues - used to develop prods. for the diagnosis and treatment of aPL antibody-mediated pathologies such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AuG-1997 (first entry) Antiphospholipid analogue peptide ACA-6501 phage library clone 2G12. Antiphospholipid analogue peptide ACA-6501 phage library clone 2G12. apt.; antibody mediated pathology; systemic lupus erythematosus; antiphospholipid antibody syndrome; stroke; foetal loss; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a correctly folded prod
Disclosure: Page 131-146; 202pp; English.
Various domains and domain clusters of human alpha-2-MR protein have been PCR amplified using the primers given in Q71252-65.
alpha-2-macroglobulin receptor/low density lipoprotein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 11; Length 4544;
Pred. No. 1.63e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 43; DB 22; Length 9;
. No. 2.11e+02;
Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                       Holtet TL, Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LI 14
WIO404 standard; peptide; 9 AA.
WIO404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 15
W67128 standard; peptide; 9 AA.
W77128:
18-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%;
llarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%;
Similarity 83.3%;
5; Conservative
                                                                                                                              04-FEB-1994; DK0054.
04-FEB-1993; DK-000130.
05-FEB-1993; DK-000139.
03-DEC-1993; WO-G02492.
```

ô

ö

ö

0; Gaps

Search completed: Thu May 20 13:17:04 1999 Job time: 110 secs.

****	(TM)	****
* * * *	, 	4 4 4 4
* * * * *	<u> </u>	4444
******		****

******		+++++++
***************************************		***************************************
******		********
*****		********

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Thu May 20 13:17:22 1999; MasPar time 3.83 Seconds MPsrch_pp Run on:

Tabular output not generated.

>US-09-099-053-2 (481-488) from US09099053.pep (6 of 6) 68 1 HAIHRCHP 8 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

116695 seqs, 37453910 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 20.442; Variance 28.322; scale 0.722 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.27e+00	3.58e+00	3.58e+00	3.58e+00	3.58e+00	3.58e+00	5.62e+00	5.62e+00	5.62e+00	8.76e+00	8.76e+00	1.36e+01	1.36e+01	1.36e+01	1.36e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	3.21e+01
	Description	Llprotein (alternati	hypothetical protein	hômeotic protein mec-	alkylglycerone-phosph	genome polyprotein -	genome polyprotein -	ig epsilon chain C re	obable ql	polyprotein(NS1, NS3,	hypothetical protein	protein A - flock hou	pdx; protein - Aquife	hypothetical protein	transducin homolog sa	hypothetical 65.4K pr	otei	GC-rich sites (of HIV	H+-transporting ATPas	bindin fertilization	SEC23 protein homolog	DNA-directed DNA poly	DNA-directed DNA poly	DNA-binding protein r
	QI	836502	S21833	S28390	JC5829	GNWVTB	GNWVNE	EHMSS	B70770	A46105	S78471	S41397	S38929	B48290	A49367	JQ1879	A28918	JE0235	855969	B40552	I60247	WMAD12	DJAD51	S72734
	DB	. 2	7	П	~	Н	Н	٦	~	N	~	~	7	~	~	N	~	ო	~	~	~	٦	Н	~
	Query Match Length DB	594	142	321	597	3412	3414	423	731	3415	966	866	87	197	519	581	97	283	345	œ	573	ഗ	1056	9
dР	Query Match	73.5	72.1	72.1	72.1	72.1	72.1	70.6	70.6	70.6	69.1	ი	67.6	7	67.6	ζ.	66.2	ė.		Ģ.		66.2	ė.	64.7
	Score	50	49	49	49	49	49	48	48	48	47	47	46	46	46	46	45	45	45	45	45	45	45	44
	Result No.	-	7	m	4	S	9	7	æ	თ	10	11	12	13		15		17	18	19	20	21	22	23

Score 49; DB 2; Length 142; Pred. No. 3.58e+00;

Query Match Best Local Similarity 71.4%;

24	44	64.7	929	7	A41870	dnaA protein - Strept	3.21e+01
25	44	64.7	751	7	I48748	semaphorin E - mouse	
26	44	64.7	796	~	57	P	
27	44	64.7	46	~	B70588	probable mbtF protein	
28	44	64.7	63	-	A42545	genome polyprotein -	3.21e+01
29	44	64.7	79	7	JC4743	fatty-acid synthase (
30	44	64.7	4544	٦	S02392	alpha-2-macroqlobulin	3.21e+01
31	44	64.7	54	7	S25111	alpha-2-macrodlobulin	
32	43	63.2	440	Н	TWBYM1	transcription factor	4.89e+01
33	43	63.2	454	7	A69017	dihydroorotase - Meth	
34	43	63.2	510	~	A42750	insulinoma-associated	4.89e+01
35	43	63.2	533	~	S42404	thromboxane-A synthas	4.89e+01
36	43	63.2	533	7	JN0683	thromboxane-A synthas	4.89e+01
37	43	63.2	880	7	S56828	finger protein YJL056	4.89e+01
38	43	63.2	45	7	S65571	pattern formation pro	
39	43	63.2	53	~	E70874	probable ppsB protein	4
40	43	63.2	54	7	~	serine proteinase (EC	4
4	43	63.2	76	~	A31494	DNA-directed RNA poly	4
42	43	63.2	76	~	-	DNA-directed RNA poly	4.89e+01
	43	63.2	76	~	18		4.89e+01
44	43	63.2	1766	7	m	DNA-directed RNA poly	4.89e+01
45	43	63.2	57	7	73	hypothetical polyprot	4.89e+01
					ALIGNMENTS		
	,						
RESULT	ч	836502	02	‡ ‡	#tvpe complete		

S36502 #type complete Liprotein (alternative) - human papillomavirus type Liprotein (alternative) - human papillomavirus type 20-Feb-1955 #sequence_revision 20-Feb-1995 #text_c? 20-Feb-1997 856502 S36502 S36469 Delius, H.; Hofmann, B. Submitted to the EMBL Data Library, August 1993 n Primer-directed sequencing of human papillomavirus S36502 S36502 Le_type DNA S36503 sseferences EMBL:X74473; NID:g396964; PID:g396971 #sequencing Papillomavirus LI protein late protein #length 594 #molecular-weight 67098 #checksum 780 #length 594 #molecular-weight 67098 #checksum 780 imilarity 83.3%; Pred. No. 2.27e+00;	74 LHRCHP 79 : 483 IHRCHP 488 2 S21833 #type complete hypothetical protein - Mycobacterium tuberculosis hypothetical protein - Mycobacterium tuberculosis 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995 S21833
TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #aubmission #description #accession #accession #arccession #arccession CLASIFICATION KEYWORDS SUMMARY QUETY MATCH BEST LOCAL SIM	Db 74 LHRCHP OY 483 IHRCHP IIIII OY 483 IHRCHP ENTER TITLE ORGANISM DATE ACCESSIONS REPERENCE #authors #authors #submission #accession #accession #status ##nolecule ##rolecule ##rolecule ##rolecule ##rolecule ##rolecule

```
*Habel N4B\
*product nonstructural protein NS5 *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #label N2A\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #label NS3/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #cross-references MUID:90101381
#accession A33776
                                                                                                                                                             72.1%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A33776; S06414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMM/
                                                                                                                               #length 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A33776
                JC5829
                                                                                                                                                                                                                                338 AIQRCOP 344
                                                                                                                                                                                                                                                                482 AIHRCHP 488
                #accession
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1688-1955
1775-1780
1779-1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2260-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2511-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1359-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1490-2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1191-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1671-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2111-2259
                                                                                                                                                                                                                                                                                                                 ഹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777-1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2-112
113-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281-776
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                 COMMENT
                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE
                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Vet, E.C.J.M.; Prinsen, H.C.M.T.; van den Bosch, H.
Biochem. Biophys. Res. Commun. (1998) 242:277-281
Nucleotide sequence of a cDNA clone encoding a Caenorhabditis
                                                                                                                                                                                                                                             Xue, D.; Finney, M.; Ruvkun, G.; Chalfie, M.
EMBO J. (1992) 11:4969-4979
Regulation of the mec-3 gene by the C. elegans homeoproteins
UNC-86 and MEC-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIM1\
LIM2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82/3; 106/3; 190/3; 228/3; 300/1
#superfamily homeotic protein mec-3; homeobox homology; LIM
metal-binding repeat homology
DNA binding; duplication; homeobox; nucleus; transcription
regulation; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
##residues 'MPRLHDIWLLT',20,'DLLQESS',28,'ITASSKNSFTIXFQ',44-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans homolog of mammalian
alkyl-dihydroxyacetonephosphate synthase: Evolutionary
                                                                                                                     528390 #type complete
homeotic protein mec-3 - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
14-Nov-1997
528390; A27662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alkylglyceron-phosphate synthase (EC 2.5.1.26) -
Caenorhabditis elegans
alkyldihydroxyacetonephosphate synthase
#formal_name Caenorhabditis elegans
20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
05-Jun-1998
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain LIM metal-binding repeat homology #label #domain LIM metal-binding repeat homology #label #domain homeobox homology #label HOX #label #length 3121 #molecular-weight 37088 #checksum 1652
                                                                                                                                                                                                                                                                                                                                                                                                               Way, J.C.; Chalfie, M. Cell (1988) 54:5-16
mec-3, a homeobox-containing gene that specifies
mifferentiation of the touch receptor neurons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
 ö
                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:L02877; NID:g156488; PID:g156489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.1%; Score-49; --- DB.1; -Length 321; larity 83.3%; Pred. No. 3.58e+00; Conservative 1; Mismatches 0; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GB:M20244; NID:g156363; PID:g156364
 ö
                                                                                                                                                                                                                                                                                                                                nucleic acid sequence not shown
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #type complete
                                                                                                                                                                                                                                                                                                                                                               1-321 ##label XUE
 .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##label WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #cross-references MUID:88253425
   Conservative
                                                                                                                                                                                                                                                                                                                                ##status nucle
##molecule_type mRNA
##residues 1-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                $28390
                                                                                                                                                                                                                                                                                                                 528390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JC5829
                                                                                                                                                                                                                                                                                                                                                                                                 A27662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A27662
                                 104 ALQRCHP 110
                                                  |::||||
482 AIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:1111
481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 HSIHRC 89
 ..
ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                   #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
29-79
89-145
218-274
'MARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
#journal
#title
                                                                                                                                                                                                                                                                #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                 m
                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #introns
                                                                                                                                                                                                                ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
   Matches
                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                  TITLE
                                                                                                                                 ENTRY
                                                                                                                                                                                DATE
                                   g
                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
```

٠ ۲,

ÿ

```
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type genomic RNA
##residues
1-3412 ##label PLE
##residues
1-3412 ##label PLE
##residues
CLASSIFICATION #superfamily yellow fever virus genome polyprotein; DEAD/H
box halicase homology
KEYWORDS
ATP; capsid protein; envelope protein; glycoprotein;
nonstructural protein; P-loop; polyprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capsid protein C; envelope protein M; envelope protein prM; major envelope protein E; nonstructural protein NS1; nonstructural protein NS2; nonstructural protein NS3; nonstructural protein NS3; nonstructural protein NS3; nonstructural protein NS4; nonstructural protein NS4; aformal_name tick-borne encephalitis virus 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #product capsid protein C #status predicted #label CPC
#product envelope protein prM #status predicted #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNWVIB #type complete
genome polyprotein - tick-borne encephalitis virus (strain
Sofjin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #product nonstructural protein NS1 #status predicted
#label NS1\
#product nonstructural protein NS2a #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #product nonstructural protein NS2b #status predicted
#label N2B\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pletnev, A.G.; Yamshchikov, V.F.; Blinov, V.M. Yarology (1990) 174:250-263 Nucleotide sequence of the genome and complete amino acid sequence of the polyprotein of tick-borne encephalitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *product nonstructural protein NS3 *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *product envelope protein M *status predicted *label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major envelope protein E #status predicted PPE\
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *region nucleotide-binding motif A (P-loop)\
#domain DEAD/H box helicase homology #label DEAD\
#region nucleotide-binding motif B\
#region DEAH motif\
                                                                                                                                                                                                                                            #molecular-weight 66559 #checksum 3790
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #product nonstructural protein NS4a #status
#label N4A\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *product nonstructural protein NS4b *status
                                                                                                                                                                                                                                                                                                Score 49; DB 2; Length 597;
Pred. No. 3.58e+00;
2; Mismatches 0; Indels
switching of peroxisomal targeting signals
```

ന

```
##molecule_type DNA
##residues 1-42
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115-183
220-288
325-396
23-75,122-181,
227-286,332-394 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|:|
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                  144,434,641,753,
861,983,999,1649,
1988,2044,2447,
2529,2686,2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
KEYWORDS
FEATURE
                                                                                                                    1688-1695
1775-1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##note
                                                          1490-2110
                                                                                                                                                                              2111-2259
                                                                                                                                                                                                                                                             2512-3414
                  1359-1489
                                                                                                                                                                                                                        2260-2511
                                                                                                 1688-1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETICS
#introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-77
                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Mandl, C.W.; Heinz, F.X.; Stoeckl, E.; Kunz, C.
#journal Virology (1989) 173:291-301
#title Genome sequence of tick-borne encephalitis virus (Western subtype) and comparative analysis of nonstructural proteins #arcoss-references MUID:90051080
#accossion A32596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #product capsid protein C #status predicted #label CPC\
#product membrane protein M precursor #status predicted
#label MPP\
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                 GNWVNE #type complete
genome polyprotein - tick=borne"encephalitis virus"(subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; P-loop; polyprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type genomic RNA
##residues 767-3414 ##label MAN2
##cross-references GB:M27157
##CTATION #superfamily yellow fever virus genome polyprotein; DEAD/H
box helicase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *product nonstructural protein NS2a *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain nonterminal signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BPE\
#domain transmembrane #status predicted #label TM2\
#product nonstructural protein NS1 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                Western, strain Neuderfl)
capsid protein C: envelope protein E: membrane protein M;
nonstructural protein NS2; nonstructural protein NS2;
nonstructural protein NS2b; nonstructural protein NS2;
nonstructural protein NS4e; nonstructural protein NS3;
nonstructural protein NS5
#formal_name tick-borne encephalitis virus
31-pec-1989 #sequence_revision 30-Jun-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #label SIG\
#product membrane protein M #status predicted #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain transmembrane #status predicted #label TM1\
#product envelope protein E #status predicted #label
                                                                                                 #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Mandl, C.W.; Heinz, F.X.; Kunz, C.
#journal virology (1988) 166:197-205
#title Sequence of the structural proteins of tick-borne encephalitis virus (Western subtype) and comparative analysis with other flaviviruses.
#cross-references MuID: 88322870
#accession A31052
                                                                                                                    predicted
#length 3412 #molecular-weight 377979 #checksum 7007
                                                                                                                                                                            Score 49; DB 1; Length 3412; Pred. No. 3.58e+00; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type genomic RNA
##residues
##cross-references GB:M21498
#label NS5\
                                                                                                                                                                              72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-May-1998
A31052; A32596
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                           1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                481 HAIHRCHP 488
              144,434,641,753,861,983,999,1228,1649,1988,2044,2052,2447,2466,2685,2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1129-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738-751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-116
117-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246-264
281-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206-280
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                       SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                             සු
                                                                                                                                                                                                                                                                                                  ò
```

```
*superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91/1; 199/1; 307/1
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers g.
                                                           *product nonstructural protein NS3 *status predicted *label NS3\
*domain DRAD/H box helicase homology *label DEAD\
*region nucleotide-binding motif A (P-loop)\
*region nucleotide-binding motif B\
*region DEAH motif\
*product nonstructural protein NS4a *status predicted
N2A\
nonstructural protein NS2b #status predicted
N2B\
                                                                                                                                                                                                                                              nonstructural protein NS4b #status predicted
                                                                                                                                                                                                                                                                                          protein NS5 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                     #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted
#length 423 #molecular-weight 47681 #checksum 7738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain immunoglobulin homology #label IMM1\
#domain immunoglobulin homology #label IMM2\
#domain immunoglobulin homology #label IMM3\
#domain immunoglobulin homology #label IMM3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.6%; Score 48; DB 1; Length 423; Best Local Similarity 71.4%; Pred. No. 5.62e+00; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #disulfide_bonds #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                          predicted #length 3414 #molecular-weight 378383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 1; Leng
Pred. No. 3.58e+00;
3; Mismatches 1;
                                                                                                                                                                                                                                                                   #label N4B\
roduct nonstructural
#label NS5\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-423 ##label ISH
                                                                                                                                                                                                                         #label N4A\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.1%;
Similarity 50.0%;
4; Conservative
                                             #label
                                                                                                                                                                                                                                                                   #label
```

4

```
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                       481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 HKIHHCRP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #description
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
#submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                   1688-1956
1688-1695
1776-1781
1780-1783
                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE
                                                                                                                                                                                                                                                                                                                                                                                                                       DATE
                                                                                                                                                                                                                                                         а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                   Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III. C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Kroph, A.; McLean, J.; Muurphy, T.; Oliver, S.; Osborne, J.; Quall, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squres, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. #cross-references MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mandl, C.W.; Holzmann, H.; Kunz, C.; Heinz, F.X.
Virology (1993) 194:173-184
Complete genomics sequence of Powassan virus: evaluation of
genetic elements in tick-borne versus mosquito-borne
                                                                                                                                          probable glgB protein - Mycobacterium tuberculosis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AL123456; NID:g3261576; PID:e245020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsid protein C, large envelope protein E, membrane-anchored protein M precursor) - Powassan virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type genomic RNA
##residues 1-3415 ##label MAN
##cross-references GB:L06436; NID:g309916; PID:g309917
##cross-references cguence extracted from NCBI backbone (NCBIN:130654,
##note NCBIP:130655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A46105 #type complete polyprotein(NS1, NS3, NS5, NS2A, NS2B, NS4A, NS4B, small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Powassan virus
07.Apr-1994 #sequence_revision 25.Apr-1997 #text_change
22-May-1998
                                                                                                                                                                          #formal_name Mycobacterium tuberculosis
17-Jn1-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
B70770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glgB
#length 731 #molecular-weight 81729 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.6%; Score 48; DB 2; Lent
larity 62.5%; Pred. No. 5.62e+00;
Conservative 1; Mismatches 2;
                                                                                                                             #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##experimental_source strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-731 ##label COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##IPSITUMES
##CIOSS-references GB:Z73902; GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUID:93242744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flaviviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                                                       A70500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B70770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A46105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A46105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 NDIYRCHP 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 HAIHRCHP 488
                                     :|||| |
482 AIHRCHP 488
                105 SIHRCDP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSIONS
REFERENCE
#authors
                                                                                                                                                                                                                                   ACCESSIONS
REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #gene
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #title
                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTRY
                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                  음
                                                    ŏ
```

₹ .

Ų

```
Dasmahapatra, B.; Dasgupta, R.; Ghosh, A.; Kaesberg, P.
J. Mol. Biol. (1985) 182:183-189
Structure of the black beetle virus genome and its functional
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
#superfamily yellow fever virus genome polyprotein; DEAD/H
box helicase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dasgupta, R. submitted to the EMBL Data Library, January 1994 submitted to the EMBL Data Library, January 1994 mear identity in the polymerase gene of two serologically distinct nodaviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S41397 #type complete protein A - flock house virus #formal_name flock house virus 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S78471 #type complete
hypothetical protein A - black beetle virus
#formal_name black beetle virus
11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change
05-0un-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
##molecule_type genomic RNA
##residues 1.998 ##label DAS
##cross-references EMBL:X77156; NID:g450500; PID:g450501
##cross-references EMBL:X77156; NID:g450500; PID:g450501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #checksum 4131
                                                                                         #domain DEAD/H box helicase homology #label D:
#region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B\
#region DEAH motif
#length 3415 #molecular-weight 378568 #checksum
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                 Length 3415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dasgupta, R. submitted to the EMBL Data Library, July 1986
                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-998 ##label DAS ##cross-references EMBL:X02396; NID:g60679; PID:g60680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type genomic RNA
##residues 1-883,'AALRRIPWINRYQC' ##label DAW
##cross-references EMBL:X02396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA biosynthesis
#length 998 #molecular-weight 112196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 2; LA Pred. No. 8.76e+00;
                                                                                                                                                                                                                                 Score 48; DB 2; L
Pred. No. 5.62e+00;
                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type genomic_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           implications.
S28728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S78471; S28728
                                                ATP; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S78471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S41397
S41397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S28728
                                                                                                                                                                                                                                                                                                                                  1597 HKIHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S78471
```

S

```
JQ1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ1879
                                                                                                                                                                                                                                                                                                                                                                       358 HTTQRCH 364
                                                                                                                                                                                                                                                                                                                                                                                              481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 HVVHQCH 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #start_codon
                                                                                                                                                                                                     #gene
CLASSIFICATION
                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                           ACCESSIONS
REFERENCE
#authors
                                                                                  #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *authors
                                                                                                                                                                                                                                 FEATURE
77-110
258-291
361-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETICS
                                                                                                                                                                                                                                                                                         SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE
                                                                                                                                                                                                                                                                                                                                                                          염
                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liebl, U.; Mockensturm-Wilson, M.; Trost, J.T.; Brune, D.C.; Blankenship, R.E.; Vermaas, W. Proc. Natl. Acad. Sci. U.S.78 (1993) 90:7124-7128 Single core polypeptide in the reaction center of the photosynthetic bacterium Heliobacillus mobilis: structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                **scatus preliminary; not compared with conceptual translation ##molecule_type DNA ##residues | 1-197 ##1-c-1 --- |
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 197 - Heliobacillus mobilis
#formal_name Heliobacillus mobilis
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references GB:L19604
.Y #length 197 #molecular-weight 22200 #checksum 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 implications and relations to other photosystems. B48290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                              Bocchetta, M.
submitted to the EMBL Data Library, July 1993
S38929
Score 47; DB 2; Length 998;
Pred. No. 8.76e+00;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2; Length 87; Pred. No. 1.36e+01; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 2; Length 197
Pred. No. 1.36e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A49367 #type complete
transducin homolog sazD - human
#formal_name Homo sapiens #common_name man
                                                                                                                                                                                                                                                                                                                                                                                   #length 87 #checksum 4629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type complete
                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:X74277
##experimental_source strain KO1SA
                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-87 ##label BOC
                                                                                                                                                                                                                                                                                                                                                                                                           67.6%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.6%;
Similarity 83.3%;
5; Conservative
Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                 06-Jun-1997
S38929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-Dec-1997
B48290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 4; Conser
                                                                    | ||:|:|
481 HAIHRCHP 488
                                                      257 HKIHHCRP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::|||
481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||||
481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 HPVHRC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 QAIHRC 53
                                                                                                                                                                                                                                                                                                                                                                       #start_codon
                                                                                                                                                                                                                                                          #submission
                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                  ACCESSIONS
REFERENCE
#authors
                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                            #variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #title
                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                            GENETICS
                                                                                                                                                                                                                                                                                                                                                          #dene
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                       RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTRY
                                                                                                                                                                                         DATE
                                                      g
                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JQ1879 #type complete
hypothetical 65.4K protein - pea enation mosaic virus
#formal_name pea enation mosaic virus, PEMV
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
12-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demler, S.A.; Rucker, D.G.; de Zoeten, G.A.
J. Gen. Virol. (1993) 74.1-14
The chimeric nature of the genome of pea enation mosaic
Virus: The independent replication of RNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily barley yellow dwarf virus RNA-directed RNA
polymerase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain barley yellow dwarf virus RNA-directed RNA polymerase homology #label BYD #length 581 #molecular-weight 65404 #checksum 4973
                                                                                                                                                                                 autosomal dominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #checksum 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.6%; Score 46; DB 2; Length 581; Best Local Similarity 57.1%; Pred. No. 1.36e+01; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 2; Length 519
Pred. No. 1.36e+01;
2; Mismatches 1; Indels
                                                                        A49367
Weinstat-Saslow, D.L.; Germino, G.G.; Somlo,
                                                                                                                                                                                                                                                         #domain WD repeat homology #label WDIV
#domain WD repeat homology #label WD2V
#domain WD repeat homology #label WD2V
#length 519 #molecular weight 56047 #chec
                                                                                                                                                Genomics (1993) 18:709-711
A transducin-1ike gene maps to the auto
polycystic kidney disease gene region
A49367
                                                                                                                                                                                                                                                                                                                                                                                                                     #superfamily WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: Thu May 20 13:18:43 1999 Job time : 81 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
##residues 1-581 ##label DEM
##experimental_source strain WSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.6%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                     09-Apr-1998
A49367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #map_position segment RNA2
```

ö

ö

US-09-099-053-2-06.rsp

*****	(TM)	*****
***************************************		***************************************
******	\[\]	******
******		4444444
******		****
*****		********
******		********
******		*******

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Thu May 20 13:19:01 1999; MasPar time 2.42 Seconds93.310 Million-cell-updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated.

>US-09-099-053-2 (481-488) from US09099053.pep (6 of 6) 68

1 HAIHRCHP 8 Description: Perfect Score: Sequence: PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 21.282; Variance 25.495; scale 0.835 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result		Query					
. ! 8	Score	Match	Match Length	BB	ΩI	Description	Pred. No.
Т	20	73.5	594	-	VL1_HPV27	MAJOR CAPSID PROTEIN L.	7.71e-01
7	49	72.1	321	Н	MEC3_CAEEL	MECHANOSENSORY PROTEIN	1.28e+00
М	49	72.1	3412	Н	POLG_TBEVS	GENOME POLYPROTEIN [CO	1.28e+00
4	49	72.1	3414	Н	POLG_TBEVW	GENOME POLYPROTEIN [CO	1.28e+00
S	49	72.1	3414	Н	POLG_TBEVH	GENOME POLYPROTEIN [CO	1.28e+00
9	48	70.6	376	Н	LYMP_HUMAN	LYMPHOPAIN PRECURSOR (2.12e+00
7	48	70.6		Н	GLGB_MYCTU	PROBABLE 1,4-ALPHA-GLU	2.12e+00
80	48	9.07	m	Н	POLG_POWVL	GENOME POLYPROTEIN [CO	2.12e+00
6	46	67.6		Н	SAZD_HUMAN	WD-REPEAT PROTEIN SAZD	5.66e+00
10	46	67.6	1551	Н	YQ12_CAEEL	HYPOTHETICAL 175.7 KD	5.66e+00
11	46	67.6		Н	LRP2_HUMAN	LOW-DENSITY LIPOPROTEI	5.66e+00
12	45	66.2	345	Н	VATX_YEAST	VACUOLAR ATP SYNTHASE	9.16e+00
13	45	66.2	485	П	BIND_STRFN	BINDIN PRECURSOR.	9.16e+00
14	45	66.2	1056	Н	DPOL_ADE05	DNA POLYMERASE (EC 2.7	9.16e+00
15	45	66.2	1056	-	DPOL_ADE02	DNA POLYMERASE (EC 2.7	9.16e+00
16	44	64.7	360	Н	LEU3_AZOVI	3-ISOPROPYLMALATE DEHY	1.47e+01
17	44	64.7	369	-1	RUVB_MYCLE	HOLLIDAY JUNCTION DNA	1.47e+01
18	44	64.7	656	М	DNAA_STRCO	CHROMOSOMAL REPLICATIO	1.47e+01
19	44	64.7	3414	Н	POLG_LANVT	GENOME POLYPROTEIN (CO	1.47e+01
20	44	64.7	4544	٦	LRP1_HUMAN	LOW-DENSITY LIPOPROTEI	1.47e+01
21	43	63.2	320	٦	Y013_NPVOP	HYPOTHETICAL 36.6 KD P	2.35e+01
22	43	63.2	438		ILL1_ARATH	IAA-AMINO ACID HYDROLA	2.35e+01
23	43	63.2	439	Н	ILL2_ARATH	IAA-AMINO ACID HYDROLA	2.35e+01

321 AA.

PRT;

RESULT 2 ID MEC3_CAEEL STANDARD; I AC P09088; DI 01-NOV-1988 (REL. 09, CREATED)

:|||||| 483 IHRCHP 488 74 LHRCHP 79

g á

24 43 63.2 440 1 NANI, YEAST NANI PROTEIN PRECUISOR 2 356+01 25 43 63.2 644 1 PRECUMENTH PROPERTIES E 2356+01 28 43 63.2 644 1 PRECUMENTH PRECUIATOR OF G-PROTEIN 2 356+01 28 43 63.2 647 1 PRECUIATOR OF G-PROTEIN 2 356+01 29 43 63.2 533 1 THAS, MOUSE THROHORANDER S SYNTHASE 2 356+01 30 43 63.2 533 1 THAS, MOUSE THROHORANDER S SYNTHASE 2 356+01 31 43 63.2 547 1 CO3_BORSE COMPLEMENT COMPONENT C 2 356+01 32 43 63.2 1451 1 EM30_ARAPH PATTERN FORMATION PROF 2 356+01 34 43 63.2 1451 1 EM30_ARAPH PATTERN FORMATION PROF 2 356+01 35 43 63.2 1451 1 EM30_ARAPH PATTERN FORMATION PROF 2 356+01 36 43 63.2 1451 1 EM30_ARAPH PATTERN FORMATION PROF 2 356+01 37 42 61.8 341 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 38 42 61.8 341 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 37 42 61.8 341 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 38 42 61.8 342 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 39 42 61.8 342 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 30 42 61.8 342 1 LAIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROF 2 356+01 31 42 61.8 372 1 VOIL SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILE SANGE SEPTION FORMATION PROFILES SANGE SEPTION FORMATION PROFILES SANGE SEPTION FORMATION PROFILES SANGE SEPTION FORMATION PROFILES SANGE SEPTION

~

```
A24055
                                                             FLAVIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
PFAM;
PFAM;
PFAM;
PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                       -!- FUNCTION: MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH RECEPTOR NEURONS. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86 TO SITES IN THE MEC-3 GENE PROMOTER.
-!- SUBCELLULAR LOCATION: UNCLEAR.
                                                                                                                 gene that specifies differentiation of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                           XUE D., FINNEY M., RUVKUN G., CHALFIE M.; "Regulation of the mec-3 gene by the C.elegans homeoproteins UNC-86 and MEC-3.";
                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                    EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 3412 AA.
Q88476; Q88477; Q88478; Q88479; Q88877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC, TO1076; -.
HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN;
REPEAT; LIM MOTIF; METAL-BINDING; ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLU-RICH (ACIDIC).
24F3D4B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Lk
Pred. No. 1.28e+00;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLG_TBEVS STANDARD; PRT; 3412 AA. P07721; P07721; Q88475; Q88476; Q88477; Q88477; Q884701-1-1988 (REL. 07, CREATED) CHAY-1998 (REL. 18, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
28, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A27662; A27662.

PIR; S28390; S28390.

PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50028; LIM_DOMAIN_1; 2.

PROSITE; PS50071; HOMEOBOX_2; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

PRAM; PF00446; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L02877; G156489; -.
EMBL; M20244; G156364; ALT_SEQ.
                                                                                                     WAY J.C., CHALFIE M.; "mec-3, a homeobox-containing the touch receptor neurons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37088 MW;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%;
larity 83.3%;
Conservative
                                                                                                                                                                                                              EMBO J. 11:4969-4979(1992)
                    MECHANOSENSORY PROTEIN 3
                                         CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315
321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                     93099872.
                                                                                   SEQUENCE FROM N.A. MEDLINE; 88253425.
01-FEB-1994 (REL. 01-OCT-1996 (REL.
                                                                                                                                       CELL 54:5-16(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSIHRC
                                                                                                                                                            REVISIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                   IONS.
                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
ID PO
AC PC
DT 01
DT 01
οy
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICK-borne encephalitis virus genome. The nucleotide sequence coding for virion structural proteins.";

TICK-borne encephalitis virus genome. The nucleotide sequence coding for virion structural proteins.";

LL FEBS LETT. 200:317-321(1986).

C. !- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HUDOPHOBIC. SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

C. !- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROFIEN BAND GLYCOPROFIEN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN M AND GLYCOPROFIEN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

C. !- THE NOWSTRUCTURAL PROTEINS NSI PRESENTS TWO ALTERNATIVE CLEAVAGE SITES FOR ITS C-TERMINUS, WHICH MAY DEFINE A SOLUBLE OR A MEMBRANE-BOUND FORM OF NSI.
GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRICTURAL PROTEINS NS1, NS2A, NS2B, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.77.48) (NSS)].
TICK BORNE ENCEPHALITIS VIRUS (STRAIN SOFJIN) (TBEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 88319988.
YAMSHCHIKOV V.F., PLETNEV A.G.;
"Nucleotide sequence of the genome region encoding the structural proteins and the NSI protein of the tick borne encephalitis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P14336; ISVB.
POLYPROTEIN; GLYCOPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.

INIT_MET 1 REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                                                                                                                                                                                                                                                                          PLETNEV A.G., YAMSHCHIKOV V.F., BLINOV V.M.; "Nuclocide sequence of the genome and complete amino acid sequence of the polyprotein of tick-borne encephalitis virus."; VIROLOGY I74:250-263(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-683 AND 777-1002 FROM N.A. MEDLINE; 86220766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins and the NS1 protein of the tinucLEIC ACIDS RES. 16:7750-7750(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00869; Flavi_glycoprot; 1.
PF00948; Flavi_NS1; 1.
PF00949; Flavi_helicase; 1.
PF00972; Flavi_NS5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01003; Flavi_capsid; 1.
PF01004; Flavi_M; 1.
PF01005; Flavi_NS2A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALT_SEQ.
ALT_SEQ.
ALT_SEQ.
ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALT_SEQ.
ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-1190 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01002; Flavi_NS2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07755; E11928; A
EMBL; X07755; E11929; Al
EMBL; X07755; E11929; Al
EMBL; X07755; E11931; Al
EMBL; X03870; G62107;
EMBL; X03870; E12109; Al
EMBL; X03870; E12100; Al
EMBL; X03870; E12101; Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07755; G62026;
EMBL; X07755; G62027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A33776; GNWVTB
PIR; A24055; A24055
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90101381.
```

m

```
resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
PROPEP
CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (REL. 13, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
115-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS, CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBIYPE) (TBEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANDL C.W., HEINZ F.X., KUNZ C.; "Sequence of the structural proteins of tick-borne encephalitis virus (western subtype) and comparative analysis with other flaviviruses."; VIROLOGY 166:197-205(1988).
                                                                                                                                                                                                              HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE, 90051080.
MANDL C.W., HEINZ F.X., STOECKL E., KUNZ C.;
"Genome sequence of tick-borne encephalitis virus (Western subtype) and comparative analysis of nonstructural proteins with other
                                                           MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NSI (OR 1190).
NONSTRUCTURAL PROTEIN NS2A (OR 1191).
NONSTRUCTURAL PROTEIN NS2B.
                                                                                                                    HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 3412;
Pred. No. 1.28e+00;
3; Mismatches 1; Indels
CELLULAR AMINOPEPTIDASE. CAPSID PROTEIN C.
                                             ENVELOPE GLYCOPROTEIN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> S (IN REF. 3).
-> D (IN REF. 3).
7740BE97 CRC32;
                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                 DEAH BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 767-3414 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-779 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                        71128
1358
1489
2110
2259
2510
3412
1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381
850
                                                                                                                                                                                                                                                                                                                                                                                                              983
999
1228
1228
122
2447
2466
246
381
381
850
3412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NEUDOERFL;
MEDLINE; 88322870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NEUDOERFL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLG_TBEVW
P14336;
                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                  CHAIN
CHAIN
NP_BIND
SITE
                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                              FRANSMEM
                                                                                                        CHAIN
                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMBL; M33668; G335165; -.

REMBL; M33668; G335165; -.

REMBL; M31052; GNWVNE.

REMBL; M31052; GNWVNE.

REPA; PFO0869; Flavi_glycoprot; 1.

REPA; PFO0949; Flavi_NS1; 1.

REPA; PFO0972; Flavi_NS5; 1.

REPA; PFO1003; Flavi_NS25; 1.

REPA; PFO1004; Flavi_NS25; 1.

REPA; PFO1005; Flavi_NS25; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REPA; PFO1005; Flavi_NS26; 1.

REMOVED FROM CAPSID ROY PROTEIN C BY THE CELULAR ANNOPEDTIDASE.
                                                                                               MEDLINE; 95272700.

REY F.A., HEINZ F.X., MANDL C.W., KUNZ C., HARRISON S.C.;

"The envelope glycoprotein from tick-borne encephalitis virus at 2-A
                                                                                                                                                                                                                                                                                                                       K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL)
                                                                                                                                                                                                    NATURE 375:291-298(1995).

-1- FUNCTION: THE SMALL PROTEINS NS2B, NS2B, NS4B AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-1- SUBUNT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C. AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-DIRECTED RNA POLYMERASE (NS5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENVELOPE GLYCOPROTEIN M.
MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4A.
                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 281-680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
W; 3DB27DA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVOLVED IN FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPSID PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL)
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378379
flaviviruses.";
VIROLOGY 173:291-301(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M27157; G335161; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
```

4

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute.. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            ó
                                                                                                                                                                                                                                           01-02T-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2.7.7.48) (NS5)].
TICK-BORNE ENCEPHALITIS VIRUS (STRAIN HYPR) (TBEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 3357-3414 FROM N.A. MEDLINE; 91303656.
MANDL C.W., KUNZ C., HEINZ F.X.;
MANDL G.P., FROM C., HEINZ F.X.;
Tresence of poly(A) in a flavivirus: significant differences between the 3' noncoding regions of the genomic RNAs of tick-borne encephalitis virus strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encephalitis virus strains...;

J. VIROL. 65:4070-4077(1991).

-! FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

-! SUBDUILT: THE VIRIAN OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS.

-! THE VIRIAN OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A PROTEIN AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

-! THE NONSTRUCTURAL PROTEINS NSI PRESENTS TWO ALTERNATIVE CLEAVAGE SITES FOR ITS C-TERMINGS, WHICH MAY DEFINE A SOLUBLE OR A MEMBRANE-BOUND FORM OF NSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPROTEIN; GLYCOPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; HELICASE; ATP-BINDING; CORT PROTEIN; PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.

1 I REMOVED FROM CAPSID PROTEIN C BY THE
                                            Gaps
                                            ö
  Length 3414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MADLARER G., MANDL C.W., ECKER M., HOLZMANN H., STIASNY K.,
KUNZ C., HEINZ F.X.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELLULAR AMINOPEPTIDASE CAPSID PROTEIN C.
  Score 49; DB 1; L. Pred. No. 1.28e+00; 3; Mismatches 1
                                                                                                                                                                                                           PRT; 3414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M76660; G335159; --
PFAM; PF00869; Flavi_Glycoprot; 1.
PFAM; PF00948; Flavi_NS1; 1.
PFAM; PF00949; Flavi_halicase; 1.
PFAM; PF00972; Flavi_NS2; 1.
PFAM; PF01002; Flavi_NS2B; 1.
PFAM; PF01004; Flavi_Capsid; 1.
PFAM; PF01004; Flavi_MS2B; 1.
Query Match 72.1%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U39292; G1066075; -.
                                                                                                                                                                                                           STANDARD;
                                                                                  1597 HEVHQCQP 1604
                                                                                                                           481 HAIHRCHP 488
                                                                                                                                                                                                         POLG_TBEVH
Q01299;
                                                                                                                                                                                                                                                                                                                                                                                                                                      FLAVIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
PROPEP
                                                                                    쉼
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                     HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL)
       MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1 (OR 1190).
NONSTRUCTURAL PROTEIN NS2A (OR 1191).
NONSTRUCTURAL PROTEIN NS2B.
HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 1; Length 3414;
Pred. No. 1.28e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BROWN J., MOLGAARD H.V., PRICE C.M., BUTTLE D.J., MATUTES
ENVER T.;
ENVELOPE GLYCOPROTEIN M.
                                                                                                                                                                                                                                                                                                                                                    MW; CF8A6A36 CRC32;
                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 AA
                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYMPHOPAIN PRECURSOR (EC 3.4.22.-).
                                                                                                          DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF013611; G2582045; -. EMBL; AF015954; G2582181; -.
                                                                                                                                                                                                                                                                                                                                                                         72.1%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                     378539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
7
1120
1130
1130
1130
1130
1130
11489
11489
11489
11489
11489
11699
11689
11689
11689
11689
11689
                                                                                                                                                                                                                                                                                                                   2447 244
2529 252
2726 272
3414 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|:|:|
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYMP_HUMAN
P56202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELLS
                                                                                                                               TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
SEQUENCE
                                                                                    CHAIN
NP_BIND
SITE
                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                     TRANSMEM
                                                                                                                                                                DISULFID
                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
ò
```

S

```
FLAVIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                     Mismatches 0; Indels ... 0; -- Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLGB OR MTCY130.11C.
MYCOBACTERLUM TUBERCULOSIS.
BACTERIA: FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN
BRANCHING ENZYME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
-!- SUBUNIT: MONDER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-H37RV;
MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-:- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUGOSIDIC LINKAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                            Score 48; DB 1; Length 376; Pred. No. 2.12e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.12e+00;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00128; alpha-amylase; 1.
GLYCOGEN BIOSYNTHESIS; TRANSFERASE; GLYCOSYLTRANSFERASE.
PROSITE; PS00139; THIOL_PROTEASE_CYS; FALSE_NEG.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
                                                                    GLYCOPROTEIN; SIGNAL. POTENTIAL.
                                                                                           LYMPHOPAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.

ACJECTC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 BY SIMILARITY.
464 BY SIMILARITY.
532 BY SIMILARITY.
81729 MW; 1ABB7637 CRC32;
                                                                                                                                                                                                                                                                                                                                                                           731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48;
                                         PFAM; PF00112; Cys-protease; 1
HSSP; P14080; 1YAL.
                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.6%;
62.5%;
                                                                                                                                                                                                                                           70.68;
                                                                    HYDROLASE; THIOL PROTEASE;
                                                                                                                                                                                                                                                       Local Similarity 100.0%;
                                                                                                                                                                                                                  42099
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z73902; E245020; -
                                                                                  21
376
153
153
331
191
191
352
352
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532
731 AA;
                                                                                                                                                                                     50
205
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               224 HRCHP 228
                                                                                                                                                                                                                                                                                                                         484 HRCHP 488
                                                                                                                                                                                                                                                                                                                                                                           GLGB_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                            Query Match
                                                                                SIGNAL
                                                                                               CHAIN
                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                         ô
```

612 NDIYRCHP 619

g

```
481 HAIHRCHP 488
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
POLG_POWL

POLG_POWL

POLG_POWL

Q0453B,

Q10453B,

Q10453B,

Q1-FEB-1995 (REL. 31, CREATED)

Q1-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

Q1-FEB-1998 (REL. 31, LAST ANNOTATION UPDATE)

GENOME POLYPROTEIN (CONTAINS CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED TICK-BORNE POWASSAN VIRUS (STRAIN LB).

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                     MANDL C.W., HOLZMANN H., KUNZ C., HEINZ F.X.;

"Complete genomic sequence of Powassan virus: evaluation of genetic elements in tick-borne versus mosquito-borne flaviviruses.";

VIROLOGY 194:173-184 (1993).

-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEBCAPSID COVERED BY A LIPPOPROTEIN ENVELOPE. CONSISTS OF TWO PROTEINS.

-!- FUNCTION AND GLYCOPROTEIN E. THE NUCLEBCAPSID IS A COMPLEX OF PROTEIN CAND AND MAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-DIRECTED RNA POLYMERASE (NSS).
HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPROTEIN; GLYCOPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE;
CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NONSTRUCTURAL PROTEIN NSI.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAJOR ENVELOPE PROTEIN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENVELOPE GLYCOPROTEIN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPSID PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONSTRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM, PF000869; Flavi_glycoprot; 1. PFAM; PF00948; Flavi_NS1; 1. PFAM; PF00949; Flavi_helicase; 1. PFAM; PF00972; Flavi_NS5; 1. PFAM; PF01002; Flavi_NS2B; 1. PFAM; PF01004; Flavi_Capsid; 1. PFAM; PF01004; Flavi_M; 1. PFAM; PF01005; Plavi_NS2A; 1. HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L06436; G309917; -. PIR; A46105; A46105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1128
1358
1489
2111
2260
2512
3415
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 93242744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    776
1129
11359
1490
2112
2261
2513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
```

ဖ

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1276 RNVYRCHP 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: | | | | | | 481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96305376
                            HTTQRCH 364
                                                1::|||
481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-KIDNEY;
 ..
                                                                                                    LT 10
YQ12_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                          C05C10.2
                            358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
 Matches
                                                                                                    THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE SULL THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                            g
                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                          ô
                                            HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOMLO S., REEDERS S.T.;
autosomal dominant polycystic
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                             Length 3415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 94140377.
WEINSTAT SASLOW D.L., GERMINO G.G., SOMLO S., REEDERS S.1.
"A transducin-like gene maps to the autosomal dominant pot kidney disease gene region."; GENOMICS 18:709-711(1993).
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                            ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                MW; A6887372 CRC32;
                                                                                                                                                                                                                                                                                                          Score 48; DB 1; Labred. No. 2.12e+00; 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1; L
Pred. No. 5.66e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2C1429C5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
WD-REPEAT PROTEIN SAZD.
                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 AA.
                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                         POTENTIAL.
                            POTENTIAL
                                                                          POTENTIAL
                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WD1.
WD2.
WD4.
WD5.
WD6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00678; WD_REPEATS; 2.
PFAM; PF00400; G-beta; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW.
                                                                                                                                                                                                                                                                                  378564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.68;
57.18;
                                                                                                                                                                                                                                                                                                             70.68;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56047
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
23
67
109
290
336
393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U02609; G414536;
                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
79
260
305
363
447
519 AA;
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       HKIHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT; WD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                  481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                3415
1453
2161
2191
2244
2347
2434
1688
1780
281
                                                                                                                                                                                                                                                                                                                                                                                                                                 9
SAZD_HUMAN
Q12788;
15-,TT
                                                                                                                                                                            DISULFID
                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                     NP_BIND
SITE
                                                                                                                  DISULFID
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                               Query Match
                                            TRANSMEM
                                                         TRANSMEM
                                                                         TRANSMEM
                                                                                                                                   DISULFID
                                                                                                                                                DISULFID
                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                       1597
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRP2_HUMAN STANDARD; PRT; 4655 AA.
P98164, 000711, 016215;
01-0CT-1996 (REL. 34, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
115-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
10W-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
(GLYCOPROTEIN 330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HJABLM G., MURRAY E., CRUMLEY G., HARAZIM W., LUNDGREN S., ONYANGO I., EK B., LARSSON M., JUHLIN C., HELLMAN P., DAVIS H., AEKERSTROEM G., RASK L., MORSE B.;
"Cloning and sequencing of human gp330, a Ca(2+)-binding receptor with potential intracellular signaling properties.";
EUR. J. BIOCHEM. 239:132-137(1996).
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATTHEWS P.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 1; Length 1551
Pred. No. 5.66e+00;
2; Mismatches 2; Indels
   Indels
                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
11 YPOTHETICAL 175,7 KD PROTEIN GOSCIO.2 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).
   ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z48178; E1351581; -.
WORNPEP; CO5C10.2; CE01466.
HYPOTHETICAL PROTEIN; ATP-BINDING; HELICASE.
NP_BIND 1021 1028 ATP (BY SIMILAR
      Mismatches
                                                                                                                                                                                                                                                                  PRT; 1551 AA
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1551 AA; 175699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 2705-4453 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 Match 67.6%;
Local Similarity 50.0%;
les 4; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAENORHABDITIS ELEGANS
```

```
(POTENTIAL).
      LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCIUM-BINDING
                          PROTEIN 2.
EXTRACELLULAR (POTENTIAL)
                                                                            (POTENTIAL)
                                                                                                      H 4 5 5 6 7
                                                                                                                                                                                                                                                                              H 4 M 4 M
                                                                                                                                                                                                                                                                                                                                                                                             9 1 8 6
                                                                                            LDL-RECEPTOR CLASS A 1
LDL-RECEPTOR CLASS A 2
LDL-RECEPTOR CLASS A 3
LDL-RECEPTOR CLASS A 4
LDL-RECEPTOR CLASS A 4
LDL-RECEPTOR CLASS A 5
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 4
LDL-RECEPTOR CLASS B 4
LDL-RECEPTOR CLASS B 5
LDL-RECEPTOR CLASS B 6
LDL-RECEPTOR CLASS B 6
LDL-RECEPTOR CLASS B 7
LDL-RECEPTOR CLASS B 9
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 1
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 2
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
LDL-RECEPTOR CLASS B 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             m m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
CLASS L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDL-RECEPTOR C
LDL-RECEPTOR C
LDL-RECEPTOR C
LDL-RECEPTOR C
LDL-RECEPTOR C
EGF-LIKE 11.
EGF-LIKE 11.
CGF-LIKE 11.
CGF-LIKE 12, C
LDL-RECEPTOR C
LDL-RECEPTOR C
                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1519
1608
1608
1695
1741
1831
1929
                                                                                                220012
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
22022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
2022
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1269
1310
1349
1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2342
2431
2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1478
1521
1566
1610
1700
1790
1833
1883
1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2018
2157
2157
2202
2246
2290
                                                        RANSMEM
                                                                                                DOMAIN
                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
    A MCDUNAS M.2., LOURINOVA E.B., STEFANSSON S., HARMONY J.A.K.,

A REWER B.H., STRICKLAND D.K., ARGRAVES W.S.;

BREWER B.H., STRICKLAND D.K., ARGRAVES W.S.;

T adolipoprotein J/clusterin.";

J. BIOL. CHEM. 270:13070-13075(1995).

C. -! FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY, BUT ALSO LIGANDS IN COMMON WITH OTHER FAMILY MEMBERS: PLASMINOGEN,

EXTRACELLULAR MATRIX COMPONINTS, PLASMINOGEN ACTIVATOR PLASMINOGEN,

EXTRACELLULAR MATRIX COMPONINTS, PLASMINOGEN ACTIVATOR INHIBITOR TYPE I COMPLEX, APOLIPOPROTEIN E-ENRICHED

C. - FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLIBASIC DRUGS SUCH AS

APROTININ, AMINOGLYCOSIDES AND POLIFMXXIN B (BY SIMILARITY).

C. - FUNCTION: MAY PARTICIPATE IN REGULATION OF PARATHYROID-HORMONE AND

PRARA-THYROLD-HORMONE-EREATED PROTEIN RELEASE.

C. - SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-

ASSOCIATED PROTEIN (RAP).

C. - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN MITH A RECEPTOR-

SOCIAL SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN WITH A RECEPTOR-

ASSOCIATED PROTEIN (RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics...and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           family
                                                                                                                                                                                                                                                                      MEDLINE; 9424704.
LUNGCREN S., HJALM G., HELLMAN P., EK B., JUHLIN C., RASTAD J., KLARESKOG L., AKERSTROM G., RASK L.; "A protein involved in calcium sensing of the human parathyroid and placental cytotrophoblast cells belongs to the LDL-receptor protein
                                                                                                               KORENBERG J.R., ARGRAVES K.M., CHEN X.N., TRAN H.,
STRICKLAND D.K., ARGRAVES W.S.;
"Chromosomal localization of human genes for the LDL receptor
member glycoprotein 330 (LRP2) and its associated protein RAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; PO1130; 1AJJ.
GLYCOPROTEIN; REPEAT; ENDOCYTOSIS; COATED PITS; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL PROXIMAL TUBULES.
KNAAK C., ARGRAVES W.S.;
SUBMITTED (DEC-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A 1-- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B 1-- SIMILARITY: CONTAINS 17 EGF-LIKE REPEATS.
-!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR; EGF-LIKE DOMAIN; SIGNAL; POLYMORPHISM SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                           EXP. CELL RES. 212:344-350(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00010; ASX_HYDROXYL; 4
PROSITE; PS01022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 9.
PROSITE; PS01209; LDLRA_1; 31.
PROSITE; PS50068; LDLRA_2; 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00057; ldl_recept_a; 36
PFAM; PF00058; ldl_recept_b; 37
                                                                                                                                                                                                                                                      SEQUENCE OF 4139-4406 FROM N.A.
                                                        SEQUENCE OF 3833-4453 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U33837; G1809240; -.
EMBL; U04441; G1389559; -.
EMBL; S73145; G685061; -.
                                                                                                                                                                                                                GENOMICS 22:88-93(1994).
                                                                            TISSUE-KIDNEY;
MEDLINE; 95048397
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95286588
                                                                                                                                                                                                                                                                                                                                                                         superfamily
                                                                                                                                                                                             (LRPAP1)
```

```
POTENTIAL
                                                                                                                                                                                                               HYDROLASE; HYDROGEN ION TRANSPORT.
                                                                                                                                                                                                                                              39790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERM; SIGNAL; FERTILIZATION. SIGNAL 1 20
                                                                                                                                 EMBL, L11584; G173171; -.
EMBL, U22382; G717067; -.
PIR; S35105; S35105.
PIR; A45994; A45994.
SGD; L0002461; VMA6.
                                                                                                                                                                                                                                                                            66.2%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M59490; G161443; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACROSOME GRANULE.
                                                                                                                                                                                                                                                345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B40552; B40552
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRONGY LOCENTROTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 92130802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                              129
                                                                                                                                                                                                                                                                                                                                                                ::||||
483 IHRCHP 488
                                                                                                                                                                                                                                                                                                                                              124 LORCHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                         BIND_STRFN P23118;
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MADELINE; 93286119.

A BAUERLE C., HO M.N., LINDORFER M.A., STEVENS T.H.;

BAUERLE C., HO M.N., LINDORFER M.A., STEVENS T.H.;

BAUERLE C., HO M.N., LINDORFER M.A., STEVENS T.H.;

The Ascolar conveces cerevisiae Was6 gene encodes the 36-kDa subunit of the vacuolar H(+)-ATPRASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPATIBLE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPATIBLES IN BUNARYOTIC CELLS. THE ACTIVE ENZYME CONSISTS OF A CATALYTIC VI DOMAIN ATTACHED TO AN INTEGRAL MEMBRANE COMPONENT OF THE MEMBRANE PORE DOMAIN AND IS REQUIRED FOR PROPER ASSEMBLY OF THE WEMBRANE PORE DOMAIN AND IS REQUIRED FOR PROPER ASSEMBLY OF VI SUBUNITS ONTO THE MEMBRANE SECTOR OR ALTERNATIVELY MAY PREVENT THE PASSAGE OF PROTONS THROUGH VO PORES.

C. I. SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.

C. I. SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.

C. I. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS V-ATPASE SUBUNIT C.
LDL-RECEPTOR CLASS B 32.
LDL-RECEPTOR CLASS B 33.
LDL-RECEPTOR CLASS B 34.
EGF-LIKE 13.
LDL-RECEPTOR CLASS A 26.
LDL-RECEPTOR CLASS A 29.
LDL-RECEPTOR CLASS A 30.
LDL-RECEPTOR CLASS A 31.
LDL-RECEPTOR CLASS A 31.
LDL-RECEPTOR CLASS A 31.
LDL-RECEPTOR CLASS A 31.
LDL-RECEPTOR CLASS A 33.
LDL-RECEPTOR CLASS A 34.
LDL-RECEPTOR CLASS A 34.
LDL-RECEPTOR CLASS A 35.
LDL-RECEPTOR CLASS A 36.
LDL-RECEPTOR CLASS A 36.
LDL-RECEPTOR CLASS A 36.
LDL-RECEPTOR CLASS A 36.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECEPTOR CLASS B 37.
LDL-RECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                          CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT) (V-ATPASE AC39
VMA6 OR YIE447C OR L934.8.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (REL. 27, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
VACUOLAR APP SYNTHASE SUBUNIT AC39 (EC 3.6.1.34) (V-ATPASE AC39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                           CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 4655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 93286119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                   33418
3550
3550
3550
3532
3716
3716
3756
3756
                                                                                                                                                                                                               33923
33923
340064
420064
4233
44233
4424
44268
44411
4526
4526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 HDVHKCSP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 HAIHRCHP 488
                                                                                                                                                                                                                                 3926
3966
4007
4154
4197
                                                                                                                                                                                                                                                                                                                                                           1742
4526
4598
                                                                                                                                                                                                                881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VATX_YEAST
P32366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: remainder
                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                           SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
    DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ά
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELIMINARY SEQUENCE OF 248-320.

VACCUIER V.D., MOY G.W.;

(IN) DIRKSEN E.R., PRESCOTT D., FOX C.F. (EDS.);

CELL REPRODUCTION. PP.12:379-389, ACADEMIC PRESS, NEW YORK (1978).

-!- FUNCTION: SPECIES-SPECIFIC SEA URCHIN SPERM PROTEIN REQUIRED FOR ADHESION OF SPERM TO THE EGG SURFACE DURING FERTILIZATION. BINDIN COATS THE ACROSOMAL PROCESS AFTER IT IS EXTERNALIZED BY THE PLOYSACCHARIDES ON THE VITELIANE LAYER RECEPTOR PROTEGLYCANS.

WHICH COVER THE EGG PLASARA MEMBRANE.

-!- SUBCELLULAR LOCATION: MAJOR PROTEIN COMPONENT OF THE LUMEN OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINOR J.E., FROMSON D.R., BRITTEN R.J., DAVIDSON E.H.;
"Comparison of the bindin proteins of Strongylocentrotus
"Itanciscanus, S. purpuratus, and Lytechinus variegatus: sequences
involved in the species specificalty of fertilization.";
MOL. BIOL. EVOL. 8:781-795(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRONGYLOCENTROTUS FRANCISCANUS (SEA URCHIN).
EUKARYOTA, METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
EUECHINOIDEA; ECHINACEA; ECHINOIDA; STRONGYLOCENTROTIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N -> T (IN REF. 1).
76C2B483 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1; L
Pred. No. 9.16e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 20, CREATED)
(REL. 20, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO OTHER SEA URCHINS BINDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
```

```
Search completed: Thu May 20 13:19:13 1999 Job time : 12 secs.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      MEDLINE; 84183604.

DEKKER B.M.M., VAN ORMONDT H.;

DEKKER B.M.M., VAN ORMONDT H.;

The nucleotide sequence of fragment HindIII-C of human adenovirus type 5 DNA (map positions 17.1-31.7).";

GENE 27:115-120(1984).

-!-CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -

N PYROPHOSPHATE + DNA (N).

-!-THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.

-!-SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                       HUMAN ADENOVIRUS TYPE 5.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN ADENOVIRUS TYPE 2.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.
 BINDIN.
FUCOSE-BINDÎNG DOMAIN (POTENTIAL)
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00116; DNA_POLYMERASE_B; 1.
TRANSFERASE; DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION;
DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 1; Length 1056; Pred. No. 9.16+00; 4; Mismatches 0; Indels
                                                             Score 45; DB 1; Length 485;
Pred. No. 9.16e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1056 AA; 120400 MW; 822A9B85 CRC32;
                          POLY-GLU.
60193AAB CRC32;
                                                                                                                                                                                                                    13-AGC-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1056 AA
                                                                                                                                                                                              PRT; 1056 AA
248 485 BIX
371 379 FUG
399 406 POI
485 AA; 51940 MW; (
                                                               66.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.2%;
Similarity 42.9%;
3; Conservative
                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X02996; G58495; -.
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN ADENOVIRUS TYPE
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 3; Conser
                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 83056843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::|||:
481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 QPVHRCQ 87
                                                                                                                  146 VHRCH 150
                                                                                                                                  :||||
483 IHRCH 487
                                                                                                                                                                                 RESULT 14
ID DPOL_ADE05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPOL_ADE02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
 CHAIN
DOMAIN
                            DOMAIN
                                                                                         Matches
 SFF
                                                                                                                  8
                                                                                                                                           δ
                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
GINGERAS T.R., SCIAKY D., GELINAS R.E., BING-DONG J., YEN C.E., KELLY M.M., BULLOCK P.A., PARSONS B.L., O'NETLL K.E., ROBERTS R.J.; "Nucleotide sequences from the adenovirus-2 genome."; ". B. D.C. CHEM. 257:13475-13491(1982).
                                                                                                                                                                                                               MEDLINE; 83056844.

ALESTROM P., AKUSJARVI G., PETTERSSON M., PETTERSSON U.:

"DNA sequence analysis of the region encoding the terminal protein
and the hypothetical N-gene product of adenovirus type 2.";
J. BIOL. CHEM. 257:13492-13498(1982).

-! CATALYICA CATIVITY: N DEOXXNUCLEOSIDE TRIPHOSPHATE -

N PYROPHOSPHATE + DANA(N).

-! THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.

-: SIMILARITY: BELONGS TO DNA POLYWERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A00711; WMAD12.
PROSTE: PS00116; DNA_POLYMERASE_B; 1.
TRANSFERASE; DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION;
DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1; Length 1056;
Pred. No. 9.16e+00;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1056 AA; 120432 MW; C53DE5E4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.2%;
Best Local Similarity 42.9%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J01917; G209822; -.
                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::|||:
481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 QPVHRCQ 87
```

****	(TM)	*****
*****		*****
***	·=====================================	****
* * * * * *	'	****
*****		******
******		******
***************************************		***************************************
******		******
******		*****

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 20 13:19:31 1999; MasPar time 5.62 Seconds 77.652 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-099-053-2 (481-488) from US09099053.pep (6 of 6) Description: Perfect Score:

1 HAIHRCHP 8 Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 Post-processing:

summaries

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 20.687; Variance 24.857; scale 0.832

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

; SUMMARIES

1.92e+00 1.92e+00 1.92e+00 1.92e+00 1.92e+00 1.92e+00 5.29e+00 5.29e+00 5.29e+00 5.29e+00 5.29e+00 5.29e+00 6.29e+00 6.20e+00 6.2 1.42e+01 1.42e+01 1.42e+01 FRUCTOSE-BISPHOSPHATE
ALKYL-DIHYDROXYACETONE
POLYPROTEIN.
POLYPROTEIN.
HYPOTHETICAL 45.4 KD P
SPADETAIL. PROTEIN A.
SIMILAR TO LIGAND-GATE
PROTEIN A.
65KDA VIRAL REPLICASE
REVERSE TRANSCRIPTASE
EPSTEIN-BARR VIRUS LAT
EXPRESSED SEQUENCE TAG
CORE PROMOTER BINDING ORF IS HOMOLOGOUS TO U T-BOX CONTAINING PROTE SIMILARITY TO GALECTIN Description 0000818 000224 0002240 00452187 0088493 010388 010388 0003383 0004620 0093383 0004620 0004620 004620 004620 004620 004620 004620 004620 004620 004620 004620 004620 006631 006631 006631 006631 006631 006631 006631 006631 006631 006631 006631 006631 006631 143 2 346 5 346 5 3414 14 3414 14 470 13 470 13 6932 16 993 16 998 14 1046 15 173 11 Query Match Length DB Score Result

1.42e+01	1.42e + 01	1.42e + 01	1.42e+01	1.42e+01	1.42e+01	1.42e + 01	1.42e + 01	۳.	2.30e+01	2.30e+01	2.30e+01	ĕ.	2.30e+01	٣.		۳.	3	3.71e+01	.7	3.71e+01	. 7	3.71e+01	3.71e+01	3.71e+01
BCD ORF2.	HYPOTHETICAL 25.3 KD P	F54B8.2 PROTEIN.	WOSB10.4 PROTEIN.	ZINC FINGER PROTEIN.	DNA-BINDING PROTEIN CP	HYPOTHETICAL 136.8 KD	STILL LIFE TYPE 2.	SEMAPHORIN E.	SEMAPHORIN E PRECURSOR	COLLAPSIN-2.	BIOTIN SULFOXIDE REDUC	STK9 PROTEIN.	C44H9.4 PROTEIN.	CllE4.6 PROTEIN.	HYPOTHETICAL 156.7 KD	FATTY ACID SYNTHASE.	LOW DENSITY LIPOPROTEI	ORF27.	MATRIX PROTEIN.	CELL DIVISION CYCLE 37	CELLULOSE SYNTHASE ISO	METALLOPROTEASE-DISINT	PUTATIVE GUANINE-NUCLE	PC6B (FRAGMENT).
043839	080201	045560	P91575	035819	099612	042649	22	099985	062181	090663	025163	~	018633	093203	005819	048926	061291	036377	083833	024276	022989	088839	P87141	062040
4	σ	Ŋ	'n	11	4	m	Ŋ	4	11	13	~	4	Ŋ	Ŋ	~	7	11	14	14	'n	10	11	m	11
215	216	253	255	283	290	1194	2044	751	751	761	196	1030	1106	1125	1461	2796	4545	292	364	389	730	815	1313	1548
9	•	66.2	9	ė.	66.2	9		64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	ω.	63.2		63.2	m	63.2	63.2
45	45	45	45	45	45	45	45	44	44	44	44	44	44	44	44	44	44	43	43	43	43	43	43	43
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ö

ö

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLAVIVIRUS
                                                                                                                                                                                                                                                                                                      ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 5
Q88493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RE
   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
               MEDLINE; 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAINES C., BERKS M., COULSON A., WILSON R., AINSCOUGH R., ANDERSON K., BAINES C., BERKS M., COULSON A., EDNTELED J., BURTON J., CONPELL M., COPERT T., COPER J., COLLSON A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., PREKY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., STADEN R., SULGTON J., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULGTON J., THOMAS K., VAUUDIN M., VAUGHAN K., WATERSTON R., WATERSTON R., WATERSTON P., SHOWNKEEN R., STADEN R., WEINSTOK L., WHIKKINSON SPROAT J., WHOLDMAN P.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; SPIRURIA; SPIRURIDA;
FILARIOIDEA; ONCHOCERCIDAE; ONCHOCERCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 5; Length 360;
Pred. No. 1.92e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.T 4 PRELIMINARY; PRT; 597 AA. 045218. 01-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) ALKYL-DIHYDROXYACETONEPHOSPHATE SYNTHASE (EC 2.5.1.26) (ALKYLGLYCERONE-PHOSPHATE SYNTHASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-FOREST;
JOSEPH G.T., HUIMA T., LUSTIGMAN S.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U96178; G1945479; -.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
PROSITE; PS00274; g1ycolytic_enzy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01157;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOVATION UPDATE)
FRUCTOSE-BISPHOSPHATE ALDOLASE (FRAGMENT).
ONCHOCERCA VOLVULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 5; L
Pred. No. 1.92e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 281054; E1345139; -.
PROSITE; PS00027; HOMEOBOX_1; 1.
HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN.
SEQUENCE 346 AA; 39989 MW; 71016FFF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 AA; 39166 MW; 090B2E33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE). CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 HDVHRCQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|||:
481 HAIHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||||
481 HAIHRC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 HSIHRC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT

1D 04

AC 04

AC 04

DT 01

DT 01

DD AL

OC EU

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

CA RH

C
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
STRAIN-NEUDOERFL;
MEDLINE: 96036491.
WALLENER G., MANDL C.W., KUNZ C., HEINZ F.X.;
WALLENER G., MANDL C.W., KUNZ C., HEINZ F.X.;
"The flavivirus 3'-noncoding region: extensive size heterogeneity independent of evolutionary relationships among strains of tick-borne encephalitis virus.";
VIROLOGY 213:169-178(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANDL C.W., HEINZ F.X., KUNZ C.; "Sequence of the structural proteins of tick-borne encephalitis virus (western subtype) and comparative analysis with other flaviviruses."; VIROLOGY 166:197-205(1988)
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANDL C.W., HEINZ F.X., STOCKL E., KUNZ C.; "Genome sequence of tick-borne encephalitis virus (Western subtype) and comparative analysis of nonstructural proteins with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TICK-BORNE ENCEPHALITIS VIRUS (TBEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                           Score 49; DB 5; Length 597; Pred. No. 1.92e+00; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANDL C.W.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U27495; G975238; -
PPRM; PF00869; Flavi_glycoprot; 1.
PFAM; PF00948; Flavi_NSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, CREATED)
01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                   597 AA; 66559 MW; AFFB98EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 3414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00949; Flavi_helicase; 1.
PF00972; Flavi_NS5; 1.
PF01002; Flavi_NS2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01003; Flavi_capsid; 1. PF01004; Flavi_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 773-3414 FROM N.A.
                                                                                                                                                                                                                                                                                                                             72.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-790 FROM N.A. STRAIN-NEUDOERFL; MEDLINE; 88322870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIROLOGY 173:291-301(1989).
                                                                                                                                                                                                                                      EMBL; AJ002686; E1248248;
                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q88493;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=NEUDOERFL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NEUDOERFL;
MEDLINE; 90051080.
                                                                                                                                                                                                                                                                                                                                                                                                                       338 AIQRCQP 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 AIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flaviviruses.
                                                                                                                                                                                                                                                           TRANSFERASE.
SEQUENCE 5
```

g

```
STEALN 263;
MEDLINE; 96036491.
WALLINER G., MANDL C.W., KUNZ C., HEINZ F.X.;
"The flavivirus 3'-noncoding region: extensive size heterogeneity independent of evolutionary relationships among strains of tick-borne independent of evolutionary relationships
                                                                                                                          IICK-BORNE ENCEPHALITIS VIRUS (TBEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 14; Length 3414;
Pred. No. 1.92e+00;
3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 5; Length 393;
Pred. No. 5.29e+00;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 45.4 KD PROTEIN C30G12.7 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATREILLE P.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03C4BD6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AD83C19E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 AA
                                                                                                                                                                                                                                                                                                                                                                    oncephalitis virus.";
VIROLOGY 213.169-178(1995).
PRAM; PRO0869; Elavi_Glycoprot; 1.
PRAM; PRO0948; Flavi_Glycoprot; 1.
PRAM; PRO0949; Flavi_Losi. 1.
PRAM; PRO0972; Flavi_NS5; 1.
PRAM; PRO1002; Flavi_NS5; 1.
PRAM; PRO1003; Flavi_NS2B; 1.
PRAM; PRO1004; Flavi_Lospsid; 1.
PRAM; PRO1005; Flavi_Cappsid; 1.
PRAM; PRO1005; Flavi_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3414 AA; 378064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.1%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U21319; G687839; -.
WORMPEP; C30G12.7; CE01838.
PFAM; PF00806; PUF; 8.
HYPOTHETICAL PROTEIN; REPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYPROTEIN.
SEQUENCE 3
                                                                                                                                                                             FLAVIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 8
Q09487
Q09487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C30G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
     ACCOORDINATION OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF THE STAND OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOUPING ILL VIRUS (LI).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
FLAVIVIRUS.
                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97321792.
MEDLINE; 97321792.
GRITSUN T.S., VENUGOPAL K.; DE ZANOTTO P.M., MIKHAILOV M.V.,
SALL A.A., POLKINGHORNE I., FROLOVA T.V., POGODINA V.V.,
LASHKEVICH V.A., GOULD E.A.;
"Complete sequence of two tick-borne flaviviruses isolated fire solution the UK: analysis and significance of the 5' and 7'-ITTRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 14; Length 3414;
Pred. No. 1.92e+00;
3; Mismatches 1; Indels (
                                                                                              Score 49; DB 14; Length 3414;
Pred. No. 1.92e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRITGUN T.S.;
GRITGUN T.S.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; YO7863; E281315; --
EMBL; YO7863; E281315; --
PFAM; PF00949; Flavi_Allicase; 1.
PFAM; PF00949; Flavi_Lalicase; 1.
PFAM; PF00949; Flavi_Lalicase; 1.
RPFAM; PF00075; Flavi_NS29; 1.
RPFAM; PF01003; Flavi_NS29; 1.
RPFAM; PF01003; Flavi_Lapsid; 1.
RPFAM; PF01004; Flavi_Layi_M; 1.
RPFAM; PF01005; Flavi_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPEID (CORE) PROTEIN.
PREMEMBRANE PROTEIN.
MENURANE PROTEIN.
ENVELOPE PROTEIN.
NONSTRUCTURAL PROTEIN.
NONSTRUCTURAL PROTEIN.
NONSTRUCTURAL PROTEIN.
NONSTRUCTURAL PROTEIN.
NONSTRUCTURAL PROTEIN.
NONSTRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA POLYMERASE.
MW; 7D0A5DDE CRC32;
                                                  9CA32E8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN; MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                         01-001-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                3414 AA; 378320 MW;
PFAM; PF01005; Flavi_NS2A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1128
1358
1358
2110
2210
2259
2511
378410 P
                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.1%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3'-UTRS.";
VIRUS RES. 49:27-39(1997).
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-369/T2;
                                                                                                                                                                                               1597 HEVHQCQP 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1597 HEVHQCQP 1604
                                                                                                                                                                                                                                481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|:|
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1359
1490
2111
2250
3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF01004
PFAM; PF01005
POLYPROTEIN; E
CHAIN 11
CHAIN 12
                            POLYPROTEIN
                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       010383;
                                                                                                                                                                                                                                                                                                                         LT 6
010383
```

SOUPLIE CHARLE SOUPLE S

ö

Gaps

ö

ö

Gaps

ö

164 HVIHRC 169

g

PRT; 3414 AA.

PRELIMINARY;

LT 7 Q88489

RESULT ID Q8

셤 ò

CHAIN

4

O93389;

481

οy

```
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
SIMILARITY TO GALECTIN-3 BINDING PROTEIN.
A_IGOOZNO1.13.
A_RABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; ENBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIINA; RHABDITOIDEA; RHABDITIIDAE; PELODERINAE; CAENORHABDITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLACK BEETLE VIRUS (BBV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE: NODAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 893-897 FROM N.A.
GUARINO L.A., GHOSH A., DASMAHAPATRA B., DASGUPTA R., KAESBERG
VIROLOGY 139:190-203(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
MEDLINE; 85210903.
DASWHAPATRA B., DASGUPTA R., GHOSH A., KAESBERG P.;
"Structure of the black beetle virus genome and its functional implications.";
                                                                                                                                                                                                                                                                                                                                                                Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 14; Length 897
Pred. No. 5.29e+00;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
SCHEET P., MAGGI L.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                       SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF007269; G2191134; -.
SEQUENCE 705 Aa; 78735 MW; 6559COCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04, CREATED)
04, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 10; Le
Pred. No. 5.29e+00;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 AA; 101870 MW; 54B851CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEINS. 2C196.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                897 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. MOL. BIOL. 182:183-189(1985)
EMBL; K02560; G210670; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02,
02,
08,
                                                                                                                                                                                                                                                                                                                                                                69.1%;
similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.1%;
Similarity 62.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 PRELIMINARY;
001623 001623;
01-011-1997 (TREMBLREL. 0
01-JUL-1997 (TREMBLREL. 0
01-JUL-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JUT 12
096631
096631;
01-FEB-1997 (TREMBLREL. 0
01-FEB-1997 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
WATERSTON R.;
SUBMITTED (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||:|:|
481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 HKIHHCRP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::||||
482 AIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                    306 GVRRCHP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NODAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                              BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ÀCTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
GRIFFIN K.J.P., ANACHER S.L., KIMMEL C.B., KIMELMAN D.;
GRIFFIN K.J.P., ANACHER S.L., KIMMEL C.B., KIMELMAN D.;
Molecular identification of spadetail: regulation of zebrafish trunk
and tail formation by T-box genes.";
DEVELOPMENT 125:0-0(1998).
EMBL, AF077225; G3396048; -.
EMBL, AF077225; G3396048; -.
EMBL, F901281; PS01264; TBOX_L; 1.
SEQUENCE 470 AA; 52579 MW; F76B4182 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the zebrafish tbx16 gene and evolution of the vertebrate T-box family.";
DEV. GENES EVOL. 208:99-99(1998).
EMBL: AF044977; G3273697; -..
PROSITE: PS01264; TB0X_2: 1.
PROSITE: PS01208; TB0X_1: 1.
SEQUENCE 470 AA, 55618 MW; 74BBB7AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 13; Length 470;
Pred. No. 5.29e+00;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
T-BOX CONTAINING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 11 004620 PRELIMINARY; PRT; 705 AA. 004620 004620. 01-JUL-1997 (TREMBLREL. 04, CREATED) 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 13; I
Pred. No. 5.29e+00;
2; Mismatches 1;
                                                                          470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO)
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 98237855.
RUVINSKY I., SILVER L.M., HO R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.1%;
larity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.1%;
larity 62.5%;
Conservative
                                                                                                       01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, SPADETAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 HSMHRYHP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 HSMHRYHP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 HAIHRCHP 488
   HAIHRC
```

093303; ,T 10 093303

TBX16

RESULLT ON THE O

Matches

g

ò

RESULT

E P P E

1

Query Match

Matches

원 ò ô

Gaps

0

ö

Gaps

ö

```
F57C2.6 PROTEIN.
F57C2.6.
                                                                                                                                                              BAYNES
    DDE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE READ BE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ά
         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN-BRISTOL N2;

X MEDLINE; 9415071B

A MILGON R., AINDERSON K., BAYNES C., BERKS M.,

A MILGON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

A GARTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,

A GARDNE M., RERSHAW J., KIRSTEN Y., LAISTER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAITERILLE P.,

RA PARSONS J., PERCY C., RIFKEN L., STOOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., SONNHAMMER E., STADEN R., SHOWNKEEN R.,

RA MALDON N., SMATH A., SONNHAMER E., STADEN R., SHOWNKEEN R.,

RA THIERRY-MIEG J., THOMAS R., VAUDIN M., VAUGHAN K., WATERSTON P.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLOCK HOUSE VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; NODAVIRIDAE;
NODAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 5; Length 932; Pred. No. 5.29e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
WATERSTON R.;
WATERSTON R.;
EMBL, 097007; G1938466; --
EMBL, 097007; G1938466; --
PFAM; PF00060; 11g_chan; 2.
SEQUENCE 932 AA; 106836 MW; 469F21FA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DASGUTA R.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X77156; G450501; -.
SEQUENCE 998 AA; 112187 MW; D6FAA9FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 14; I
Pred. No. 5.29e+00;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08,
09,
                                                                                                                                                                                                                                                                                                                                                                                                                                :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.1%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 69.1%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
ID 045243
AC 045243; 045597;
DI 01-0NN-1998 (TREMBLREL. 06
DT 01-NOV-1999 (TREMBLREL. 06
DT 01-JAN-1999 (TREMBLREL. 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL. (
TREMBLREL. (
TREMBLREL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 HAIHRCHP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 HKIHHCRP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          867 IHRCH 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 IHRCH 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
ID Q66929
AC Q66929;
DT 01-NOV-1996 (
DT 01-NOV-1996 (
DT 01-NOV-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MURRAY J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
```

```
ö
                                                                                                                                                                                                                                                                         MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPERT T., COOPER J., COULSON A.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JOIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

EARSON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

THERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2. L. M. Of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                             EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 5; Length 513; Pred. No. 8.70e+00; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z83110; E3347306; ...
EMBL; Z81462; E1347306; JOINED.
EMBL; Z81462; E1343632; ...
EMBL; Z8110; E1343632; JOINED.
SEQUENCE 513 AA; 57037 MW; EDE4821B CRC32;
                                                                                                                                                                                                              SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: Thu May 20 13:21:35 1999 Job time: 124 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.6%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans.";
NATURE 368:32-38(1994).
CAENORHABDITIS ELEGANS.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 PLQRCHP 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 AIHRCHP 488
```

*****	(TM)	

****	'	

*****		****
****) 	****

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Thu May 20 16:27:55 1999; MasPar time 3568.62 Seconds 1202.402 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-099-053-1 (1-1548) from US09099053.seq 1548 Description: Perfect Score: N.A. Sequence:

1 GCTCGCGGGCTCCCATGCC.......CCAACGCTCTGGGCTCCAGC 1548
CGAGCGCCCGAGGGTACCGG.......GGTTGCGAGACCCGAGGTCG

TABLE jmetric Gap 60 Scoring table:

Dbase 0; Query 0 Nmatch STD 646147 seqs, 1385953633 bases x Searched:

N

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_huml 6:em_hum2 7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph 13:em_tpl 14:em_ro 15:em_sts 16:em_vi

Database:

17:gb_bal 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1 22:gb_ln2 23:gb_om 24:gb_ov 25:gb_pat 26:gp_ph 27:gb_pl 22:gb_pl 29:gb_pl 20:gb_pl 20:

Mean 9.259; Variance 3.020; scale 3.066 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	le-11	3.91e-11	10e-02	2.11e-01	2.11e-01	1.40e-02	1.23e+00	L.23e+00	23e+00	23e+00	.23e+00	.23e+00	.23e+00
		Pre	π	m	3.4	~	7	θ,	-	4	-	ä		~1	Н
		Description	Mouse mRNA for tyrosin	Mouse mRNA for srm (ty	Syrian golden hamster	Drosophila melanogaste	Drosophila melanogaste	Homo sapiens clone DJ0	Mus musculus protein t	Rous sarcome virus Pra	Human hemopoietic cell	Human hemopoietic cell	H.sapiens HCK gene for	Xiphophorus c-fyn (Xfy	Duck adapted Rous sarc
		OI.	MUSTSPK	MUSSRM	HAMNEU	DME132670	AC006494	AC004929	MUSPTKV	RERSVSRC	HUMHCKB	HUMHCKA	HSHCKE11	XHCFYN	RSVPRSRC
		DB	32	32	32	21	20	19	32	37	29	29	30	24	37
		Match Length DB	2393	2560	4062	5423	162815	183180	211		1926			2526	2545
æ	Query	Match	2.1	2.1	1.4	1.4	1.4	1.4	1.3	1.3	1.3	1.3	1.3	1.3	1.3
		Score	32	32	22	21	21	22.	20	20	20	20	20	20	20
	Result	No.		7	ю	4	_C	و ن	7	ထ	თ	10	11	12	13

Mol. Cell. Biol. 14 (10), 6915-6925 (1994)
95021220
Submitted (24-Dec-1993) to DDBJ by:
Nachiro Kohmura
Dapartment of Neurobiology and Behavioral Genetics National Institute for Physiological Sciences
Myodaiji, Okazaki 444

JOURNAL MEDLINE COMMENT

Location/Qualifiers
1. 2393
/organism="Mus musculus"
/db_xref="taxon:10090"

source

FEATURES

Japan Phone:0564-55-7741 Fax: 0564-55-7744

	14	0		64		DRAJ503	1.23	
	15	20	6.1	3123	32		r H-19 provi	
υ	17			35		HSDRD2I	M. auratus H-19 provira 1.23 H. sapiens DRD2 gene, 1 1.23	
	18	0 0		51			1.23	
	200			3.5			1.6	
•	21			391			1.23	
	22	0		962			Rous sarcoma virus (Pr 1.23	
υ	23		•	92		AF050737	Homo sapiens dopamine 1.23	
O	25	ാത		808			Homo sapiens RET proto 6.74	
	26	. n		0.2		CHKMYO	Chicken mRNA for myoge 6.74	
	27	o n 1	•	16			H.sapiens mRNA cdk3 fo 6.74	
	28	on c		57			Drosophila melanogaste 6.74	
	30	ת מי		7 89 7 89			Human DNA repair and r 6.74	
	31	, o		76			Homo sapiens RGS-GAIP 6.74	
	32	σ.	•	17			Mus musculus c-Src kin 6.74	
υ	33	on c	٠	84			S.galbus DSM 40480 gen 6.74	
C		nσ	•	85			Actomolias caviae nemoi o./4	
	36	n 01		127			Rat mRNA for protein-t 6.74	
	37	a		044			Methanobacterium therm 6.74	
	38	on.	•	175			Human DNA sequence fro 6.74	
υ	39	መ	7	4363			Homo sapiens chromosom 6.74	
	40	ത	7	0238			Drosophila melanogaste 6.74	
	41	თ (7	1132			Human Chromosome 11 BA 6.74	
υ	2.5	a c	ų,	5118			Human DNA sequence *** 6.74	
	2 4 4 2 4 4	ח מ		151965			Homo sapiens clone DJU 6.74	
	45	n or		9285			Homo sapiens FAC Cione 0.74	
	!		!					
٠						ALIGNMENTS	Ŋ	
RESULT	LT 1							
LOCUS	Ñ		Ϋ́	23	93]	mRNA	ROD	
DEFI	DEFINITION		mRN.	A for	tyr	sine-speci	fic protein kinase, complete cd	
NID	1010							
VERSION	NOI	D26186.1 GI:529072	5.1	GI:52	907	2		
KEYW	KEYWORDS	tyrosi	lne-s	specif	10	rotei		
SOURCE	5	Mus mi	iscu.	lus ad	ult	Lung	cDNA to mRNA, clone_lib:5' stretch.	
Š	Ę	Fukare	musculus ryota · M	rus . Mota	0	. chordata.	400	
		Rodent	ia;	Sciur	000	Rodentia; Sciuroquathi; Muridae; Mu	urinae; Mus.	
REFE		1 (be	ses	1 to	239	3)		
AU	AUTHORS	Kohmui	ra, N					
II.		Direct	lns :	omissi GALD	g c	74 04 16001	TOO CHART & SECTION TOWNS T	
2		Kohmut	ָם מיקי	7.4.7 Va†ion	ے ر ام	Thatitute fo	o/Embr/cembank darabases	5
		Neurok	piole	ogy &	Beh	avioral Gene	; 38 Nishigonaka, Myodaiji	
		Okazak	¢i, λ	Aichi	444	Japan (Te	4-55-7744, Fax:0564-55-77	
REFE	REFERENCE	2 (be	ses	1 1 1	239	3)		
AU		Kohmui	z z	Yag, ر.	T, 1	., Tomooka,	, Oye	
II	TILE	A novel nonreceptor t	3, N.	onrece	a to	., ikawa,i. d r tyrosine ki	Ĭ	
		disruption	otion					
50	JOURNAL	Mol. C	[e]]	. Biol	٦.	4 (10), 6913	5-6925 (1994)	

N

```
9493236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                       polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                              QIPLVQDEWERPRSEFVFGRKLGEGFFGEVWEGLWLGSIPVAVKVIKSADMKLADLTK
EIBALKSLRHERLIRLHAICSLGEPVYIVTELMGKGNLQVYLGSSEGKALSLPHLLGF
ACQVAEGMSYLEERRVVHRDLAARNVLVGDDLTCKVADFGLARLLKDDVYSPSSGSKI
                                                                                                                                                                                                                                                                                                                                                                   PVKWTAPEAANYRVESQKSDVWSFGILLYEVFTYGQCPYEGMTNHETLQQISRGYRLP
RPAVCPAEVYVLMVECWKGSPEERPTFAILREKLNAINRRLHLGLT"
                                                                                                                                                                                                                                      /translation-"MEPFLRKRLTFLSFFWDKIWPADESEEDIPRIOGHDDNPVPEQA
AAVEPCSFPAPRARLFRALYDFTARCAEELSVSGGDRLYALKEEGDYIFAQRLSGPPS
TGLVPVTYLAKATPEPPSDQPWYFSGISRAQAQQLLLSPANAPGAFLIRPSESSIGGY
                                                                                                                                                                                                                                                                                               SLSVRAQAKVCHYRICMAPSGSLYLQEGQLFPSLDALLAYYKTNWKLIQNPLLQPCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-FEB-1995) to the DDBJ/EMBL/GenBank databases. Yasuhiro Kawachi, Institute of Clinical Medicine, University of Tsukuba, Department of Dermatology; 1-1-1, Ten-nodai, Tsukuba city, Ibaraki 305, Japan (E-mail:nakauchi@ttcsl.riken.go.jp, 72: (Dases 1 to 2560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of a novel cDNA clone encoding protein tyrosine kinase in murine skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             srm; tyrosine kinase.
Mus musculus (strain:C57BL/6) adult male thymus cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                               /product-"tyrosine-specific protein kinase"
/protein_nd=BaA0531.1"
/db_xref="PID:d1005873"
/db_xref="PID:g529073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSSRM 2560 bp mRNA ROD 1
Mouse mRNA for srm (tyrosine kinase), complete cds.
D49427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 32;
Pred. No. 3.91e-11;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Invest. Dermatol. 21, 533-538 (1995)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawachi, Y., Nakauchi, H. and Otsuka, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014 GGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTC 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 GGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTC 803

    .2560
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="srm"
/protein_id="BAA08406.1"
/clone_lib="5' stretch"
/dev_stage="adult"
/tissue_type="lung"
279. .1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="thymus"
447. .1937
                                                                                                                                                                                                                     /db_xref="G1:529073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6"
                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                         gene="srm"
                                                                                                                                                                                                                                                                                                                                                                                                       1934. .2008
2369. .2374
                                                                                                             /gene="srm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%;
Best Local Similarity 100.0%;
Matches 32; Conservative
                                                                                              .1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:684971
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 889
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawachi,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g684971
D49427.1
                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
polyA_signal
polyA_site
BASE COUNT 525 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
/db_xref="PID: 9684972"
/db_xref="PID: 9684972"
/db_xref="TiD: 9684972"
/db_xr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-receptor; cellular oncogene; neu-differentiation factor/heregulin; p-185; tyrosine kinase. Mescoricetus auratus (individual_isolate animal 14) peripherall nerve neoplastic Schwann cell cell-line 14-2 (library: NIH3T3) cDNA to mRNA, clone pSHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-MAY-1993) to the DDBJ/EMBL/GenBank databases. Takurc Makamura, Faculty of Medicine, University of Tokyo, Department of Pathology, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111(ex:3356), Fax:03-3815-8379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura,T., Ushijima,T., Ishizaka,Y., Nagao,M., Arai,M., Yamazaki,Y. and Ishikawa,T. Cloning and activation of the Syrian hamster neu proto-oncogene Gene 140 (2), 251-255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euthe:
Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus
1 (bases1 to 4062)
Nakamura,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMNEU 4062 bp mRNA for p-185, complete cds. D16295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="neoplastic Schwann cell" /clone_lib="NIH3T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 32; Ler
Pred. No. 3.91e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mesocricetus auratus"
/isolate="animal 14"
/db_xref="taxon:10036"
/cell_line="14-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="peripherall nerve" 33. .3797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takuro Nakamura
Department of Pathology
Faculty of Medicine, University of Tokyo
7-3-1 Hongo
Bunkyo-ku Tokyo 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1182 GGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTC 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94193007
Submitted (19-May-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               772 GGGGAGGTGTGGGAAGGCCTGTGGCTGGGCTC 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-3812-2111 x3356
03-3815-8379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="neu"
33. .86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 4062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D16295.1 GI:493236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 a
```

```
Pfeiffer,B., Poon,L., Seg
Svirskas,R.R., Wan,K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1277 GETCCTTCGGCGTCCTGCTGC 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGTCCTTCGGCGTCCTGCTGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                    .>2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                .2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1378 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94544352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
REFERENCE
AUTHORS
                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                       mRNA
      REFERENCE
                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                 IARRAY PARARLEPTOCHEROCAGGTOPERHSOTCACHENISGICELHPRALYTYON
IARRAY PARARLEPTOCHEROCAGGTOPERHSOTCACHENISGICELHPRALYTYON
DYFESSMRYBEGRATEGASCYTTCPYNYLSTFYGSCTLVCPLINQEVTAEDGTORCEKC
SKSCARVCYGLGMEHLRGARALTSANIOGEFAGCKKITEGSLAFLPESFDGNESSGTAFL
TPEDCLOVETLEETIGYLY TSANIOGEFAGCKKITEGSLAFLPESFDGNESSGTAFL
TPEDCLOVETLEETIGYLY TSANIOGEFACKKITEGSLAFLPGSASGTAFL
TPEDCLOVETLEETIGYLY TSANIOGEFACKTROLEVIRGE TO PROLOVETLEETIGYLCH TRANICACHENISGIC TO PROLOVETLEETIGYLCH TRANICACHENISGIC TO PROLOVETLEETIGY TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVETLE TRANICACHENISGIC TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO PROLOVET TO 
                                                                                                                                                                                                                                                            /db_xref="G1:747595"
/translation="MELAAWCGWGLLLALLSPGASGTQVCTGTDMKLRLPASPETHLD
                                                                                                                                                                                                                                                                                                                  IVRHLYQGCQVVQGNLELTYLPANATISFLÖDIQEVOGYMLIAHSQVRHYPLQRLRIY
RGTQLFEDKYALAVLDNRDPLDNVTTATGRTPEGLRELQLRSLTEILKGGVLIRGNPQ
LCYQDTVLWKDVFRKNNQLAPVDIDTNRSRACPPCAPACKDNHCWGASPEDCQTLTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELGMGATKGPQSISPRDLSPLQRYSEDPTLPLPTETDGYVAPLACSPQPEYVNQPEVR
PQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGGAVENPEYLVPRGGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 5423)
Zhang, Y.Q.
Direct Submission
Submitted (06 FEB-1999) Zhang Y.Q., Biology, University of Utah, 257 South 1400 East, Salt Lake City, Utah 84112-0840, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tracheata; Hexapoda; Insecta;
Muscomorpha; Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 32; Length 4062;
Pred. No. 3.40e-02;
0; Mismatches --0; Indels---0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQPHPPALCPAFDNLYYWDQDPSERGSPPNTFEGTPTAENPEYLGLDVPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94454137
AJ132670.1 GI:4454137
buttonless gene; homeodomain; 1(3)L4910; P-element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DME132670 5423 bp DNA INV
Drosophila melanogaster buttonless gene, exon 1.
AJ132670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative; transmembrane domain"
2058. .3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="extracellular domain"
1989. .2057
/gene="neu"
                                                                                                                                             /product="p-185 precursor"
/protein_id="BAA03801.1"
/db_xref="PID:d1004317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cytoplasmic domain"
1209 c 1182 g 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda;
Pterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                    /db_xref="PID:9747595"
                              'product-"putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2524 AGGGCATGAGCTACCTGGAGGA 2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1055 AGGCCATGAGCTACCTGGAGGA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product-"p-185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fruit fly.
Drosophila melanogaster
                                                                                                                  /codon_start=1
"neu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87. .3794
/gene="neu"
                                                                                    /gene="neu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "gene="neu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.4%;
Best Local Similarity 100.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dene="neu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516. .1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
```

```
ACO06694.3 GI:4544352
ACO06694.3 GI:4544352
HTG; HTGS_PHASEI.

SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.

I (bases 1 to 162815)
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Howston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Shir,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="First-tanger" | /db_xref="First-tanger" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /db_xref="G1:4454138" | /d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster; Chromosome 3R; Region 94Al2-B5; BAC clone BACR48cl7, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T (bases I to 162815)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weinburg, T., Zhang, R., Zieran, L.L. and
2 (bases 1 to 5423)
Zhang.Y.Q. and Broadie,K.S.
Cloning, mapping and tissue-specific expression of Drosophila
clathrin-associated protein AP50 gene
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 21; Length 5423;
Pred. No. 2.11e-01;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. :5423
/organism="brosophila melanogaster"
/note="l(3)L4910"
/db_xref="taxon:7227"
/chromosome="3R"
/map="948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="homeodomain protein"
/protein_id="CAA10727.1"
/db_xref="PID:e1386970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1786. .>2262
/gene="buttonless"
/note="plamid_rescue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="buttonless"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="buttonless"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="buttonless"
```

Louis,

TITLE JOURNAL

COMMENT

```
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183180)
                                                                                                                                                                                                                                                                                                                                Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently a consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 1551 bp in length
gap of unknown length
contig of 1484 bp in length
gap of unknown length
gap of unknown length
contig of 1855 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 1565 bp in length
gap of unknown length
gap of unknown length
contig of 1556 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 20146 bp in length
unknown length
of 20271 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 10772 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 11568 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 4043 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 5261
                                                                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                (bases 1 to 183180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1551:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6491:
8058:
8077:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1598:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10701:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34915
                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                 Waterston, R.H.
                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22418
224437
224023
224042
25502
25521
27115
27115
27115
27115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
37115
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44239
44258
55030
55049
66617
66636
86782
86782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1552
1571
3055
3074
4599
4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12431
14172
14191
15847
15866
17521
17540
19117
19136
20815
                                                        ORGANISM
                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                            SOURCE
                                                                                                                                                                                                              Direct Submission
Submitted (03-FBP-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 30, 1999 this sequence version replaced gi:4454430.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 400 bases, phrap computed error
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC004929 183180 bp DNA HTG 12-JUN-1998
Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
DOYLE,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Feiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Syirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rate <= 1/10.
* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 20; Length 162815;
Pred. No. 2.11e-01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2722 37766: contig of 15045 bp in length 7767 37846: gap of unknown length 7847 54413: contig of 16567 bp in length 444 54493: gap of unknown length 7754: contig of 23071 bp in length 7645 162815: contig of 85171 bp in length 645 162815: contig of 85171 bp in length 665 162815: contig of 85171 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BACR48C17 (D504) RPCI-98 48.C.17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
of 8064 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 1187 b
gap of unknown 1
contig of 2530 b
gap of unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown ll contig of 3713 by gap of unknown ll gap of 6827 by gap of unknown ll contig of 8064 by gap of unknown ll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35560 c 35024 g 45746 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="y2;~cn-bw-sp". ---/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22842 GGTCCTTCGGCGTCCTGCTGC 22862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1277 GGTCCTTCGGCGTCCTGCTGC 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="94A12-B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome="3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC004929.1 GI:3213068
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7670:
14497:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%;
Matches 21: Constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14577:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22641:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .162815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1188
1268
3798
3878
7591
7671
14498
114578
22642
22722
37767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54414
54494
77565
77645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45843 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC004929
93213068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pieces.
```

source

FEATURES

BASE COUNT

ORIGIN

9

RESULT

g οy DEFINITION

ACCESSION

KEYWORDS VERSION

Ŋ

```
/codon_start=1
/function="novel member of src family of PTK"
/function="novel member of src family of PTK"
/function_id="novel.tyrosine kinase"
/function_id="novel.tyrosine kinase"
/function_id="novel.tyrosine kinase"
/function="projection="novel.tyrosine kinase"
/function="id="novel.tyrosine"
/function="id="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 08-NOV-1994
kinase (HCK) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
1 (bases 1 to 1653)
Hackett, P.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (14-MAR-1989) Hackett P.B., University of Minnesota,
Department of Genetics and Cell Biology, 250 Biosciences Centre,
Paul MN 55108-1095, U.S. A.
Liu,z.J. and Hackett,P.B.
Sequence variation of the Rous sarcoma virus PrA src gene
Nucleic Acids Res. 17 (10), 3986 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                        55. .58
//gene="PTK"
//note="Aside from wobble changes, this catalytic domain
sequence has one codon change when compared to c-yes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 37; Length 1653;
Pred. No. 1.23e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMHCKB 1926 bp mRNA PRI Human hemopoietic cell protein-tyrosine kinase (cds. clone HK24. M1659. gl83913 M16592.1 GI:183913 kinase; protein kinase; protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 20; DB 32; I
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers

1. 1653
/organism="Rous sarcoma virus"
/db_xref="taxon:11886"
a 516 c 500 g 283 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene (pp60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                PIKWTAPEAALYGRFTIKSDVWSFGI"
                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KERSVSRC 1653 bp RNA ROUS SARCOME VITUS Pra SrC 9
                                                                                                                                                                                                                                                                                                                                                            р
                                                                                                                                                                                                                                                                                                                                                         46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1273 TGCAAGGTGGCTGACTTCGG 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1264 AAGTCAGACGTCTGGTCCTT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1138 TGCAAGGTGGCTGACTTCGG 1157
                                                                                                                                                                                                                                                                                    putative"
/citation=[1]
/citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AAGTCAGACGTCTGGTCCTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
Matches 20: Constant
                                                                                                                                                                                                                                                                                                                                                       41 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X14718.1 GI:61714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89282411
*map: 7054-8706.
                                                                                                                                                                                                                                                                                                                                                            ಡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 a
                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    src gene.
                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g61714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification de quatorze tränscrits codant pour des proteine
tyrosine kinases chez les cellules E-5; characterisation partielle
de trois nouveaux transcrits
Thesis (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .211
/Organism="Mus musculus"
/db_xref="taxon:10090"
/ceil_line="E-5"
/ceil_type="murine thymic medullary epithelial cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 211)

Hebert, B., Bergeron, J., Tijssen, P. and Potworowski, E.F.

Protein tyrosine kinases transcribed in a murine thymic medullary

epithelial cell line

Gene 143, 257-260 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Motifs VI thru IX of the catalytic domain.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSPTKV 211 bp mRNA ROD 12-At
Mus musculus protein tyrosine-kinase mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183180;
gap of unknown length
contig of 33094 bp in length
gap of unknown length
contig of 330921 bp in length
gap of unknown length
contig of 1528 bp in length
gap of unknown length
contig of 1519 bp in length
contig of 1719 bp in length
gap of unknown length
contig of 1729 bp in length
contig of 1729 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 19; Length 18:
Pred. No. 3.40e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             gap of unknown length contig of 1577 bp in length gap of unknown length contig of 1458 bp in length.
                                                                                                                                                                                                                                                         contig of 2230 bp in length
gap of unknown length
contig of 1889 bp in length
gap of unknown length
                                                                                                                                                                                                              of 1729 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42477 g 49890 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="DJ0917G04"
41389 c 42477 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51540 CCTTCACCCAGCTTCCTCCCAA 51561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase.
Mus musculus cDNA to mRNA.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    764 CCTTCACCCAGCTTCCTCCCAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                             181722:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PTK"
<1. .>211
                                                                                                                                                                                                                                                                                                         80109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.4%;
Best Local Similarity 100.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L25762.1 GI:413748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus.
1 (bases 1 to 211)
Hebert, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             putative"
                                                                                                                                                                                                                                                                                                                          180110
180128
181705
181723
                                                                     140204
171125
171143
172671
172689
174208
                                                                                                                                                                                                                               175955
175973
178203
                        107091
                                                140185
                                                                                                                                                                                                                                                                                                         178221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48785 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L25762
9413748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

셤 ď

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

mRNA gene

CDS

```
Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria:
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria:
Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 2167)

St Hradetzky,D.

Direct Submission

NL Submitted (14-JUN-1991) D. Hradetzky, Chemotherapeutisches
Forschungsinstitut, Georg-Speyer-Haus, Paul Ehrlich Str 42-44, 6000
Frankfurt 70, Federal Republic of Germany

E 2 (bases 1 to 2167)

The genomic locus of the human hemopoletic specific cell protein
tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
exon-intron structure among human PTKs of the src family

Gene 113 (2), 275-280 (1992)
                                                                                                                                                                                                                                                         /protein_id="AAA52643.1"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="PlD:g306832"
/db_xref="Plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper-plo:gaper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proto-oncogene; src family; T-cell receptor alpha-chain; Tyrosine kinase; V-alpha gene segment; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSHCKEll 2167 bp DNA PRI 16-JUL-1992
H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 bp upstream of BamHI site; chromosome 20q11-q12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 29; Length 201
Pred. No. 1.23e+00;
0; Mismatches 0; Indels
                                                                                                                                                                /note="protein-tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also X58736-X58740, X58744-X58769
See also X58741 and X58743.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="spleen"
/clone_lib="genomic; TS48"
/clone="D640 H"
/map="q11-12"
/lumber=9
/formber=9
/formber=9
/gene="HCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 t
                                                                                                                                                                                                                                 /db_xref="GDB:G00-119-303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
   mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1264 AAGTCAGACGTCTGGTCCTT 1283
                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414 AAGTCAGACGTCTGGTCCTT 1433
                                                             /gene="HCK"
169. 1686
                                                                                                   169. .1686
/gene="HCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
      'note-"HCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X58742.1 GI:32043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMHCKA 2015 bp mRNA PRI 08-NOV-1994
Human hemopoletic cell proteit.tyrosine kinase (HCK) gene, complete
cds, clone lambda-a2/la.
M16591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSVRDYDPRQGDTVKHYKIRTLDNGGFYISPRSTFSTLQELVDHYKKGNDGLCQKLSV
PCMSSKPQKPWEKDAWEIPRESLKLEKKLGAGQFGEVWMATYNKHTKVAVKTMKPGSM
SVEAFLAEANVMKTLQHDKLVKLHAVVTKEPIYIITEFWAKGSLLDFLKSDEGSKQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKLIDFSAQIAEGMAFIEQRNYIHRDLRAANILVSASLVCKIADFGLARVIEDNEYTA
REGAKFPIRWTAPEALINFGSFTIKSDVWSFGTLLMETVTYGRIPYFGHSUPEVIRALE
RGYRMPRPENCPEELYNIMMRCWKNRPEERPTFEYIQSVLDDFYTATESQYQQOP"
497 a 522 c 520 g 387 t
1 bp upstream of EcorI site; chromosome 20q11-q12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGCMKSKFLQVGGNTFSKTETSASPHCPyrvPDPTSTIKPGPNS
HNSNTPGIREAGSEDIIVVALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEGY I PSNYVARVDSLETEEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETIKGSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotas; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. L bases 1 to 2015)
Quintrell, N., Lebo, R., Varmus, H., Bishop, J.M., Pettenati, M.J., Le Beau, M.M., Diaz, M.O. and Rowley, J.D.
Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and is expressed in hemopoletic cells Mol. Cell. Biol. 7 (6), 2267-2275 (1987)
                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1926)
Ziegler.S.F. Marth,J.D., Lewis,D.B. and Perlmutter,R.M. Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin
Mol. Cell. Biol. 7 (6), 2276-2285 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Human mitogen-stimulated leukocyte, cDNA to mRNA, clone HK24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g183911
M16591.1 GI:183911
Kinase; protein kinase; protein-tyrosine kinase.
Human hemopoietic cell, cDNA to mRNA, clone lambda-a2/la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 29; Length 1926;
Pred. No. 1.23e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="protein-tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:GOO-119-303"
/protein_id="AAA52644.1"
/db_xref="PID:g306833"
/db_xref="GI:306833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .2015
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20q11-q12"
<1. .2015
                                                                                                                                                                                                                                                                                                                                                             1. .1926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20q11-q12"
<1. .1926
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="HCK mRNA"
76. .1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 AAGTCAGACGTCTGGTCCTT 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1264 AAGTCAGACGTCTGGTCCTT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HCK"
76. .1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 1.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                       source
```

BASE COUNT ORIGIN

spurce

mRNA

MEDLINE

FEATURES

JOURNAL

TITLE

DEFINITION

ó 셤

ACCESSION

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

ö

Gaps

.. 0

ö

Gaps

```
/LEGISTACTION="MGCVOCKDREATKLTDDRDASISQGAGYRYGADPTPOHYPSEGY
TAIPNYNNEHAPYGOGVIYFGGVNTSSHTGTLRTRGGTGVTLFYALYDYBRRTEDDLS
FRKGERFQILUSTEGDWWDASLTTGGGSTIEDNYAPVDIGAEDWYFGKLGRKDAE
FROLLSTGNPRGTYLIRESTTKGAFSLIROWDDEKGDHYKHYKIRKLDGGGYYTTTR
AQFDTLQQLVQHYSDRAAGLCCRLVVPCHKGMPRLADLSVKTKDVWEIPRESLQLIKR
IGNGQFGEVWMGTWNGTTKVAVKTLKPGTMSPESFLEEAQIMKKLRHDKLVQLYAVVS
BEDIYTYTEXMSKGSLLDFLKDGEGRARLFLDNIVDMAAQYAAGMAYIERMYIHRDLR
SFGILLTEDLIVCKIADFGLARLIEDNEYTARQGAFFPIKWTAPFAALYGRPTIKSDVW
SFGILLTEDLYFTATEPQYQPGNNNREVLEQVERGYRMPCPQDCPASLHELMLQCWKKDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA36154.1"
/db_xref="PID::g61897"
/db_xref="G1::G1887"
/db_xref="G1::G1882"
/db_xref="SPTREMBL::Q07461"
/translation="MGSSKSKPRDPSQRRHSLEPPDSTHHGGFPASQTPDETAAPDAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-MAR-1990) Zubak S., Institute Mol. Biol. & Genet.,
Academy of Science Ukr SSr, 252627 Kiev, Str Zabolotnogo 150, U S S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLNPENPRGTFLVRKSETAKGAYCLSVSDFDNAKGPNVKHYKIYKLYSGGFYITLRT
GRSSLAQLVAHYSKRADGLGHRLINVCTSKPOTYGGLAKDAWEIPRESKLEAFT ?~~
CEGEVWMGTWNGTTRYALKTLRPGTMSDEAFLQEAQVMKKFHHEKLVQLYSEEPI
YIVIEYMSKGSLLDFLKGEMGKYLRLPQLVDMAAQIASGMAYVERMIYVHRDLRAANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPSRSFGTVATEPKLFWGFNTSDTVTSPQRAGALAGGVTTFVALYDYESWTETDLSF
KKGERLQIVNNTEGYWWLAHSLTTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGI
LLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKDPEERPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961896
X51861.1 GI:61896
XFG gene.
Rous sarcoma virus.
Valusses: Retriod viruses: Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSVPRSRC 2545 bp RNA VRL 10-SEP-1992
Duck adapted Rous sarcoma virus (Pr-RSV-C) src gene and 3'-LTR.
X51861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_line="Khaki Campbell duck embryo fibroblasts"
50. 142
/rpt_type=DIRECT
282. 1862
282. 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 2545)
Kashuba,V.I., Serge,Z.V., Rynditch,A.V., Kavsan,V.M. and Hlozanek,I.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                     Score 20; DB 24; Length 2526; Pred. No. 1.23e+00;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .2545
/organism="Rous sarcoma virus"
/strain="pr-RSV-C"
/isolate="da Pr-RSV-C"
/db_xref="taxon:11886"
    /db_xref="PID:g64482"
/db_xref="G1:64482"
/db_xref="SWISS-PROT:P27446"
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                               472 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
                                                                                                                                                                                                                                                                                   ρ
                                                                                                                                                                                                                                                                               707
                                                                                                                                                                                                                                                                                                                                                                                                                    1443 GACTICGGCCTGGCCCGGCT 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                         1150 GACTTCGGCCTGGCCCGGCT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282. .1862
/gene="scr"
                                                                                                                                                                                                                                                                               673 c
                                                                                                                                                                                                                                                             2466
                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                               674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zubak, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                             polyA_site
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (22-OCT-1990) Schartl M., Max-Planck-Institut fuer
Biochemie, Cenzentrum, Am Klopferspitz 18a, D-8033 Martinsried, FRG
2 (bases 1 to 2250)
Hannig, G., Ottilie, S. and Schartl, M.
Conservation of structure and expression of the c-yes and fyn genes in lower vertebrates
Oncogene 6 (3), 361-369 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fyn oncogene; oncogene.
Xiphophorus helleri.
Xiphophorus helleri
Eukaryota: Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XHCFYN 2526 bp mRNA VRT 22
Xiphophorus c-fyn (Xfyn) mRNA for protein p59(Xfyn).
X54971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.3%; Score 20; DB 30; Length 216
Best Local Similarity 100.0%; Pred. No. 1.23e+00;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xiphophorus helleri"
/strain="Rio Lancetilla"
/isolate="Db-"
                                                                                                                                                                                                                                                                                                                                                                                                                  579 t
                                                                                                                                                                                                                                              /unumcet_n.
/usedin=X58741:HCK_cds
/usedin=X58741:HCK_mRNA
1066. .>2167
/unmber=11
1281. .1592
/note="ALU repeat VI"
/note="ALU repeat VI"
/note="ALU repeat VII"
a 626 c 485 9 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="p59(Xfyn)"
/protein_id="CAA38715.1"
                                                          /usedin=X58741:HCK_cds
/usedin=X58741:HCK_mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:8084"
/clone="lambda 3911"
                                                                                                                                                       203. .430
/note="ALU repeat V"
934. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .2526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .>2526
/note="p59(Xfyn)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="xfyn"
222. 1835
/gene="xfyn"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        996 AAGTCAGACGTCTGGTCCTT 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1264 AAGTCAGACGTCTGGTCCTT 1283
                                                                                           170. .933
/gene="HCK"
16. .169
/gene="HCK"
/number=10
                                                                                                                                                                                                                  /gene="HCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2526)
Schartl, M.
                                                                                                                                     'number-10
                                                                                                                                                                                                                                        /number-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g64481
X54971.1 GI:64481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                   intron
                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
    exon
                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

œ

ö

Gaps

ö

Indels

30-MAY-1996

BASE COUNT ORIGIN

14

g οχ DEFINITION

ACCESSION

SOURCE ORGANISM

KEYWORDS

VERSION

TITLE JOURNAL

AUTHORS

REFERENCE

REFERENCE AUTHORS TITLE

```
/translation="MGSSKSKPKDPSQRRRSLEPPDSTHHGGFPASQTPDETAAPDAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Mesocricetus auratus"
/db_xref="taxon:10036"
/db_xref="taxon:10036"
/haplotype="21-22 hypodiploid"
/tissue_type="mesenchymal"
/cell_type="sarcoma cells induced by XC rescued PR-RSV-C"
/cell_line="H19"
/clone="H19cl2:1"
/clone="H19cl2:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (26-MAY-1989) Bodor J., Institute of Molecular Genetics
Czechoslovak Academy of Sciences, Flemingovo 2, 166 37 Prague,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The H-19 proviral seg was generated in the hamster genome by src mRNA reverse transcription and integration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bodor, J., Poliak, E., Pichrtova, J., Geryk, J. and Svoboda, J. Complete nucleotide sequence of LTR, v-src, LTR provirus H-19 Nucleic Acids Res. 17 (21), 8869 (1989)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
1 (bases 1 to 3123)
                                                                                                                                                                                                                                                                          315145.1 GI:61706
long terminal repeat; oncogene; provirus; src oncogene; src
oncogene viral.
                                                                                                                                                                   RERSVH19 3123 bp RNA ROD
Hamster H-19 proviral DNA (LTR- v-src -LTR).
X15345
  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mesocricetus auratus"
/db_xref="taxon:10036"
1. 3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rous sarcoma virus"
/db_xref="taxon:11886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rous sarcoma virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  831. .2411
/note="pp60v-src (AA 1-526)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:P25020"
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359. 379 .//note="direct repeat 2 (R)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352. 357
/note="pot. polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA33404.1"
/db_xref="PID:g61707"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |21]. .126
/note="direct repeat 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref-"taxon:11886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329. .335
/note="put. TATA-box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756. .2992
/note="exon (v-src)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .120
/note="hamster DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:61707
  ;
0
                                             2394 GCTCATGCTGGAGTGCTGGA 2413
                                                                                        1419 GCTCATGCTGGAGTGCTGGA 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127. .459
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 3123)
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /proviral
                                                                                                                                                                                                                                                                                                                                                       golden hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bodor, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                      LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                        δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVIGADISSLVEVRGSCVDHSEQEVPKMICGADGEMIVPIGNCLCNFGYEERNEGC
QVCKYGYTKELSSDVGCRKCPLHSYSVYKGATGCODKGYTRGETDPAAMPCTREPSA
PHNLISNNNETSVLLDMSPPLSSGGRODLTYNVVCCOVRDTOCSPCGDDVRYSPQR
LSLRSTRVSVHQLQAHTNYTRQIMAVNGVSKHNRSPEQAVSTLTTNQAAPSWWGNQ
KSDTTRHTLALFWDQPEKPNOVILLEYSWYYRENDOMESSYSTUTLLALFWDGPRSPANDIKDLTPL
TSYVEHPRARTAAGYGESPSAPFESSNYVAAPVVGGWSSAVLLLLIJAGCVVVLLLII
IITFIITKRRSYSKTKQGEDKNOVQCVRIYVDPTYEDPNQAREFAREINTSCIKLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIHLEGVVTKCKPVMITTEYMENGSLDMFLRKNDCRFTVIQLVGILRGIASGMKYLSD
SKYTHRDAARNILVMSNUKVCKVSDFCMSRVLEDBFGARYTRGKRIP BRWTAPBAIT
YRKTYSASDVWSYGIVWWEVYGYGRRPYWDKSNQDVIRAIEGGYRLPPPMECPLALHQ
IMLECWMRERADRPKFSQIVNMLDKLIRNPATLKRTAGGASRSHPSTINHAPSECSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIKFTLRDCNSLPGVIGTCKETFNLYYLESDSDNERYAHESRFSKIDTVAADESFTQV
DIGDRIMKLNTEVRDVGVLSRAGFYLAFQDVGACIALVSVHVFYKKCPLAVRNLAQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKVIGIGEFGEVCSGRLKLPGKREICVAIKTLKAGFTEQQRLDFLSEASVIGQFDHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="EVSIMDEKNIPIRTYQVCNVMEPSQNNWLRTHWIQRGAAQRIYI
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Coperenygii: Teleostei; Buteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooke, J.E., Xu,Q., Wilson,S.W. and Holder,N.
Cooke,J.E., Xu,Q., Wilson,S.W. and Holder,N.
Characterisation of five novel zebrafish Eph-related receptor
tyrosine kinasagests roles in patterning the neural plate
Dev. Genes Evol. 206, 515-531 (1997)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-MAR-1998) Cooke J.E., University College London, Department of Anatomy and Developmental Biology, Gower Street, London, WCLE 6BT, UK
                                                                                                                                                                                                                                                                                                                                                                           DRAJ5030 2640 bp MRNA VRT 27-MAY-1998 Danio rerio MRNA for Eph-like receptor tyrosine kinase rtk4, partial.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Eph-like receptor tyrosine kinase rtk4"
/protein_id="CAA06303.1"
/db_xref="PID:e1285052"
                                                                                                                                                                                                              ö
                                                                                                                                                            Score 20; DB 37; Length 2545; Pred. No. 1.23e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2640;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 24;
Pred. No. 1.23e+00;
                                                                                                                                                                                                            Mismatches
                                                                                        517 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:93005933"
/db_xref="GI:3005933"
/db_xref="SPTREMBL:073879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eph-like receptor tyrosine kinase.
zebrafish.
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLASVDDWLKLIGLEQYRENFNTA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2640
/organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                    752 9
FKYLQAQLLPACVLEVAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 g
                1944. .2043
/rpt_type=DIRECT
2212. .2545
                                                                                                                                                                                                                                                       1479 TGCAAGGTGGCTGACTTCGG 1498
                                                                                                                                                                                                                                                                                  1138 TGCAAGGTGGCTGACTTCGG 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĀJ005030.1 GI:3005932
                                                                                                                                                            Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .>2640
                                                                                    693 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                        583 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cooke, J. E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43005932
                        repeat_region
```

source

CDS

JOURNAL

FEATURES

BASE COUNT ORIGIN

```
RNPSRSFGTVATEPKLEWGENTSDTVTSPQRAGALAGGVTTFVALYDVESWTETDLSF
KKGERLOIVNNTEGDWALLAHŠĪTĪTĞGTGYIPSDNYAPSDSIQAEEWYFGKITRRESER
LLALDFBRRGFFTTRSTAGANCLSVSDEDBAAGGPWTKHYKTLKZKSGGFTTTSRT
OFGSLOQIVAAYSKHADGLCHRLINUCPTSRPOTGLAKDAWEIPRESIRLEAKLGGG
CFGEVWMGTWNGTTRVAIKTLKFGTWSPEAFLOEAQWKKLRHEKLVQLIAAVSEEPI
YIVIETSKSKGSLLDFLKGEMGKYKIRLPOLVDWAAQIASGMAYVERMYVHRDLKAANI
LVGENLVCKVADFGLARLIEDNEYTARGGAKFPIKWTAPEAALYGRFTIKSDVWSFGI
LLTELTTKGRYPPFGANVREVLDQVERAYRMPCPPECPESLHDLMCQCWRKDPEERPT
FKYLQAQLLPACVLEVAE"

Anote="put. TATA-box"

Anote="put. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 20; DB 32; Length 3123; Best Local Similarity 100.0%; Pred. No. 1.23e+00; Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
```

Search completed: Thu May 20 18:37:08 1999 Job time: 7753 secs.

g οχ

```
......CCAACGCTCTGGGCTCCAGC 1548
************************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### Sparts 3:parts 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part8 14:part8 15:part9 10:part10 11:part11 12:part12 13:part13 14:part8 15:part9 20:part20 21:part21 22:part22 23:part23 24:part24 25:part22 23:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part28 30:part38 31:part31 32:part31 33:part31 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39 40:part40 41:part41 42:part47 48:part48 45:part45 46:part46 47:part47 48:part48 45:part45 56:part56 57:part52 53:part58 59:part59 60:part50 60:part50 67:part57 58:part58 59:part59 60:part60
                                                                                                            (TM)
                                                                                                                                                                                                                                           MasPar time 411.24 Seconds
806.566 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.00e+00
3.96e-02
3.96e-02
3.96e-02
3.96e-02
1.99e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

    n.a. database search, using Smith-Waterman algorithm

                                                                                                                                                              Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAD encoding cD
SAD probe 5557.
SAD PCR primer
SAD PCR primer
SAD PCR primer
SAD PCR primer
SAD PCR primer
SAD PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mean 7.892; Variance 3.155; scale 2.502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
Human
Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  271905 segs, 107135622 bases x
                                                                                                                                                                                                                                                                                         >US-09-099-053-1
(1-1548) from US09099053.seq
1548
                                                                                                                                                                                                                                                                                                                                       1 GCTCGCGGGCTCCCATGGCC.
                                                                                                                                                                                                                                             Thu May 20 19:34:52 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V81743
V81769
V81771
V81773
V81774
V81770
V81770
                                                                                                                                                                                                                                                                                                                                                                                                                        Dbase 0; Query 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \sigma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                               TABLE jmetric
Gap 60
                                                                                                                                                                                                                                                                       not generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n-geneseq35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1548
30
21
21
21
21
21
21
21
21
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing:
                                                                                                                                                                                                                                                                                                              Description:
Perfect Score:
N.A. Sequence:
                                                                                                                                                                                                                                                                       Tabular output
                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                            ••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1548
30
31
21
21
21
21
21
21
21
21
                                                                                                                                                                                                                                                                                                                                                                                                                        STD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Statistics:
                                                                                                                                                                                                                  MPsrch_nn
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database:
                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                        Nmatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 2 4 2 9 7 8 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000
```

```
4 . 3.7 e + 0.0

4 . 3.7 e + 0.0

5 . 5.7 e + 0.0

6 . 3.7 e + 0.0

7 . 3.7 e + 0.0

8 . 3.7 e + 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

9 . 5.4 e - 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.7 e + 0.0

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1

1 . 3.0 e + 0.1
                                                         Human C-srcfl oncogen Partial sequence of e Methods for diagnosin Chicken pp60 c-src gene Mouse Actrila recept Mouse Actrila recept Mouse Actrila recept Mouse Actrila recept Mouse Actrila recept Mouse Actrila recept Human intracellular thuman intracellular thuman intracellular the SV-2 strain 25766 gh Mouse alpha-1 collage Eph-related PTK Cek5-thuman canalicular mul Human SAD PCR primer Human SAD PCR primer Human SAD PCR primer Human Done morphogeni Human Prelated PTR Cek5-thuman SAD PCR primer Human SAD PCR primer Human Done morphogeni Human Prelated PTR Cek1-thuman SAD PCR primer Human Bone morphogeni
 Human SAD PCR primer
Human SAD RACE primer
Human SAD RACE primer
TB4X gene specific ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine tracheal antim
Insulin like growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partial human FRAZZLE
113 kD ISGF-3alpha ge
V81768
V81761
V81760
V69680
V20456
T133754
T183754
C46687
V71969
                                                                                                                                                                 V71968
V71968
V71968
V71969
V73673
V73652
V73652
V73650
V73651
V7360
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62154
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62134
V62
 340
3840
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
13
24
                                                                                                                                                                   53
                                                                                                                                                                                                13
30
30
13
                                                                                                                                                                                                                                                                         18
18
19
255
656
1177
1602
                                                                                                                                    1969
3268
3370
4989
 RESULT
    0000 00
                                                                                                                                                                                                                                                                                                                        0 0 0 0 0 0 0 0 0 0 0 0 0
```

```
TRESULT 1

ID W1143 standard; CDNA; 1548 BP.

YO W1743;

YO W1743;

DI 10-MAR-1999 (first entry)

DE Human SAD encoding CDNA.

W TYPO I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; where is the intington's disease; neuronal survival; Alzheimer's disease; where is the intington's disease; ss.

KW PTPO4; PTPO5; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; KW reprodegenerative disease; neuronal survival; Alzheimer's disease; KW neurodegenerative disease; neuronal survival; Alzheimer's disease; KW parkinson's disease; neuronal survival; Alzheimer's disease; FF Key 49.1515

FF COS 49.1515

FF COS 49.1515

FF COS 49.1522

PR 23-OCT-1997; US-049472

PR 20-MAY-1997; US-049916.

PR 20-MAY-1997; US-049916.

PR 20-MAY-1997; US-049916.

PR 11-JUN-1997; US-049916.

PR 20-MAY-1997; US-049916.

PR 11-JUN-1997; US-049916.

PR 11-JUN-1997; US-049916.

PR 18-JUN-1997; US-049914.

PR 19-OCH 34/01.

PR 18-JUN-1997; US-049914.

PR 19-OCH 34/01.

PR 18-JUN-1997; US-049914.

PR 18-JUN-1997;
```

 $^{\circ}$

```
1141
                                                                                                                                                                                                                                                                                                                                                              1321
                                                                                                                                                                                               1081
                                                                                                                                                                                                                                                                               1201
                                                                                                                                                                                                                                                                                                                                                                                                       1381
                                                                                                                                                                                                                                                                                                                                                                                                                          1381
                                                                                                                                                                                                                                                                                                                                                                                                                                               1441
            781
                                841
                                                    841
                                                                        901
                                                                                           901
                                                                                                               961
                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                   δ
                                                                       g
                                                                                           ò
                                                                                                              g
                                                                                                                                   Qγ
                                                                                                                                                       g
                                                                                                                                                                           ò
                                                                                                                                                                                              g
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                           οχ
                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                          ο
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
present sequence encodes human SAD. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPS) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      780
                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              840
                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                            9
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                         CTCAGGAGGCGGCTGGCTTCTTCTTTTTGGACAAGATCTGGCCGGCGGCGGC
                                                                                                                                                                                                                                                                                                   gagooggaccatggcaccccggggtccctggaccccaacactgacccagtgcccacgctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtcagtcggacccaggcacagcagctgctcctctcccacccdacgaaccaggggcttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctcatccggcccagcgagagcagcctcgggggctactcactgtcagtccgggcccaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaggtctgccactaccgggtctccatggcagctgatggcagcctctacctgcagaaggga
                                                                                                                                                                                                                                                                                                                                  ccgccgagccttgcagccccttccctcagctcttccttgcgctctatgacttcacggcg
                                                                                                                                                                                                                                                                                                                                                     CCCGCCGAGCCTTGCAGCCCCTTCCCTCAGCTCTTCCCTTGCGCTCTATGACTTCACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCATCCGGCCCAGCGAGAGCAGCCTCGGGGGCTACTCACTGTCAGTCCGGGCCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTCTGCCACTACCGGGTCTCCATGGCAGCTGATGGCAGCCTCTACCTGCAGAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cggctctttcccggcctggaggagctgctcacctacaaggccaactggaagctgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCTCTTTCCCGGCCTGGAGGAGCTGCTCCTACTACAAGGCCAACTGGAAGCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagaaccccctgctgcagccctgcatgccccagaaggccccgaggcaggacgtgtgggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAACCCCCTGCTGCAGCCCTGCATGCCCCAGAAGGCCCCCGAGGCAGGACGTGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgggaaggcctgtgggctcgctgcccgtggcgatcaaggtcatcaagtcagccaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                        acceaegtegecaaggettetectgagaegeteteagaeceaecetggtaetttageggg
                                                                                                                                                                                     ;
0
                                                                                                                                                                 DB 59; Length 1548;
                                                                                                                                              263 T;
                                                                                                                                                                                     0; Indels
                                                                                                                                              494 G;
                                                                                                                                                                Score 1548; DB 59;
Pred. No. 0.00e+00;
0; Mismatches (
                                                                                                                                             533 C;
                                                                                                                                             258 A;
                                                                                                                                                                 100.08;
                                                                                                                                                                           Best Local Similarity 100.0%;
Matches 1548; Conservative
                                                                                                                                              1548 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.
                                                                                                                                               Sequence
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
  g
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음.
                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                   οχ
                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
840
                                                                                                               900
                                                                                                                                                               980
                                                                                                                                                                                                         960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-1999 (first entry)

Human SAD probe 5557.

Hupptd; PrP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; Synthetic.
ctcatccggctgcacgcagtgtgctcggggggggcctgtgtacatagtcacggaactc
                                                                                                                                                                                                                                                         atgogcaaggggaacctgcaggccttcctgggcacccccgagggccgggccctgcgtctg
                                                                                                                                                                                                                                                                                                                                              1441 AGCAGCCCCGAGGAACGGCCCTCCTTTGCCACGCTGCGGGAGAAGCTGCACGCCATCCAC
                                                                                                                                                                                                         CTCATCCGGCTGCACGCAGTGTGCTCGGGCGGGGGGCCTGTGTACATAGTCACGGAACTC
                                                                                                                                                                                                                                                                                                    ATGCGCAAGGGGAACCTGCAGGCCTTCCTGGGCACCCCCGAGGGCCGGGCCCTGCGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             cgcgttgtgcaccgggacttggccgccggaacgtgctcgtggacgacggcctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggtggctgacttcggcctggcccggctgctcaaggacgacatctactccccgagcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 AAGGIGGCIGACTICGGCCIGGCCCGGCTGCICAAGGACGACGACTCIACTCCCCGAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agcagccccgaggaacggccctcctttgccacgctgcgggagaagctgcacgccatccac
                                                                       atgaagctcactgacctcgccaaggagatccagacactgaagggcctgcggcacgagcgg
                                                                                                                 ATGAAGCTCACTGACCTCGCCAAGGAGATCCAGACACTGAAGGGCCTGCGGCACGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agctccaagatcccggtcaagtggacagcgcctgaggcggccaattatcgtgtcttctcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201 AGCTCCAAGATCCCGGTCAAGTGGACAGCGCCTGAGGCGGCCAATTATCGTGTCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgccgcgcccggctgcctgcccggcggaggtctacgtgctcatgctggaggtgctggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agatgccaccctgagtcctcacgtgacccaacgctctgggctccagc 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r 2
V81766 standard; DNA; 30
V81766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998; U08439.
23-CCT-1997; US-065595.
28-APR-1997; US-044428.
20-MAY-1997; US-047222.
11-JUN-1997; US-049477.
11-JUN-1997; US-0499756.
18*JUN-1997; US-049914.
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
WO9849317-A2.
05-NOV-1998.
```

 \sim

```
Homo sapiens.
W09849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                          ខ្លួនទីទីទីទី
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                   New nucleic acid encoding specific protein tyrosine phosphatases -

"seful for identifying specific modulators for treatment and

"prevention of Cancer and neurodegenerative disease

"prevention of Cancer and neurodegenerative disease

"Example 6; Page 87; 193pp; English;

The present invention describes isolated, enriched or purified nucleic

acids encoding PPPO4, SAD, PPPO5, PPTO10, ALD and ALK-7 proteins. The

acids encoding PPPO4, SAD, PPPO5, PPTO10, ALD and ALK-7 proteins. The

acids encoding PPPO4, SAD, PPPO5, PPTO10, ALD and ALK-7 proteins. The

acids encoding PPO4, SAD, PPPO5, PPTO10, ALD and ALK-7 proteins. The

acids encoding PPPO4, SAD, PPPO5, PPTO10, ALD and ALK-7 proteins. The

acids and antaqonists, including NBP) in vivo or in vitro.

These substances are used to treat or prevent diseases associated with

abnormal signal transduction pathways that involve the proteins,

particularly cancer (e.g. leukaemia and lymphoma), while modulators of

ALK-7 (which is a type i receptor serine/threonine kinase) are used to

promote neuronal survival, particularly for treating Alzheimer's,

Parkinson's or Huntington's diseases. Nucleic acid fragments of the

polymuclectides encoding the proteins can be used as probes. Lo. identify

and clone related sequences; to detect protein-encoded RNA; to generate

transgenic animals and in gene therapy (optionally after mutation). Ab

are account of the proteins. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mew nucleic acid encoding specific protein tyrosine phosphatases - weeful for identifying specific modulators for treatment and research in the present increased and neurodegenerative disease.

Example 6; Page 88; 193pp; English.

Example 6; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 88; Page 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1999 (first entry)

Human SAD PCR primer 6642.

BTP04, PTP05, PTP10, SAD, ALP, ALK-7, protein tyrosine phosphatase;
type I receptor serine/threonine kinase; cancer; leukaemla; lymphoma;
neurodegenerative disease; neuronal survival; Alzheimer's disease;
Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.9%; Score 30; DB 59; Length 30; 00.0%; Pred. No. 4.57e-09; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998; U08439.
23-OCT-1997; US-063595.
28-APR-1997; US-044428.
20-MAY-1997; US-044428.
11-JUN-1997; US-049477.
11-JUN-1997; US-049914.
(SUGE-) SUGEN INC.
APP H, Clary D, Courtneidge SA, Hui TH, Jallal B, Markby, D, Ontust S, Peles E, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
9
App H, Clary D, Courtneidge SA, Hui <u>TH, Jallal B, Markby D, Onrust S, Peles E, Plowman GD;</u>
WPI; 99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tgggagcggccacactccgaattcgccctt 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .r. 3
V81769 standard; DNA; 21 BP.
V81769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe for human SAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

```
PER 23-OCT-1998; U08439.

PR 23-OCT-1997; US-063595.

PR 28-APR-1997; US-0644428.

PR 28-APR-1997; US-049472.

PR 10-UNN-1997; US-049472.

PR 11-UNN-1997; US-04947.

PR 11-UNN-1997; US-04944.

PR 1
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a PCR primer for human SAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR'1999 (first entry)

Human SAD PCR primer 6643.

PTP04; PTP05; PTP10; SAD; ALP, ALK-7; protein tyrosine phosphatase;
type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
neurodegenerative disease; neuronal survival; Alzheimer's disease;
Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                               Score 21; DB 59; Length 21;
Pred. No. 3.96e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 59;
Pred. No. 3.96e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                  8
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
G;
                                                                                                                                                                                                  5
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ς;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 aggccaactggaagctgatcc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atggagccgttcctcaggagg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР.
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ATGGAGCCGTTCCTCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 AGGCCAACTGGAAGCTGATCC
                                                                                                                                                                                                  4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
ID V81773 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 4
V81771 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for human SAD. Sequence 21 BP; 6 A;
                                                                                                                                                                                                  21 BP;
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Sp
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SaD, PTP05, PTP10, ALP and ALK-7 proteins. The acids encoding PTP04, SaD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases.

(i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to parkinson's or Huntington's diseases. Nucleic acid fragments of the polymoulectides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). A continuation of the proteins. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
         10-MAR-1999 (first entry)

Human SAD PCR primer 5284.

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease, neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR'1999 (first entry)
Human SAD PCR primer 5285.
Pyroty, Prpt05, Prpt10, SAD: ALP; ALK-7; protein tyrosine phosphatase;
type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease;
Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                     D 03-NOV-1939; U08439.

R 23-OCT-1997; US-044228.

R 20-MAY-1997; US-0444728.

R 11-JUN-1997; US-049472.

R 11-JUN-1997; US-049475.

R 11-JUN-1997; US-049476.

R 11-JUN-1997; US-049914.

A (SUGE-) SUGEN INC.

A (SUGE-) SUGEN INC.

I App H, Clarry D, Courtneidge SA, Hui TH, Jallal B, Markby D, Onrust S, Peles E, Plowman GD;

R MPI; 99-009434/01.

R WPI; 99-009434/01.

T New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

T SEXAMPLE T, U33Pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 59; Length 21;
Pred. No. 3.96e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  857 TCGCCAAGGAGATCCAGACAC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tegecaaggagatecagacae 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V81774 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%;
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for human SAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.

W0984917-A2.

05-NOV-1998.

27-APR-1998; U08439.

23-OCT-1997; US-044428.

20-MAY-1997; US-044428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-049914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-049477
                                                                                                       Homo sapiens.
WO9849317-A2.
                                                                                                                               05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer
                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
The present invention describes isolated, enriched or purified nucleic acids encoding PPP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The acids encoding PPP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatuses.

CPTPS) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with particularly cancer (e.g. leukaemia and lymphoma), while modulators of articularly cancer (e.g. leukaemia and lymphoma), while modulators of particularly cancer (e.g. leukaemia and lymphoma), while modulators of particularly cancer (e.g. leukaemia and lymphoma), while modulators of promote neuronal survival, particularly for treating Alzheimer's, parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). A contraction of the present sequence represents a proper contraction of the present sequence represents and the proteins. The present sequence represents and the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          read nucleic acid encoding specific protein tyrosine phosphatases restinging the control of cancer and neurodegenerative disease.

Transple 6: Page 88: 193pp; English.

Transple 6: Page 88: 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTPO4, SAD, PTPO5, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases.

(PTPS) and are used to identify substances that modulate their activity (TPS) and are used to identify substances that modulate their activity.

These substances are used to treat or prevent diseases associated with abornal signal transduction pathways that involve the proteins.

Darticularly cancer (e.g. leukaemia and lymphoma), while modulators of promote neuronal survival, particularly for treating Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1999 (first entry)
Human SAD PCR primer 6644.

Human SAD PTPO5: PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease, neuronal survival; Alzhelmer's disease; Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer neurodegenerative disease Example 7; page 90; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 59;
Pred. No. 3.96e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              App H, Clary D, Courtneidge SA, Hui TH, Jallal Markby D, Onrust S, Peles E, Plowman GD; WPI; 99-009434/01.
                                     Jallal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
6
App H, Clary D, Courtneidge SA, Hui TH, Markby D, Onrust S, Peles E, Plowman GD; WPI; 99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 GAAGTCAGCCACCTTGCAGGC 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V81770 standard; DNA; 21 BP
V81770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gaagtcagccaccttgcaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%; ses 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer for human SAD.
Sequence 21 BP; 5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998.
27-APR-1998; U08439.
23-CCT-1997; US-063595.
28-APR-1997; US-044428.
20-MAY-1997; US-047222.
11-JUN-1997; US-049477.
11-JUN-1997; US-049976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

Ŋ

88888888

RESULT

엄 S

```
New nucleic acid, and acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

They are seen invention describes isolated, enriched or purified nucleic acids encoding PTPD4, SAD, PTPD6, PTPD7, AD and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPS) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of the promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymore can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Above the proteins can be used to determine the proteins. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1999 (first entry)
Human SAD PCR primer 6119.
PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine Kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease:
                                                       10-MAR-1999 (first entry)

Human SAD PCR primer 5554.

PTP04; PTP05: PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphom: neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease; Huntington's disease; PCR primer; ss Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     App H, Clary D, Courtneidge SA, Hui TH, Jallal
Markby D, Onrust S, Peles E, Plowman GD;
WPI; 99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 10
V81768 standard; DNA; 18 BP.
V81768;
          /81765 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        783 CCACACCTCCCAAAGTA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ccacacctccccaaagta 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer for human SAD.
Sequence 18 BP; 6 A;
                                                                                                                                                                                                                                                                                    05-NOV-1998. U08439. 23-OCT-1998; US-063595. 28-APR-1997; US-044428. 20-MAY-1997; US-044428. 11-JUN-1997; US-049477. 11-JUN-1997; US-049914. (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09849317-A2.
05-NOV-1998.
27-ARR-1998; U08439.
23-OCT-1997; US-063895.
28-ARR-1997; US-044428.
20-MAY-1997; US-044428.
11-JUN-1997; US-049472.
                                                                                                                                                                                                                                            Homo sapiens.
WO9849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
          Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR 20-MAY-1997; US-044428.

PR 11-JUN-1997; US-049776.

PR 11-JUN-199776.

PR 11-JUN-1997.

PR 11-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a PCR primer for human SAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-1999 (first entry)

Human SAD PCR primer 6645.

Human SAD PCR primer 6645.

PTP04, PTP05, PTP10, SAD: ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer: leukaemia; lymphoma; neurodegenerative disease, neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 59; Leuy...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 59; Length 20; Pred. No. 1.99e-01;
                                                                                                                                                               4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                             3
G;
                                                                                                                                                             10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1548 GCTGGAGCCCAGAGCGTTGG 1529
                                                                                                                                                                                                                                                                                                                                                                 761 reacceaectrecreeaage 741
                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gctggagcccagagcgttgg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 8
V81772 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0%;
                                                                                                                                                                                                            Query Match 1.4%;
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                  1 tcacccagcttcctcccaagg
                                                                                                                                                               4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1998, U08439, 23-APR-1997; US-063595, 28-APR-1997; US-0644428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

ö

Gaps

ö

Matches

g

RESULT

7 1

ဖ

```
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Syntheti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                              RESULT
    8888888888
                                                                                                                                                                                                                g
                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                               Cb
                                                      Natively D. Onlines S., Peles E., Plowman GD;

New nucleic acid encoding specific protein tyrosine phosphatases -
reset is dentifying specific modulators for treatment and
reset is cancer and neurodegenerative disease

Example 6: Page 87: 193pp: English.

Example 6: Page 87: 193pp: English.

The present invention describes isolated, enriched or purified nucleic
above proteins, other than ALK-7, are protein tyrosine phosphatases.

The present invention describes isolated, enriched or purified nucleic
above proteins, other than ALK-7, are protein tyrosine phosphatases.

(i.e. agonists and antagonists, including NBP) in vivo or in vitro.

These substances are used to treat or prevent diseases associated with
abnormal signal transduction pathways that involve the proteins,
controllarly cancer (e.g. leukaemia and lymphoma), while modulators of
ALK-7 (which is a type I receptor serine/threonine kinase) are used to
promote neuronal survival, particularly for treating Alzheimer's,
concernment and ingene proteins can be used as probes to identify
and clone related sequences; to detect protein-encoded RMR; to generate
transgenic animals and in gene therapy (optionally after mutation). Ab
are used to determine the proteins. The present sequence represents a
conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR.1999 (first entry)

Human SAD RACE primer 5848.

Pyrpo4; Prp05; Prp10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease, neuronal survival; Alzheimer's disease; Parkinson's disease; Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 59; Length 18;
Pred. No. 4.37e+00;
0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease Example 6; Page 86; 193pp; English.
             (SUGE-) SUGEN INC.
App H, Clary D, Courtneidge SA, Hui TH, Jallal B,
Markby D, Onrust S, Peles E, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                            2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Β,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hui TH, Jallal
                                                                                                                                                                                                                                                                                                                                                                                                        6 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09843317-A2.
V5-NVV-1998.
27-APR-1998.
23-OCT-1997; US-063595.
28-APR-1997; US-044428.
20-MAY-1997; US-044428.
11-JUN-1997; US-04977.
11-JUN-1997; US-049756.
18-JUN-1997; US-049914.
SUGEP.) SUGEN INC.
APP H, Clary D, Courtneidge SA, Hui TH, Jal Markby D, Onrust S, Peles E, Plowman GD; WPI; 99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                        c;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 CTTCGAGGGCACAGAGCC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V81761 standard; DNA; 18 BP. V81761:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cttcgagggcacagagcc 18
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2%,
Best Local Similarity 100.0%,
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            4 A;
18-JUN-1997; US-049914.
                                                                                                                                                                                                                                                                                                                                                                                                          18 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
W09849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
```

```
ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a RACE primer for human SAD.
                                                                                                                                                                                                                                                                                                                                                                      PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; PCR primer; ss.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
                                                                                                                                             Score 18; DB 59; Length 18;
Pred. No. 4.37e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                               3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 59; I
Pred. No. 9.54e-01;
0; Mismatches 0;
                                                                                                             7 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
6
                                                                                                               4
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      852 AGTGAGCTTCATGTTGGCT 834
                                                                                                                                                                                                                                                                                                         V81760 standard; DNA; 19 BP. V81760;
                                                                                                                                                                                                                                           589 GGTAGAGGCTGCCATCAG 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agtgagcttcatgttggct 19
                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                        10-MAR-1999 (first entry)
Human SAD RACE primer 5556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match
Local Similarity 100.0%;
les 19; Conservative
                                                                                                                                                                                                             1 ggtagaggctgccatcag 18
                                                                                                                4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for human SAD.
9 BP; 3 A;
                                                                                                                                                                              18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1997; US-044428.
20-MAY-1997; US-047222.
11-JUN-1997; US-049477.
11-JUN-1997; US-0499756.
18-JUN-1997; US-049914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-063595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U08439
                                                                                                                Bb:
                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9849317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RACE primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998
```

```
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                        ò
                                                                                                                                                                                                                                               Tricancer composition comprising two anti-sense oligo:nucleotide(s)

Tricancer composition comprising two anti-sense oligo:nucleotide(s)

Tricancer composition and nuclear oncogene(s)

Claim 105-106; 92pp; English.

The present sequence represents an oncogene from the present invention.

The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and cytoplasmic oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, pML/RAR alpha , AMLI/MT68, E2A/pr1 and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.

Sequence 255 BP; 44 A; 86 C; 86 G; 39 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 30; 54pp; English.

Example 2; Page 30; 54pp; English.

Example 2; Page 30; 54pp; English.

Sequences V69551 to V6964 represent PCR primers used for localisation of the genes of the invention which occur on the non-recombining region of the human Y chromosome. The gene sequences fall into two classes: (1) X-homologous DNA which are expressed in many organs, having functional X-homologous and (2) testis-specific DNA sequences. Y chromosomal DNA from males with known conditions such as infertility and reduced sperm count can be assessed using the invention to determine whether the condition is associated with or caused by the occurrence of the gene or gene alteration. Candidate inhibitors of the enzymatic activity of the
                                                                     02-FEB-1999 (first entry)
TB4X gene specific right primer.
Non-recombining region; human; Y chromosome; X homologue; testis; sperm; infertility; gene alteration; inhibitor; TB4X; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            Lahn BT, Page DC; WPI; 98-568729/48. Novel genes in the non-combining region of Y chromosome - useful to diagnose if male infertility or reduced sperm count has a genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; c-src11; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 52; Length 19;
Pred. No. 4.37e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes can be assessed using in vitro assays. Sequence 19 BP; 4 A; 8 C; 3 G;
                                                                                                                                                                                                           Homo sapiens.

W09846747-A2.

22-ocr-1998.

10-ARR-1997; US-041877.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1994; 306691.
15-SEP-1994; US-306691.
(UVJE-) UNIV JEFERSON THOMAS.
Calabretta B, Skorski T;
WPI; 98-229882/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7T 14
V20456 standard; DNA; 255 BP.
V20456; JT-UJN-1998 (first entry)
Human c-srcll oncogene.
T 13
V69680 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777 CTCCCCAAAGTAGCCTTC 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ctccccaaagtagccttc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                    V69680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT

VAZ

DD 172

DD 172

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

DD 173

D
                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
```

DB 40;

1.2%; Score 18;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene for endoglin (transforming growth factor beta binding protein) - useful in diagnosis and gene therapy of hereditary hammorrhagic telangiectasia (laim 6: Page 41; 71pp: English. Oligonucleotides derived from introns of the endoglin gene can be used as primers for amplifying a single exon of the endoglin gene used as primers for amplifying a single exon of the endoglin gene encoding endoglin can be used for gene therapy of HHT which is caused by inheritance of a defective gene, e.g. endoglin, betagingen, TGF-beta type I or II receptor or TGF-beta/activin type I
                                                                                                                                                                                                                      713754;
T-DEC-1996 (first entry)
Partial sequence of endoglin.
Endoglin; TGF-beta; beta-glycan; receptor; diagnosis; detection;
gene therapy; haemorrhagic telanglectasla; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 24; Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. No. 4.37e+00;
Mismatches 0; Indels
                       Indels
Pred. No. 4.37e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-1994; US-346129.
(HSCR-) HSC RES & DEV LP.
(UYDU-) UNIV DUKE.
Letarte M, Marchuk DA, McAllister K;
WPI; 96-286827/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Thu May 20 19:49:17 1999
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 1..296
/*tag= a
/label= Intron 10.
297.554
/*tag= b
/label= Exon 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/label= Intron 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 A;
                                                                                                                                                                               T 15
T13754 standard; DNA; 656 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1523 GTGAGGACTCAGGGGTGG 1506
                                                                 148 acctgcaggccttcctgg 165
                                                                                             974 ACCTGCAGGCCTTCCTGG 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 gtgaggactcaggggtgg 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          555..656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996.
29-NOV-1995; U15428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Job time : 865 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9616975-A1.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
```

```
Insert Length: 434 Std Error: 0.00 Seq primer: -40UP from Gibco.
24
24
28
qz48f07.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
NID
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
RESULT
                          0000
                                                                                                                                                      O
                                                                                                                                                                              00 0
                                                                                                                                                                                                                                                                                                                                                              00
                                                                                                                                                                                                                                                                                                                                                                                            υu
                                                                                                                                                                                                                                                                                                              1.67e-123
5.49e-09
1.13e-05
1.13e-05
1.13e-05
1.13e-05
1.13e-04
1.28e-02
                                                                                                                                                                                                                            MasPar time 2885.34 Seconds 1257:120 Million cell updates/sec
                                                                                                         (ME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:9b_est1 9:9b_est10 10:9b_est11 11:9b_est12 12:9b_est13 13:9b_est14 14:9b_est15 15:9b_est16 16:9b_est17 17:9b_est18 18:9b_est15 19:9b_est2 20:9b_est2 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1
genbank-est111
                                                                                                                                                                                                     - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qz48f07.x1 NCI_CGAP_K1
zbl2c04.r1 Soares_feta
zk26h10.r1 Soares_preg
ak13g03.s1 Soares_para
zl41g09.r1 Soares_preg
RPCIII-158L24.rU RPCII
                                                                                                                                                     Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cSRL-17ell-u cSRL flow
UI-R-C1-1f-a-11-0-UI.s
HUM137H10B Clontech hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mean 9.358; Variance 1.389; scale 6.737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                              ×
                                                                                                                                                                                                                                                                                                                                                                                                           segs, 1171580779 bases
                                                                                                                                                                                                                                                                 >US-09-099-053-1
(1-1548) from US09099053.seq
1548
                                                                                                                                                                                                                                                                                                             1 GCTCGCGGGCTCCCATGGCC.
                                                                                                                                                                                                                      May 20 18:37:31 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0%
45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1373274
W17139
AA035407
AA890391
AA149096
AQ37709
BQ37480
AQ34709
BO3480
AI059300
D60912
                                                                                                                                                                                                                                                                                                                                                                                      Dbase 0; Query 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum Match
Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TABLE jmetric
                                                                                                                                                                                                                                                     not generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3332
1196
1196
1165
341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embl-est58
                                                                                                                                                                                                                                                                                                                                                                                                           2883791
                                                                                                                                                                                                                                                                                                                                                              Gap 60
                                                                                                                                                                                                                             Thu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing:
                                                                                                                                                                                                                                                                                      Description:
Perfect Score:
N.A. Sequence:
                                                                                                                                                                                                                                                   Tabular output
                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8820000000
                                                                                                                                                                                                                                                                                                                                                                                     STD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Statistics:
                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
```

Nmatch

ritle:

Run (

Result М М 1064597861

O υU υ

```
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Trissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens cDNA clone IMAGE:2030149 3' TYROSINE-PROTEIN KINASE SRM ;, mRNA
1. 28 e - 0.04

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05

1. 28 e - 0.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 332)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 15, 1998 this sequence version replaced gi:3223249
qt65d10.x1 NCI_CGAP_ES y979D06.r1 Scares brea cococos s1 NCI_CGAP_GC CIT-HSP-2343N3.TR CIT-HSP-2343N3.TR CIT-Hy-b-06-0-UI.s yuloa02.s1 Scares feta ym19911.s1 Scares feta ym19911.s1 Scares_feta record for s1 scares_feta record 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ys93d07.rl Soares neti
yf48e06.rl Soares infa
yf48e06.rl Soares infa
UI-R-C1.ky-b-06-0-U1.s
zx37c05.rl Soares tota
yp59c12.rl Soares feta
RPC1-11.168rl9.rl RPC1
mn88q08.rl Stratagene
ud80a02.rl Scratagene
ud80a02.rl Stratagene
ud80a02.rl Stratagene
mr92a07.rl Stratagene
F.rubripes GSS sequenc
F.rubripes GSS sequenc
F.rubripes GSS sequenc
F.rubripes GSS sequenc
F.rubripes GSS sequenc
F.rubripes GSS sequenc
G1896.rl Stratagene
F.rubripes GSS sequenc
F.rubripes GSS sequenc
G71611.xl Soares_feta
q971611.xl Soares_feta
ws36b06.rl Stratagene
q93la12.xl Soares_feta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ww-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 bp mRNA
NCI_CGAP_Kid11 Homo
SW:SRM_MOUSE Q62270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AÃO80464
AAZ24533
AAZ24533
AAZ24071
AA822071
AAB22071
AAAC73075
FROO17364
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
AAC150506
                                                                                                                                                                                                                                                                                                                                                                         AQ185427
AA616543
AA34576
T54433
AA159821
AA39011
H86410
R12164
H09004
AA479875
H40255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI373274
94153140
AI373274.1 GI:4153140
```

```
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ო
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                // Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Corgan: Kidney: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site=1: Not I; Site=2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (CloneIDs 1323376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Organism="Homo sapiens"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W17139
249 bp mRNA
zbl2c04.r1 Scares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:301830 5' similar to gb:M64347 FIBROBLAST GROWTH FACTOR
RECEPTOR 3 PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 249)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L....Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
On Nov 29, 1993 this sequence version replaced gi:634607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 26; Le
Pred. No. 1.67e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                     /db_xref="texon:9606"
/clone="IMAGE:2030149"
/clone=lib="NGI_CGAP_Kidll"
/lab_host="DH108" 72 t
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g1291518
W17139.1 GI:1291518
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 CTACCTGCAGAA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               585 CTACCTGCAGAA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
LOCUS
```

ŏ Dp

```
double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library /db_xref="GDB:3757717"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA035407 196 bp mRNA EST 10-MAY-1997 zk26h10.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471715 5' similar to gb:M16591 TYROSINE-PROTEIN KINASE HCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Imal: estewatson, wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 774
Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 183.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Metazoa; Chordata; Craniata; Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196)

Hiller,L., Clark,W., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
Unpublished (1995)

On Apr 5, 1995 this sequence version replaced gi:760783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 33; Length 249;
Pred. No. 5.49e-09;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                              /clone="INAGE:301830"
/clone_11b="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
48 c 65 g 46 t 44 others

    196
    /organism="Homo sapiens"

                                                                                                                                                                                                                                                          /db_xref="GDB:1246761"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1271 ACGTCTGGTCCTTCGGCGTCCTGCT 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 ACGICIGGICCIINGNNGICCIGCI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g1507064
AA035407.1 GI:1507064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.0%;
Matches 22; Conservative
```

ద ô

```
349 AGCCCAGCCACAGGCCTTCC 368
                                                                                                                                                                                                                                                                                                 802 AGCCCAGCCACAGGCCTTCC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA149096.1 GI:1719549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
                                                                                                                                                             Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.3%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                            122 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                    ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                 ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-3'), double-stranded cDNA was size selected, ligated to bloom R adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento saces and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTRACTORY Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA890391 417 bp mRNA EST 04-JAN-1999 ak13903.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405876 3', mRNA sequence.
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1404564.
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                              Length 196;
/db_xref="taxon:9606.....
/map="70303; 1"
/clone="IMAGE:471715"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                       Query Match
1.3%; Score 20; DB 35; Length 196
Best Local Similarity 100.0%; Pred. No. 1.13e-05;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 401.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
                                                                                                                                                             ų
                                                                                                                                                             44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="12p"
/clone="1MAGE:1405876"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
57 c 53 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                             1264 AAGTCAGACGTCTGGTCCTT 1283
                                                                                                                                                                                                                                                                                                                    117 AAGTCAGACGTCTGGTCCTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93017270
AA890391.1 GI:3017270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA890391
                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .467
/organism="Homo sapiens"
/noted="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA149096 467 bp mRNA EST 19-MAY-1997 2141099.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:504544 5' similar to gb:M16591 TYROSINE-PROTEIN KINASE HCK (HUMAN); , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 748 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (base; Louine, Louine); Hominidae; Homo.
Hiller, Louine, Louine, Louine, Louine, Louine, Louine, Maria, Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Materston, R., Williamson, A., Wohldmann, P., and Wilson, R., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R., Mashur Merck, Est Project
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 12, 1996 this sequence version replaced gi:1407090.
                                                                                                                                                                                                                                          ;
0
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="bH10B (ampicillin resistant)"
96 c 106 g 93 t
                                                                                                                                                                                         Length 417;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_pregnant_uterus_NbHPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                       Score 20; DB 20;
Pred. No. 1.13e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 9; L
Pred. No. 1.13e-05;
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:504544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
140 c 133 g
```

```
Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AGCCCAGCCACAGGCCTTCC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      802 AGCCCAGCCACAGGCCTTCC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 100.0%;
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g1412758
B03480.1 GI:1412758
                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                      Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
               REFERENCE
                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                           FEATURES
                                                         TITLE
                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           පු
                                                                                                                                                                                                                                                                                                                      Use of BAC End Sequences from Library RPCI11 for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from sesarch Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/Ab_xref="GDB:7560575"
/Ab_xref="taxon:9606"
/clone="R-158124"
/clone_lib="RPCI11"
/sex="Male"
                                                                                                               AQ374666 493 bp DNA GSS 05-MAR-1999
RPCIII-158L24.TJ RPCIII Homo sapiens genomic clone R-158L24,
genomic survey sequence.
                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ347709 602 bp DNA GSS 21-JAN-199
RPCII1-137G11.TV RPCI11 Homo sapiens genomic clone R-137G11,
                                                                                                                                                                                                                                                                                            de Jong, P. and
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 41; Length with Pred. No. 1.13e-05;
 Indels
                                                                                                                                                                                                                                                                     1 (bases 1 to 493)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
Venter,J.C.
 ö
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
125 c 111 q 10
                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Other_GSSs: RPCI11-158L24.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .493
 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence. AQ347709
                                          94345689
AQ374666.1 GI:4345689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ347709.1 GI:4172605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 20; Conservative
 Conservative
                           91 AAGTCAGACGTCTGGTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                                                                                                                   Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q4172605
                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
20;
                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
 Matches
                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                          NID
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                    RESULT
                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                           a
                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
```

```
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: bbe@tigr.org
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
For clone availability
Research Genetics (info@tesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                 Venter, J.C.
Use of BAC End Sequences from Library RPCI11 for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165)
Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S.,
Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,
Kupfer, K. and Garner, H.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B03480 165 bp DNA GSS 26-JUN-1996 CSRL-17e11-u CSRL flow sorted Chromosome 11 specific cosmid Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library" /db_xref="GDB:7552378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
1 (bases 1 to 602)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens genomic clone cSRL-17e11, genomic survey sequence. B03480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDermott Center for Human Growth and Development University of Texas Southwestern Medical Center At Dallas 5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1660
Fax: 214-648-1666
Emal: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu Seq primer: TY Class: cosmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 41; Length 602
Pred. No. 1.13e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sequence Sampled Map of Chromosome 11 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .602
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
144 c 137 g 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="R-137611"
/clone_lib="RPCI11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Evans GA, Shane Probst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
```

```
individually tagged normalized libraries constructed from $1.2$ and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-draw which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 341)

Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Makafohi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Makawa,H., Shin,S. and Nakamura,Y.

Fujiwara et al. (1995)
                                                                                                                                                                                                                                                                                                                                                                                         hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
643-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOUYLZ 341 bp mRNA EST 28-AUG-1995
HUM137H10B Clontech human fetal brain polyA+ mRNA (#6535) Homo
Sepiens CDNA clone GEN-137H10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Clontech human fetal brain polyA+ mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On May 18, 1995 this sequence version replaced gi:811044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 22; Length 167;
Pred. No. 1.28e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
31 c 34 g t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10116"
/clone="U1-R-C1-1f-a-11-0-U1"
/clone_lib="U1-R-C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 342 Std Error: 0.00 High quality sequence stop: 276. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="GEN-137H10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tsutomu Fujiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 ACTGGGTCAGTGTTGGGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ACTGGGTCAGTGTTGGGG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:962551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D60912.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g,
                                                                                                                                 /note="vector: SCOS-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hampster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

/db_xref="taxon:9606"
/clone="cSRL-17e1"
/clone="cSRL-17e1"
/clone="ib="cSRL flow sorted Chromosome 11 specific cosmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
University of Lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7461 319 335 8250
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9265
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 319 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 335 8260
Fax: 310 5000
Fax: 310 5000
Fax: 310 5000
Fax: 310 5000
Fax: 310 5000
Fax: 310 5000
Fax: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley"
/strain="Sprague-Dawley"
/note=Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco R1; The UI-R-C1
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-Al and UI-R-E1 libraries: The UI-R-Al library
consisted of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The UI-R-E1 library consisted of a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases) 1 to 167)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALUS9300 167 bp mRNA EST 11-FEB-1999
UI-R-C1-1f-a-11-0-UI.s1 UI-R-C1 Rattus norvegicus CDNA clone
UI-R-C1-1f-a-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="chimeric hamster somatic cell hybrid" 37 c 41 g 28 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jan 14, 1998 this sequence version replaced gi:1797766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 19; DB 37; Length 165; Best Local Similarity 100.0%; Pred. No. 4.14e-04; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
High quality sequence stop: 165.... Location/Qualifiers

    165
/organism="Homo sapiens"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 g
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g3333077
AI059300.1 GI:3333077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 CAAGGCCAACTGGAAGCTG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   639 CAAGGCCAACTGGAAGCTG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
```

g ò Gaps

ö

ø

11

RESULT

Matches

g ò DEFINITION

ACCESSION

ORGANISM

KEYWORDS SOURCE

VERSION

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

```
// Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Grain shear; // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organism= // Organis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA814869 387 bp mRNA EST 13-FEB-1998 oco6608.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1340078 3', mRNA sequence.
AA814869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: est@watson.wustl.edu
Ensert Size: 613
High quality sequence stops: 329
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INAME CONSORTIUM (info@image.llnl.gov) for further information.
Seq primer: M13RP1
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 370)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
Unpublished (1995)
On May 10, 1995 this sequence version replaced gi:806203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 30; Length 370
Pred. No. 1.28e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host-"DH10B (ampicillin resistant)"
107 c 96 g 77 t 1 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:156659"
/clone_lib="Soares breast 2NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 329.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GDB:570370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:2884465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 TCTTCTGGGACAAGATCT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCTGGGACAAGATCT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
                                                                                                        GI:848060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA814869.1
                                R73690
9848060
R73690.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R
                                                                                                                                        EST.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                   ACCESSION
                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                           ΝID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: esophagus; Vector: pCMV-SPORT6; Site_1:
Sall: Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dr. Average insert size 1.1 kb. Life Technologies
catalog dr. 11502-010"
/db_xref="faxon:9606"""
/map="MANIGG3-C4 region; MANIGC3-C4 region"
/clone_lib="NGI_CGAP_ESO2"
                                                                                                                                                                                                                                                                                                                                                                                  A1282729 364 bp mRNA EST 21-DEC-1998 45554L0.x1 NCI_CGAP_ESC2 Homo sapiens CDNA clone IMAGE:1960147 3' similar to SW:MS2_HUMAN P78325 CELL SUFFACE ANTIGEN MS2 PRECURSOR ; contains element TAR1 repetitive element ; mRNA sequence.
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1995
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS R73690 370 bp mRNA EST 05-JUN-
DEFINITION yj97b06.rl Soares breast 2NbHBst Homo sapiens CDNA clone
IMAGE:156659 5', mRNA sequence.
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                   Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 364;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 25; Length 364
Pred. No. 4.14e-04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="squamous cell carcinoma'
/lab_host="DH108"
114 c 123 g 61 t
Score 18; DB 31; Len
Pred. No. 1.28e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00

    364
    /organism="Homo sapiens"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1638 Std Error
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93920962
AI282729.1 GI:3920962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1040 CCTGCCAGGTGAGGG 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 CCTGCCAGGTGGCTGAGGG 108
                                                                                                                                                                 130 CCCGGCCTGGAGGAGCTG 147
                                                                                                                                                                                                                610 CCCGGCCTGGAGGAGCTG 627
                                Query Match 1.2%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2%;
Best Local Similarity 100.0%;
Matches 19; Conservative
                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
```

source

FEATURES

RESULT 12

g ò

BASE COUNT ORIGIN

ö

Gaps

ö

^

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

FEATURES

```
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
Unpublished (1997)
Other_GSSS: CIT-HSP-2343N3.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: madams@tigr.org
Clones are available from Research Genetics (Info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8260
Fax: 319 335 9565
Fax: 319 335 9560
Fax: 41 Fax: 41 Fax: 41 Fax: 42 Fax: 42 Fax: 42 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax: 43 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS A1058611 400 bp mRNA EST 11-FEB-1999
DEFINITION UI-R-C1-ky-b-06-0-UI.sl UI-R-C1 Rattus norvegicus CDNA clone
UI-R-C1-ky-b-06-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jan 14, 1998 this sequence version replaced gi:2043323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Sperm"
118 c 121 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="2343N3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93332388
AI058611.1 GI:3332388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1062 CATGCCTCAGCCACCTG 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 CATGCCCTCAGCCACCTG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI058611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
COMMENT
                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       සු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                    Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 387)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ054911 387 bp DNA GSS 29-JUL-1998 CIT-HSP-2343N3.TR CIT-HSP Homo sapiens genomic clone 2343N3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%; Score 18; DB 18; Length 387
Best Local Similarity 100.0%; Pred. No. 1.28e-02;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1340078"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
112 c 93 g 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 327.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnī.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93351517
AQ054911.1 GI:3351517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 CICCCCAAGIAGCCIIC 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 CICCCCAAAGIAGCCTIC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
```

RESULT 14 DEFINITION

Сp

ACCESSION

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

VERSION

BASE COUNT

ORIGIN

ö

Gaps

```
source
```

```
Notes "Vergue Dawles"

Notes "Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_2: Eco RI; The UI-R-CI library is a subtracted library derived from the UI-R-CI library which is a subtracted library derived from the UI-R-CI library, which is a subtracted library derived from the UI-R-CI library do II library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligorial rate which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which ESTS had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

    .400
    /organism="Rattus norvegicus"
    /strain="Sprague-Dawley"
```

/db_xref="taxon:10116" /map="933H10: 3; 3q12.1-3q13.32; 17q21" /clone="UI-R-C1-ky-b-06-0-UI" /clone_lib="UI-R-C1" /dev_stage="Adult"

/lab_host="DH10B (Life Technologies)" 89 c 94 q 112 + 105

BASE COUNT ORIGIN

ó Score 19; DB 22; Length 400; Pred. No. 4.14e-04; 0; Mismatches 0; Indels Query Match 1.2%; Best Local Similarity 100.0%; Matches 19; Conservative

ó

Gaps

186 TGACTTGATGACCTTGATC 204

g $^{\rm Cp}$

834 TGACTTGATGACCTTGATC 816

Search completed: Thu May 20 19:34:29 1999 Job time: 3418 secs.